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(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypep-
tides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

DESCRIPTION

PROTEIN KINASES

FIELD OF THE INVENTION

5 The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

BACKGROUND OF THE INVENTION

10 The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be or to describe prior art to the invention.

 Cellular signal transduction is a fundamental mechanism whereby external stimuli that regulate diverse cellular processes are relayed to the interior of cells. One of the key
15 biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins, which enables regulation of the activity of mature proteins by altering their structure and function.

 Protein phosphorylation plays a pivotal role in biological signal transduction. Among the biological functions controlled by protein phosphorylation are the following:
20 cell division; differentiation and death (apoptosis); cell motility and cytoskeletal structure; control of DNA replication, transcription, splicing and translation; protein translocation events from the endoplasmic reticulum and Golgi apparatus to the membrane and extracellular space; protein nuclear import and export; regulation of metabolic reactions, etc. Abnormal protein phosphorylation is widely recognized to be causally linked to the
25 etiology of many diseases including cancer as well as immunologic, neuronal and metabolic disorders.

 The most common phospho-acceptor amino acid residues are serine, threonine and tyrosine. Phosphorylation in histidine has also been observed in bacteria. The presence of a phosphate moiety modulates protein function in multiple ways. A common mechanism
30 includes changes in the catalytic properties (V_{\max} and K_m) of an enzyme leading to its activation or inactivation. A second widely recognized mechanism involves promoting protein-protein interactions. An example of this is the tyrosine autophosphorylation of the

ligand-activated EGF receptor tyrosine kinase. This event triggers the high-affinity binding to the phosphotyrosine residue on the receptor's C-terminal intracellular domain to the SH2 motif of the adaptor molecule Grb2. Grb2 in turn binds through its SH3 motif to a second adaptor molecule, such as SHC. The formation of this ternary complex
5 activates the signaling events that are responsible for the biological effects of EGF. Serine and threonine phosphorylation events have also been recently recognized to exert their biological function through protein-protein interaction events mediated by the high-affinity binding of phosphoserine and phosphothreonine to WW motifs present in a large variety of proteins (Lu, P.J. *et al.* (1999) *Science* 283:1325-1328). A third important
10 outcome of protein phosphorylation is changes in the subcellular localization of the substrate. As an example, nuclear import and export events in a large diversity of proteins are regulated by protein phosphorylation (Drier E.A. *et al.* (1999) *Genes Dev* 13: 556-568).

Protein kinases are one of the largest families of eukaryotic proteins with several
15 hundred known members. These proteins share a 250-300 amino acid domain that can be subdivided into 12 distinct subdomains that comprise the common catalytic core structure. These conserved protein motifs have recently been exploited using PCR-based and bioinformatic strategies leading to a significant expansion of the known kinases. Multiple
20 alignment of the sequences in the catalytic domain of protein kinases and subsequent parsimony analysis permits their segregation into a dendrogram reflecting the relatedness of their catalytic domains (Fig. 1). In this manner, related kinases are clustered into distinct branches or subfamilies including: tyrosine kinases, cyclic-nucleotide-dependent kinases, calcium/calmodulin kinases, cyclin-dependent kinases and MAP-kinases, serine-threonine kinase receptors, and several other less defined subfamilies.

25 We have recently completed a systematic analysis of the protein kinases present in *C. elegans*, the multicellular organism whose entire DNA sequence has been determined. We identified 473 unique kinase profiles including 398 full-length conventional kinases, and 20 additional proteins that may function as atypical protein kinases. (Plowman G.D. *et al.* (1999), *Proc. Natl. Acad. Sci.* 96:13603-13610).

30 Using parsimony analysis, the protein kinases may be divided into 4 major groups: AGC, CAMK, CMGC and tyrosine kinases. In addition, there are a number of minor yet distinct families, including the STE and casein kinase 1, families related to worm- or

fungus-specific kinases, and a family designated "other" to represent several smaller families. In addition, we designate an "atypical" family to represent protein kinases whose catalytic domain has little or no primary sequence homology to conventional kinases, including the A6 kinases and PI3 kinases.

5 The AGC kinases are basic amino acid-directed enzymes that phosphorylate residues found proximal to Arg and Lys. Examples of this group are the cyclic nucleotide-dependent kinases, G protein kinases, NDR or DBF2 and the ribosomal S6 kinases.

 The CAMK group kinases are also basic amino acid-directed kinases. They include the Ca²⁺/calmodulin-regulated and AMP-dependent protein kinases, myosin light chain
10 kinases, checkpoint 2 kinases (CHK2) and EMK-related protein kinases. The EMK family of STK are involved in the control of cell polarity, microtubule stability and cancer. One member of the EMK family, C-TAK1 has been reported to control entry into mitosis by activating Cdc25C which in turn dephosphorylates Cdc2.

 CMGC group kinases are "proline-directed" enzymes phosphorylating residues
15 that exist in a proline-rich context. They include the cyclin-dependent kinases (CDKs), mitogen-activated kinases (MAPKs), GSK3s and CLKs. Most CMGC kinases have larger-than-average kinase domains owing to the presence of insertions within subdomains X and XI.

 The tyrosine kinase group encompass both cytoplasmic (i.e. src) as well as
20 transmembrane receptor tyrosine kinases (i.e. EGF receptor). These kinases play a pivotal role in the signal transduction processes that mediate cell proliferation, differentiation and apoptosis.

 Group members that define smaller, yet distinct phylogenetic branches of conventional kinases include the elongation factor 2 kinases (EIFKs); homologues of the
25 yeast sterile family kinases (STE) which refers to 3 classes of kinases which lie sequentially upstream of the MAPKs; mixed lineage kinases (MLKs); Lim-domain containing kinases (LIMKs); Calcium-calmodulin kinase kinases (CAMKK), dual-specific tyrosine kinases (DYRK), integrin receptor associated kinase (IRAK); testis-specific kinases (TSK); UNC-51 related kinases (UNC); several families that are close
30 homologues to worm (C26C2.1, YQ09, ZC581.9, YFL033c, C24A1.3), Drosophila (SLOB), or yeast (YDOD_sp, YGR262_sc) kinases, and others that are "unique" and don't cluster into any obvious family.

SUMMARY OF THE INVENTION

Through a search of the EST database for homologies to the conserved catalytic kinase domain of protein kinases, hundreds of mammalian members of known and previously unidentified protein kinase families and groups have been identified as part of the present invention. Multiple alignment and parsimony analysis of the catalytic domain reveals that approximately half of these protein kinases cluster into 10 known groups, with the other half perhaps defining novel groups. Classification in this manner has proven highly accurate not only in predicting motifs present in the remaining non-catalytic portion of each protein, but also in their regulation, substrates, and signaling pathways. The present invention includes the partial or complete sequence of new protein kinases, their classification, predicted or deduced protein structure, and a strategy for elucidating their biologic and therapeutic relevance.

Thus, a first aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,

SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
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SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
5 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242.

By "isolated" in reference to nucleic acid is meant a polymer of nucleotides
conjugated to each other, including DNA and RNA, that is isolated from a natural source
10 or that is synthesized. The isolated nucleic acid of the present invention is unique in the
sense that it is not found in a pure or separated state in nature. Use of the term "isolated"
indicates that a naturally occurring sequence has been removed from its normal cellular
(i.e., chromosomal) environment. Thus, the sequence may be in a cell-free solution or
placed in a different cellular environment. The term does not imply that the sequence is
15 the only nucleotide chain present, but that it is essentially free (about 90 - 95% pure at
least) of non-nucleotide material naturally associated with it, and thus is distinguished
from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the
specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of
20 the total DNA or RNA present in the cells or solution of interest than in normal or
diseased cells or in the cells from which the sequence was taken. This could be caused by
a person by preferential reduction in the amount of other DNA or RNA present, or by a
preferential increase in the amount of the specific DNA or RNA sequence, or by a
combination of the two. However, it should be noted that enriched does not imply that
25 there are no other DNA or RNA sequences present, just that the relative amount of the
sequence of interest has been significantly increased. The term "significant" is used to
indicate that the level of increase is useful to the person making such an increase, and
generally means an increase relative to other nucleic acids of about at least 2 fold, more
preferably at least 5 to 10 fold or even more. The term also does not imply that there is no
30 DNA or RNA from other sources. The other source DNA may, for example, comprise
DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term
distinguishes from naturally occurring events, such as viral infection, or tumor type

growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately 10^6 -fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

By a "kinase polypeptide" is meant 10 (preferably 20, more preferably 40, most preferably 75) or more contiguous amino acids set forth in an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,

SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
5 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
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SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
10 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
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SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional
15 derivatives thereof as described herein. For sequences for which the full-length sequence
is not given, the remaining sequences can be determined using methods well-known to
those in the art and are intended to be included in the invention. In certain aspects,
polypeptides of 100, 200, 300 or more amino acids are preferred. The kinase polypeptide
can be encoded by a full-length nucleic acid sequence or any portion of the full-length
20 nucleic acid sequence, so long as a functional activity of the polypeptide is retained. By
“functional” domain is meant any region of the polypeptide that may play a regulatory or
catalytic role as predicted from amino acid sequence homology to other proteins or by the
presence of amino acid sequences that may give rise to specific structural conformations
(*i.e.*, coiled-coils). For some purposes, polypeptide domains are preferred, including, but
25 not limited to, N-terminal, catalytic/kinase and C-terminal.

The amino acid sequence will be substantially similar to a sequence selected from
the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID
NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID
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NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding
20 full-length amino acid sequence, or fragments thereof. A sequence that is substantially
similar to a sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
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ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 or portions of or the entire corresponding full-length amino acid sequences.

By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues between two sequences (either full-length or a defined domain) by the total number of residues in the known sequence, or the domain of the known sequence, and multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have replacements and substitutions, have a lower degree of identity. "Gaps" are spaces in an alignment that can result from aligning a novel sequence with a known sequence when the novel sequence has additions or deletions of amino acids in comparison with the known sequence. These gaps do not factor into the assessment of % identity using the above calculation.

Those skilled in the art will recognize that several computer programs are also available for determining sequence identity using standard parameters, for example, Blast (Altschul, *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402), Blast2 (Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410), and Smith-Waterman (Smith, *et al.* (1981) *J. Mol. Biol.* 147:195-197).

In preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding a kinase polypeptide comprising a nucleotide sequence that: (a) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID

NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
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NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID
10 NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID
NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID
NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID
NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID
NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will
15 have at least 75% identity (preferably 90%, more preferably at least 95% and most
preferably 99-100%) to the sequence selected from the group consisting of those set forth
in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID
20 NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID
NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID
NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID
25 NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID
NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID
NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID
NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID
NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID
30 NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID

NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (e) is the complement of the nucleotide sequence of (d); (f) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID

NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID
NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID
5 NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID
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NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID
NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID
NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID
10 NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID
NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID
NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID
15 NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
20 NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID
NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or
fragments thereof. (The domain demarcations of the polypeptides of the invention are
indicated in Table 2 by reference to the kinase domain.) A sequence that is substantially
25 similar to a sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
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NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ

ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID

NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,

SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (g) is the complement of the nucleotide sequence of (f); (h) encodes a polypeptide having an amino acid sequence selected from the group consisting

of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,

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5 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
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10 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
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15 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
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SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
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NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
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NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID

NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,

SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more of the domains selected from the group consisting of a N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (i) is the

complement of the nucleotide sequence of (h). The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.

The term "complement" refers to two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if all of the nucleotides of the first sequence are complementary to all of the nucleotides of the second sequence.

The term "domain" refers to a region of a polypeptide that contains a particular function. For instance, N-terminal or C-terminal domains of signal transduction proteins can serve functions including, but not limited to, binding molecules that localize the signal transduction molecule to different regions of the cell or binding other signaling molecules directly responsible for propagating a particular cellular signal. Some domains can be expressed separately from the rest of the protein and function by themselves, while others must remain part of the intact protein to retain function. The latter are termed functional regions of proteins and also relate to domains.

The term "N-terminal domain" refers to the extracatalytic region located between the initiator methionine and the catalytic domain of the protein kinase. The N-terminal domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the N-terminal boundary of the catalytic domain. Depending on its length, the N-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose N-terminal domain has been shown to play a regulatory role is PAK65, which contains a CRIB motif used for Cdc42 and rac binding (Burbelo, P.D. *et al.* (1995) *J. Biol. Chem.* 270, 29071-29074). The N-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the amino-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. Further, in some cases, portions of the N-terminal domains of the protein kinases of the invention have not been identified since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined and using the approaches described herein the N-terminal domain can be identified.

The term "catalytic domain" or "kinase domain" refers to a region of the protein kinase that is typically 25-300 amino acids long and is responsible for carrying out the phosphate transfer reaction from a high-energy phosphate donor molecule such as ATP or GTP to itself (autophosphorylation) or to other proteins (exogenous phosphorylation).

5 The catalytic domain of protein kinases is made up of 12 subdomains that contain highly conserved amino acid residues, and are responsible for proper polypeptide folding and for catalysis. The catalytic domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database. The catalytic/kinase domains of the protein kinases of the invention are identified in Table 2, herein. Further,
10 in some cases, the complete sequence of the catalytic/kinase domains of the protein kinases of the invention may not have been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the catalytic/kinase domain can be identified.

15 The term "catalytic activity", as used herein, defines the rate at which a kinase catalytic domain phosphorylates a substrate. Catalytic activity can be measured, for example, by determining the amount of a substrate converted to a phosphorylated product as a function of time. Catalytic activity can be measured by methods of the invention by holding time constant and determining the concentration of a phosphorylated substrate
20 after a fixed period of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

The term "substrate" as used herein refers to a molecule phosphorylated by a kinase of the invention. Kinases phosphorylate substrates on serine/threonine or tyrosine
25 amino acids. The molecule may be another protein or a polypeptide.

The term "C-terminal domain" refers to the region located between the catalytic domain and the carboxy-terminal amino acid residue of the protein kinase. The C-terminal domain can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C-terminal boundary of
30 the catalytic domain or of any functional C-terminal extracatalytic domain. Depending on its length and amino acid composition, the C-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose C-terminal

domain may play a regulatory role is PAK3 which contains a heterotrimeric G_b subunit-binding site near its C-terminus (Leeuw, T. *et al.* (1998) *Nature*, 391, 191-195). The C-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the carboxy-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. In some cases, the C-terminal domains of the protein kinases of the invention have not been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the C-terminal domain can be identified.

The term "signal transduction pathway" refers to the molecules that propagate an extracellular signal through the cell membrane to become an intracellular signal. This signal can then stimulate a cellular response. The polypeptide molecules involved in signal transduction processes are typically receptor and non-receptor protein tyrosine kinases, receptor and non-receptor protein phosphatases, SRC homology 2 and 3 domains, phosphotyrosine binding proteins (SRC homology 2 (SH2) and phosphotyrosine binding (PTB and PH) domain containing proteins), proline-rich binding proteins (SH3 domain containing proteins), nucleotide exchange factors, and transcription factors.

The term "coiled-coil structure region" as used herein, refers to a polypeptide sequence that has a high probability of adopting a coiled-coil structure as predicted by computer algorithms such as COILS (Lupas, A. (1996) *Meth. Enzymology* 266:513-525). Coiled-coils are formed by two or three amphipathic α -helices in parallel. Coiled-coils can bind to coiled-coil domains of other polypeptides resulting in homo- or heterodimers (Lupas, A. (1991) *Science* 252:1162-1164). Coiled-coil-dependent oligomerization has been shown to be necessary for protein function including catalytic activity of serine/threonine kinases (Roe, J. *et al.* (1997) *J. Biol. Chem.* 272:5838-5845). Coiled-coil regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "proline-rich region" as used herein, refers to a region of a protein kinase whose proline content over a given amino acid length is higher than the average content of this amino acid found in proteins (*i.e.*, >10%). Proline-rich regions are easily discernable by visual inspection of amino acid sequences and quantitated by standard computer

sequence analysis programs such as the DNASTar program EditSeq. Proline-rich regions have been demonstrated to participate in regulatory protein-protein interactions. Among these interactions, those that are most relevant to this invention involve the "PxxP" proline rich motif found in certain protein kinases (*i.e.*, human PAK1) and the SH3 domain of the adaptor molecule Nck (Galisteo, M.L. *et al.* (1996) J. Biol. Chem. 271:20997-21000).

Other regulatory interactions involving "PxxP" proline-rich motifs include the WW domain (Sudol, M. (1996) Prog. Biophys. Mol. Bio. 65:113-132). Proline rich regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "spacer region" as used herein, refers to a region of the protein kinase located between predicted functional domains. The spacer region has no detectable homology to any amino acid sequence in the database, and can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C- and N-terminal boundaries of the flanking functional domains. Spacer regions may or may not play a fundamental role in protein kinase function. Precedence for the regulatory role of spacer regions in kinase function is provided by the role of the src kinase spacer in inter-domain interactions (Xu, W. *et al.* (1997) Nature 385:595-602). Spacer regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "insert" as used herein refers to a portion of a protein kinase that is absent from a close homolog. Inserts may or may not be the product alternative splicing of exons. Inserts can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Inserts may play a functional role by presenting a new interface for protein-protein interactions, or by interfering with such interactions. Insert regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "C-terminal tail" as used herein, refers to a C-terminal domain of a protein kinase, that by homology extends or protrudes past the C-terminal amino acid of its closest homolog. C-terminal tails can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Depending on its length, a C-terminal tail may or may not play a regulatory role in kinase function. C-terminal tail regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides, more preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 50 contiguous nucleotides, most preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 100 contiguous nucleotides. In some instances, the conditions may prevent hybridization of nucleic acids having more than 5 mismatches in the full-length sequence.

By stringent hybridization assay conditions is meant hybridization assay conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM NaH_2PO_4 , pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart solution at 42 °C overnight; washing with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C. Under some of the most stringent hybridization assay conditions, the second wash can be done with 0.1X SSC at a temperature up to 70 °C (pg. 421, Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein including any figures, tables, or drawings.). However, other applications may require the use of conditions falling between these sets of conditions. Methods of determining the conditions required to achieve desired hybridizations are well-known to those with ordinary skill in the art, and are based on several factors, including but not limited to, the sequences to be hybridized and the samples to be tested.

In other preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding kinase polypeptides, further comprising a vector or promoter effective to initiate transcription in a host cell. The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding a kinase polypeptide and a transcriptional termination region functional in a cell. Specific

vectors and host cell combinations are discussed herein. The recombinant nucleic acid can also contain the full-length sequence encoding the protein kinase, or a domain, for example.

The term "vector" relates to a single or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding a kinase can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

The term "transfecting" defines a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field, detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

The term "promoter" as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different organisms. For example, in prokaryotes, the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35,

SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, encodes an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID

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NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
10 NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242, or the corresponding full-length amino acid sequence, a functional derivative
thereof, or at least 10, 20, 40, 50, 75, 100, 200, 300 or 500 contiguous amino acids of a
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
15 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
20 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
25 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID
30 NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID

NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length sequences or derivatives thereof. The nucleic acid may be isolated from a natural source by cDNA cloning or by subtractive hybridization. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the nucleic acid may be synthesized by the triester method or by using an automated DNA synthesizer.

The term "mammal" refers preferably to such organisms as mice, rats, rabbits, guinea pigs, sheep, and goats, more preferably to cats, dogs, monkeys, and apes, and most preferably to humans.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a kinase polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acid encoding kinase polypeptides are provided in Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides, even more preferably 2 out of 20 nucleotides or most preferably 1 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a kinase polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 10 (preferably 25, more preferably 50, most preferably 75) or more contiguous amino acids selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,

SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
5 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
10 SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
15 SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
20 SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof.

25 In particular, a unique nucleic acid region is preferably of mammalian origin and preferably human.

A second aspect of the invention features a nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
30 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,

SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
5 SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
10 SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
15 SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
20 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the nucleic acid
probe encodes a kinase polypeptide that is a fragment of the protein encoded by an amino
acid sequence selected from the group consisting of those set forth in SEQ ID NO:122,
SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
25 SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132,
SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137,
SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,
SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147,
SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152,
30 SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157,
SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162,
SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167,

SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177,
SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,
SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,
5 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
10 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
15 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242, or the corresponding full-length amino acid sequences. The nucleic acid probe
contains a nucleotide base sequence that will hybridize to a sequence selected from the
group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ
ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9,
20 SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ
ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID
NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25,
SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID
25 NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41,
SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ
ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID
NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57,
SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ
30 ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID
NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73,
SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ

ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, or a functional derivative thereof.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID

NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or functional derivatives thereof.

Methods for using the probes include detecting the presence or amount of kinase RNA in a sample by contacting the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to kinase RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for a kinase polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson *et al.*, in *Nonisotopic DNA Probe Techniques*, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

In a third aspect, the invention describes a recombinant cell or tissue comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,

SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
5 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
10 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242. In such cells, the nucleic acid may be under the control of the
genomic regulatory elements, or may be under the control of exogenous regulatory
elements including an exogenous promoter. By "exogenous" it is meant a promoter that is
15 not normally coupled *in vivo* transcriptionally to the coding sequence for the kinase
polypeptides.

The polypeptide is preferably a fragment of the protein encoded by an amino acid
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
20 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
25 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
30 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID

NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID
NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
5 NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID
NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID
NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID
NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID
NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID
10 NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the
corresponding full-length amino acid sequence. By "fragment," is meant an amino acid
sequence present in a kinase polypeptide. Preferably, such a sequence comprises at least
10, 20, 40, 50, 75, 100, 200, or 300 contiguous amino acids a sequence selected from the
group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
15 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
20 SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
25 SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
30 SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,

SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
5 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or of the corresponding full-
length amino acid sequence, or a functional derivative thereof.

In a fourth aspect, the invention features an isolated, enriched, or purified kinase
polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ
10 ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ
ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ
ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ
ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ
ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ
15 ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ
ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ
ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ
20 ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ
25 ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ
ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ
30 ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ
ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ

ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to a polypeptide is meant a polymer of amino acids (2 or more amino acids) conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of non-amino acid material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level

this level should be at least 2-5 fold greater (*e.g.*, in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

5 In preferred embodiments, the kinase polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,
10 SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,
15 SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
20 SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
25 SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
30 SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. Preferably, the kinase polypeptide contains at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous

amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof.

In preferred embodiments, the kinase polypeptide comprises an amino acid sequence having (a) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ

ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ

ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (c) an amino acid sequence of a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
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SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242 where the domain is selected from the group consisting of an N-terminal domain,
a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich
region, a spacer region, an insert, and a C-terminal tail; or (d) an amino acid sequence
15 selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
20 SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,
SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
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SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
25 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
30 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, an insert, and a C-terminal tail. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.)

The polypeptide can be isolated from a natural source by methods well-known in the art. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the polypeptide may be synthesized using an automated polypeptide synthesizer. The isolated, enriched, or purified kinase polypeptide is preferably selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ

ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242A.

In some embodiments the invention includes a recombinant kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,

SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. By “recombinant kinase polypeptide” is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (*e.g.*, present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a fifth aspect, the invention features an antibody (*e.g.*, a monoclonal or polyclonal antibody) having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain or fragment where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ

ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In preferred embodiments, the antibody binds specifically to domains of kinase polypeptides, that are defined *supra*.

By “specific binding affinity” is meant that the antibody binds to the target kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody fragments are polypeptides that contain regions that can bind other polypeptides. The term “specific binding affinity” describes an antibody that binds to a kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions.

The term “polyclonal” refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

“Monoclonal antibodies” are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art (Kohler *et al.*, Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term “antibody fragment” refers to a portion of an antibody, often the hyper variable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hyper variable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a kinase polypeptide or domains of a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by probing the sample with the antibody under conditions suitable for kinase-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the

kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the kinase as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

An antibody or antibody fragment with specific binding affinity to a kinase polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

Antibodies having specific binding affinity to a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

In a sixth aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain, where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID

NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; and where the domains are defined as above. By “hybridoma” is meant an immortalized cell line that is capable of secreting an antibody, for example an antibody to a kinase of the invention. In preferred embodiments, the antibody to the kinase comprises a sequence of amino acids that is able to specifically bind a kinase polypeptide of the invention.

In a seventh aspect, the invention features a kinase polypeptide binding agent able to bind to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242. The binding agent is preferably a purified antibody that recognizes an epitope
present on a kinase polypeptide of the invention. Other binding agents include molecules
that bind to kinase polypeptides and analogous molecules that bind to a kinase
15 polypeptide. Such binding agents may be identified by using assays that measure kinase
binding partner activity, such as those that measure PDGFR activity.

The invention also features a method for screening for human cells containing a
kinase polypeptide of the invention or an equivalent sequence. The method involves
identifying the novel polypeptide in human cells using techniques that are routine and
20 standard in the art, such as those described herein for identifying the kinases of the
invention (*e.g.*, cloning, Southern or Northern blot analysis, in situ hybridization, PCR
amplification, etc.).

In an eighth aspect, the invention features methods for identifying a substance that
modulates kinase activity comprising the steps of: (a) contacting a kinase polypeptide
25 selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
30 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,

SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
5 SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
10 SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
15 SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance; (b)
measuring the activity of said polypeptide; and (c) determining whether said substance
modulates the activity of said polypeptide.

20 The term “modulates” refers to the ability of a compound to alter the function of a
kinase of the invention. A modulator preferably activates or inhibits the activity of a
kinase of the invention.

The term “activates” refers to increasing the cellular activity of the kinase. The
term inhibit refers to decreasing the cellular activity of the kinase. Kinase activity is
25 preferably the interaction with a natural binding partner.

The term “modulates” also refers to altering the function of kinases of the
invention by increasing or decreasing the probability that a complex forms between the
kinase and a natural binding partner. A modulator preferably increases the probability that
such a complex forms between the kinase and the natural binding partner, more preferably
30 increases or decreases the probability that a complex forms between the kinase and the
natural binding partner depending on the concentration of the compound exposed to the

kinase, and most preferably decreases the probability that a complex forms between the kinase and the natural binding partner.

The term “complex” refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules
5 bound to one another. For instance, a protein tyrosine receptor protein kinase, GRB2, SOS, RAF, and RAS assemble to form a signal transduction complex in response to a mitogenic ligand.

The term “natural binding partner” refers to polypeptides, lipids, small molecules, or nucleic acids that bind to kinases in cells. A change in the interaction between a kinase
10 and a natural binding partner can manifest itself as an increased or decreased probability that the interaction forms, or an increased or decreased concentration of kinase/natural binding partner complex.

The term “contacting” as used herein refers to mixing a solution comprising the test compound with a liquid medium bathing the cells of the methods. The solution
15 comprising the compound may also comprise another component, such as dimethyl sulfoxide (DMSO), which facilitates the uptake of the test compound or compounds into the cells of the methods. The solution comprising the test compound may be added to the medium bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

In a ninth aspect, the invention features methods for identifying a substance that modulates kinase activity in a cell comprising the steps of: (a) expressing a kinase
20 polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,
25 SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,
30 SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,

SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
5 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
10 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
15 and SEQ ID NO:242; (b) adding a test substance to said cell; and (c) monitoring a change
in cell phenotype or the interaction between said polypeptide and a natural binding
partner.

The term “expressing” as used herein refers to the production of kinases of the
invention from a nucleic acid vector containing kinase genes within a cell. The nucleic
20 acid vector is transfected into cells using well known techniques in the art as described
herein.

In a tenth aspect, the invention provides methods for treating a disease or abnormal
condition by administering to a patient in need of such treatment a substance that
modulates the activity of a polypeptide selected from the group consisting of SEQ ID
25 NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
30 NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID

NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the disease is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer. Also included are metabolic disorders, such as diabetes mellitus, and reproductive disorders, such as infertility.

Preferably, the disease or disorder is selected from the group consisting of rheumatoid arthritis, arteriosclerosis, autoimmune disorders, and organ transplantation. Preferably the disease or disorder is selected from the group consisting of immune-related diseases and disorders, myocardial infarction, cardiomyopathies, stroke, renal failure, and oxidative stress-related neurodegenerative disorders. Most preferably, the immune-related diseases and disorders are selected from the group consisting of rheumatoid arthritis, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, arteriosclerosis, rhinitis, autoimmunity, and organ transplantation.

Substances useful for treatment of disorders or diseases preferably show positive results in one or more in vitro assays for an activity corresponding to treatment of the disease or disorder in question. Substances that modulate the activity of the polypeptides

preferably include, but are not limited to, antisense oligonucleotides and inhibitors of protein kinases.

The term “preventing” refers to decreasing the probability that an organism contracts or develops an abnormal condition.

5 The term “treating” refers to having a therapeutic effect and at least partially alleviating or abrogating an abnormal condition in the organism.

10 The term “therapeutic effect” refers to the inhibition or activation factors causing or contributing to the abnormal condition. A therapeutic effect relieves to some extent one or more of the symptoms of the abnormal condition. In reference to the treatment of abnormal conditions, a therapeutic effect can refer to one or more of the following: (a) an increase in the proliferation, growth, and/or differentiation of cells; (b) inhibition (*i.e.*, slowing or stopping) of cell death; (c) inhibition of degeneration; (d) relieving to some extent one or more of the symptoms associated with the abnormal condition; and (e) enhancing the function of the affected population of cells. Compounds demonstrating efficacy against abnormal conditions can be identified as described herein.

15 The term “abnormal condition” refers to a function in the cells or tissues of an organism that deviates from their normal functions in that organism. An abnormal condition can relate to cell proliferation, cell differentiation or cell survival. An abnormal condition may also include irregularities in cell cycle progression, *i.e.*, irregularities in normal cell cycle progression through mitosis and meiosis.

20 Abnormal cell proliferative conditions include cancers such as fibrotic and mesangial disorders, abnormal angiogenesis and vasculogenesis, wound healing, psoriasis, diabetes mellitus, and inflammation.

25 Abnormal differentiation conditions include, but are not limited to neurodegenerative disorders, slow wound healing rates, and slow tissue grafting healing rates.

30 Abnormal cell survival conditions relate to conditions in which programmed cell death (apoptosis) pathways are activated or abrogated. A number of protein kinases are associated with the apoptosis pathways. Aberrations in the function of any one of the protein kinases could lead to cell immortality or premature cell death.

The term "aberration", in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term "administering" relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

5 ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ
ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ
ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ
10 ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ
ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ
15 ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ
ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ
ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe
comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the
complements of the sequences and fragments; and (b) detecting the presence or amount of
20 the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from
the group consisting of rheumatoid arthritis, atherosclerosis, autoimmune disorders, organ
transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative
stress-related neurodegenerative disorders, metabolic disorder including diabetes,
25 reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group
consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID
NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ
ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID
30 NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20,
SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ
ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof. Hybridization conditions should be such that hybridization occurs only with the kinase genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

Hybridization conditions should be such that hybridization occurs only with the genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

The diseases for which detection of kinase genes in a sample could be diagnostic include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in comparison to normal cells. By "amplification" is meant increased numbers of kinase

DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

“Amplification” as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon

& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

5 Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul
10 and Vougioukas, U.S. Patent No. 5,316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris
15 *et al.* J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.* J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*,
20 Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); and Sikora *et al.*, Analytical Biochem. 172:344-355 (1988), all of which are incorporated
25 herein by reference in their entirety, including any drawings.

 Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

 Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432
30 (1993); and Burke *et al.* BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., " J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

The term "aberration", in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term "administering" relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the complements of the sequences and fragments; and (b) detecting the presence or amount of the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from the group consisting of rheumatoid arthritis, arteriosclerosis, autoimmune disorders, organ transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative stress-related neurodegenerative disorders, metabolic disorder including diabetes, reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof. Hybridization conditions should be such that hybridization occurs only with the kinase genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

Hybridization conditions should be such that hybridization occurs only with the genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

The diseases for which detection of kinase genes in a sample could be diagnostic include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in comparison to normal cells. By "amplification" is meant increased numbers of kinase

DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

"Amplification" as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon

& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

5 Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722
10 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris
15 *et al.* J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.* J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*,
20 Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); and Sikora *et al.*, Analytical Biochem. 172:344-355 (1988), all of which are incorporated
25 herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432
30 (1993); and Burke *et al.* BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental
5 Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., "J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992);
10 Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol.
15 Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996,
20 incorporated herein by reference in its entirety, including any drawings.

Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number
25 WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being
30 treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

formulated in animal models to achieve a circulating concentration range that initially takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors and major organs can also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows:

1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, Journal of American Veterinary Medical Assoc., 202:229-249, 1993).

Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness or toxicity. Gross abnormalities in tissue are noted and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

In a final aspect, the invention features a method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein the method comprises: (a) comparing a nucleic acid target region encoding the kinase polypeptide in
10 a sample, where the kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
15 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
20 NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
25 NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
30 NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID

NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding the kinase polypeptide, or one or more fragments thereof; and (b) detecting
5 differences in sequence or amount between the target region and the control target region, as an indication of the disease or disorder. Preferably, the disease or disorder is selected from the group consisting of immune-related diseases and disorders, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders, and cancer. Immune-related diseases and disorders include,
10 but are not limited to, those discussed previously.

The term "comparing" as used herein refers to identifying discrepancies between the nucleic acid target region isolated from a sample, and the control nucleic acid target region. The discrepancies can be in the nucleotide sequences, *e.g.* insertions, deletions, or point mutations, or in the amount of a given nucleotide sequence. Methods to determine
15 these discrepancies in sequences are well-known to one of ordinary skill in the art. The "control" nucleic acid target region refers to the sequence or amount of the sequence found in normal cells, *e.g.* cells that are not diseased as discussed previously.

The term also includes anti-sense molecules drawn thereto.

The invention has been described broadly and generically herein. Each of the
20 narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. For example, in some instances the nucleotide sequence of particular kinase polypeptides may not be part of a preferred
25 embodiment.

The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

BRIEF DESCRIPTION OF THE FIGURES

Figures 1A to 1BB shows the amino acid sequences of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

Figures 2A to 2MMMM shows the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID

NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34,
SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ
ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID
NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50,
5 SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ
ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID
NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66,
SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ
ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID
10 NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82,
SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ
ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID
NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98,
SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103,
15 SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108,
SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113,
SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118,
SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121.

20 DETAILED DESCRIPTION OF THE INVENTION

The present invention relates in part to kinase polypeptides, nucleic acids encoding
such polypeptides, cells containing such nucleic acids, antibodies to such polypeptides,
assays utilizing such polypeptides, and methods relating to all of the foregoing. The
present invention is based upon the isolation and characterization of new kinase
25 polypeptides. The polypeptides and nucleic acids may be produced using well-known and
standard synthesis techniques when given the sequences presented herein.

I. The Nucleic Acids of the Invention

30 Included within the scope of this invention are the functional equivalents of the
herein-described isolated nucleic acid molecules. The degeneracy of the genetic code
permits substitution of certain codons by other codons that specify the same amino acid
and hence would give rise to the same protein. The nucleic acid sequence can vary

substantially since, with the exception of methionine and tryptophan, the known amino acids can be coded for by more than one codon. Thus, portions or all of the kinase genes of the invention could be synthesized to give a nucleic acid sequence significantly different from one selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121. The encoded amino acid sequence thereof would, however, be preserved.

In addition, the nucleic acid sequence may comprise a nucleotide sequence which results from the addition, deletion or substitution of at least one nucleotide to the 5'-end and/or the 3'-end of the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID

NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13,
SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ
ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID
NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29,
5 SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ
ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID
NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45,
SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ
ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID
10 NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61,
SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ
ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID
NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77,
SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ
15 ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID
NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93,
SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ
ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID
NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID
20 NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID
NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID
NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a derivative thereof. Any nucleotide
or polynucleotide may be used in this regard, provided that its addition, deletion or
substitution does not alter the amino acid sequence of SEQ ID NO:122, SEQ ID NO:123,
25 SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,
30 SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
5 SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
10 SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
15 SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, that is encoded
by the nucleotide sequence. For example, the present invention is intended to include any
nucleic acid sequence resulting from the addition of ATG as an initiation codon at the 5'-
end of the inventive nucleic acid sequence or its derivative, or from the addition of TTA,
20 TAG or TGA as a termination codon at the 3'-end of the inventive nucleotide sequence or
its derivative. Moreover, the nucleic acid molecule of the present invention may, as
necessary, have restriction endonuclease recognition sites added to its 5'-end and/or 3'-
end.

Such functional alterations of a given nucleic acid sequence afford an opportunity
25 to promote secretion and/or processing of heterologous proteins encoded by foreign
nucleic acid sequences fused thereto, for example. All variations of the nucleotide
sequence of the kinase genes of the invention and fragments thereof permitted by the
genetic code are, therefore, included in this invention.

Further, it is possible to delete codons or to substitute one or more codons with
30 codons other than degenerate codons to produce a structurally modified polypeptide, but
one which has substantially the same utility or activity as the polypeptide produced by the
unmodified nucleic acid molecule. As recognized in the art, the two polypeptides are

functionally equivalent, as are the two nucleic acid molecules that give rise to their production, even though the differences between the nucleic acid molecules are not related to the degeneracy of the genetic code. This is discussed further in the "Functional Derivatives" section, herein.

5 Finally, many of the nucleic acid molecules of the invention are provided as a partial sequence only (Fig. 2A through 2QQ). However, it is standard for one of ordinary skill in the art to obtain a full-length sequence when provided with a partial sequence. Similarly, when provided with a partial or full-length sequence it is standard for one of ordinary skill in the art to obtain nucleic acid sequence coding for homologous proteins.
10 Therefore, these nucleic acid molecules are also part of the invention.

 The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore
15 presumably define new protein kinase groups.

 Additional characteristics may be found, *inter alia*, in the tables, namely Table 1, Table 2, Table 3 and Table 4, shown below.

20 II. Nucleic Acid Probes, Methods, and Kits for Detection of Protein Kinases.

 A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory,
25 Sambrook, Fritsch, & Maniatis, eds., 1989).

 In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences that correspond to N-terminal, kinase or C-terminal portions, for example, of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid probes may be used as primers in a polymerase chain
30 reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press,

Michael, *et al.*, eds., 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art ("Molecular Cloning: A Laboratory Manual", 1989, *supra*). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b) detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to

radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or streptavidin).

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

III. DNA Constructs Comprising a Protein Kinase Nucleic Acid Molecule and Cells Containing These Constructs.

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The polypeptide may be purified from cells that have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding a kinase of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a kinase of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and a sequence encoding a kinase of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a kinase of the invention, or (3) interfere with the ability of the gene sequence of a kinase of the invention to be transcribed by the promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence.

Thus, to express a gene encoding a kinase of the invention, transcriptional and translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a kinase of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells.

5 Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for kinases of the invention. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

10 In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include γ gt10, γ gt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

15 Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

20 To express a kinase of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the kinase of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage λ , the *bla* promoter of the β -lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage λ (P_L and P_R), the *trp*, *recA*, *lacZ*, *lacI*, and *gal* promoters of *E. coli*, the α -amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the ζ -28-specific promoters of *B. subtilis* (Gilman *et*
25 *al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic
30

promoters are reviewed by Glick (Ind. Microbiol. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev. Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the kinase polypeptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO or CHO-K1, or cells of lymphoid origin and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332, which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used (Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of kinases of the invention in insect cells (Jasny, Science 238:1653, 1987; Miller *et al.*, In: Genetic Engineering, Vol. 8, Plenum, Setlow *et al.*, eds., pp. 277-297, 1986).

Any of a series of yeast expression systems can be utilized which incorporate promoter and termination elements from the actively expressed sequences coding for glycolytic enzymes that are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational modifications. A number of recombinant DNA strategies exist utilizing strong promoter sequences and high copy number plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian genes and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). Several possible vector systems are available for the expression of kinases of the invention in a mammalian host.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of kinases of the invention in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer *et al.*, J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, Nature (London) 290:304-31, 1981); and the yeast gal4 gene sequence promoter (Johnston *et al.*, Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver *et al.*, Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon that encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes a kinase of the invention (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (*i.e.*, AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the kinase of the invention coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as the kinase of the invention coding sequence).

A nucleic acid molecule encoding a kinase of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule. Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (*Mol. Cell. Biol.* 3:280-, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector;

the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColEI, pSC101, pACYC 184, π VX; "Molecular Cloning: A Laboratory Manual", 1989, *supra*). *Bacillus* plasmids include pC194, pC221, pT127, and the like (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall *et al.*, J. Bacteriol. 169:4177-4183, 1987), and streptomyces bacteriophages such as ϕ C31 (Chater *et al.*, In: Sixth International Symposium on Actinomycetales Biology, Akademiai Kaido, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John *et al.* (Rev. Infect. Dis. 8:693-704, 1986), and Izaki (Jpn. J. Bacteriol. 33:729-742, 1978).

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, Miami Wntr. Symp. 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, Cell 28:203-204, 1982; Bollon *et al.*, J. Clin. Hematol. Oncol. 10:39-48, 1980; Maniatis, In: Cell Biology: A Comprehensive Treatise, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, *i.e.*, transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene(s) results in the production of a kinase of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

IV. The Proteins of the Invention

A variety of methodologies known in the art can be utilized to obtain the polypeptides of the present invention. The polypeptides may be purified from tissues or cells that naturally produce the polypeptides. Alternatively, the above-described isolated nucleic acid fragments could be used to express the kinases of the invention in any
5 organism. The samples of the present invention include cells, protein extracts or membrane extracts of cells, or biological fluids. The samples will vary based on the assay format, the detection method, and the nature of the tissues, cells or extracts used as the sample.

10 Any eukaryotic organism can be used as a source for the polypeptides of the invention, as long as the source organism naturally contains such polypeptides. As used herein, "source organism" refers to the original organism from which the amino acid sequence of the subunit is derived, regardless of the organism the subunit is expressed in and ultimately isolated from.

15 One skilled in the art can readily follow known methods for isolating proteins in order to obtain the polypeptides free of natural contaminants. These include, but are not limited to: size-exclusion chromatography, HPLC, ion-exchange chromatography, and immuno-affinity chromatography.

Further, the polypeptides of the invention include the full-length polypeptides that
20 can be identified from the full-length or partial sequences encoded by SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,
25 SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167,
30 SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,

SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,
SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
5 SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
10 SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242 (Figure 1). In addition, the polypeptides of the invention include the domains of
these polypeptides, including, but not limited to, the N-terminal, kinase/catalytic, and C-
15 terminal domains.

The characteristics of the protein kinase nucleic acid sequences of the invention are
provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI,
CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant
number of protein kinases that do not belong to any of the known groups, and therefore
20 presumably define new protein kinase groups.

Additional characteristics are shown in, *inter alia*, the tables, namely Table 1,
Table 2, Table 3 and Table 4, provided below.

V. Antibodies, Hybridomas, Methods of Use and Kits for Detection of Protein
25 Kinases

The present invention relates to an antibody having binding affinity to a kinase of
the invention. The polypeptide may have an amino acid sequence selected from the group
consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ
ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ
30 ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ
ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ
ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or a functional derivative thereof, or at least 9 contiguous amino acids thereof (preferably, at least 20, 30, 35, or 40 or more contiguous amino acids thereof). Alternatively, the antibody may bind to a part of the polypeptide not provided in the sequences above, but that is present in the full-length sequence of the polypeptide and that is easily obtained using methods standard in the art. Further, the antibody may bind specifically to particular domains of one or more of the kinases of the invention, including, but not limited to, the N-terminal, kinase/catalytic, or C-terminal domains.

The present invention also relates to an antibody having specific binding affinity to a kinase or kinase domain of the invention. Such an antibody may be isolated by comparing its binding affinity to a kinase of the invention with its binding affinity to other polypeptides. Those that bind selectively to a kinase of the invention would be chosen for use in methods requiring a distinction between a kinase of the invention and other

polypeptides. Such methods could include, but should not be limited to, the analysis of altered kinase expression in tissue containing other polypeptides.

The kinases of the present invention can be used in a variety of procedures and methods, such as for the generation of antibodies, for use in identifying pharmaceutical compositions, and for studying DNA/protein interaction.

The kinases of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting.

The present invention also relates to a hybridoma that produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line that is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth *et al.*, J. Immunol. Methods 35:1-21, 1980).

Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal that is immunized, the antigenicity of the polypeptide and the site of injection.

The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or β -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Agl4 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell that produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", *supra*, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, *see* Stemberger *et al.*, J. Histochem. Cytochem. 18:315, 1970; Bayer *et al.*, Meth. Enzym. 62:308-, 1979; Engval *et al.*, Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues that express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby *et al.*, Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as in immunochromatography.

Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides (Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspczak *et al.*, Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the kinases of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a kinase polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Altered levels of a kinase of the invention in a sample as compared to normal levels may indicate disease.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock *et al.* ("Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents that are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

VI. Isolation of Compounds That Interact With Protein Kinases

The present invention also relates to a method of detecting a compound capable of binding to a protein kinase of the invention, comprising incubating the compound with a kinase of the invention and detecting the presence of the compound bound to the kinase. The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts.

The present invention also relates to a method of detecting an agonist or antagonist of kinase activity or kinase binding partner activity comprising incubating cells that produce a kinase of the invention in the presence of a compound and detecting changes in the level of kinase activity or kinase binding partner activity. The compounds thus identified would produce a change in activity indicative of the presence of the compound.

The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts. Once the compound is identified it can be isolated using techniques well known in the art.

5 The present invention also encompasses a method of agonizing (stimulating) or antagonizing kinase associated activity in a mammal comprising administering to said mammal an agonist or antagonist to a kinase of the invention in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of kinase activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize kinase associated functions
10 is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit
15 the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S.
20 Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*).

25 Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will cause multiple side-effects as therapeutics for diseases.

30 Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin,

naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzyldene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzyldene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris *et al.*, J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.*, J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J.

Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*, Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); Sikora *et al.*, Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432 (1993); and Burke *et al.*, BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen *et al.*, Clin. Exp. Immunol. 91:141-156 (1993); Anafi *et al.*, Blood 82:12:3524-3529 (1993); Baker *et al.*, J. Cell Sci. 102:543-555 (1992); Bilder *et al.*, Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton *et al.*, Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert *et al.*, Experimental Cell Research 199:255-261 (1992); Dong *et al.*, J. Leukocyte Biology 53:53-60 (1993); Dong *et al.*, J. Immunol. 151(5):2717-2724 (1993); Gazit *et al.*, J. Med. Chem. 32:2344-2352 (1989); Gazit *et al.*, " J. Med. Chem. 36:3556-3564 (1993); Kaur *et al.*, Anti-Cancer Drugs 5:213-222 (1994); Kaur *et al.*, King *et al.*, Biochem. J. 275:413-418 (1991); Kuo *et al.*, Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall *et al.*, J. Biol. Chem. 264:14503-14509 (1989); Peterson *et al.*, The Prostate 22:335-345 (1993); Pillemer *et al.*, Int. J. Cancer 50:80-85 (1992); Posner *et al.*, Molecular Pharmacology 45:673-683 (1993); Rendu *et al.*, Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring *et al.*, J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda *et al.*, Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

VII. Biological Significance, Applications and Clinical Relevance of Novel Protein
5 Kinases

For each protein kinase in this application, we provide a classification of the protein class and family to which it belongs, a summary of non-catalytic protein motifs, a profile of its expression in several hundred tissue and cell sources, and a chromosomal location. This information can be used to suggest potential function, regulation or
10 therapeutic utility for each of the proteins.

The kinase classification and protein domains often reflect pathways, cellular roles, or mechanisms of up- or down-stream regulation. Also disease-relevant genes often occur in families of related genes. For example if one member of a kinase family functions as an oncogene, a tumor suppressor, or has been found to be disrupted in an immune,
15 neurologic, cardiovascular, or metabolic disorder, frequently other family members may play a related role.

The expression analysis organizes kinases into groups that are transcriptionally upregulated in tumors and those that are more restricted to specific tumor types such as melanoma or prostate. This analysis also identifies genes that are regulated in a cell cycle
20 dependent manner, and are therefore likely to be involved in maintaining cell cycle checkpoints, entry, progression, or exit from mitosis, oversee DNA repair, or are involved in cell proliferation and genome stability. Expression data also can identify genes expressed in endothelial sources or other tissues that suggest a role in angiogenesis, thereby implicating them as targets for control of diseases that have an angiogenic
25 component, such as cancer, endometriosis, retinopathy and macular degeneration, and various ischemic or vascular pathologies. A proteins' role in cell survival can also be suggested based on restricted expression in cells subjected to external stress such as oxidative damage, hypoxia, drugs such as cisplatin, or irradiation. Metastases-associated genes can be implicated when expression is restricted to invading regions of a
30 tumor, or is only seen in local or distant metastases compared to the primary tumor, or when a gene is upregulated during cell culture models of invasion, migration, or motility.

Chromosomal location can identify candidate targets for a tumor amplicon or a tumor-suppressor locus. Summaries of prevalent tumor amplicons are available in the literature, and can identify tumor types to experimentally be confirmed to contain amplified copies of a kinase gene which localizes to an adjacent region.

Based on these criteria several kinases immediately stand out as being of potential therapeutic relevance. The protein kinases can be divided into the following disease-relevant categories (nucleotide Seq ID #s in parentheses):

Tumor associated: Mok (SEQ ID NO:57), EPK2, AA316804 (SEQ ID NO:11), AA435956 (SEQ ID NO:48), AA278842 (SEQ ID NO:88), AA599286 (SEQ ID NO:89), AA826850 (SEQ ID NO:3), HRI (SEQ ID NO:73), MLK4 AA232253 (SEQ ID NO:82), AA883975 SGK 235 (SEQ ID NO:95), AA311714 (SEQ ID NO:101), MPSK1 (SEQ ID NO:110), R19609 (Seq ID111), AA383293 (SEQ ID NO:26).

Prostate-specific: AA234451 (SEQ ID NO:47), TSK4 (SEQ ID NO:93), RIP4 (SEQ ID NO:84), KIAA0965 (SEQ ID NO:8).

Oncogenic or proliferation associated: KIAA0781 (SEQ ID NO:38), AA789239 (SEQ ID NO:52), CCRK (SEQ ID NO:54), CLK4 (SEQ ID NO:55), H85389 (SEQ ID NO:97).

Neuronal restricted: CAMKKB (SEQ ID NO:66)

Hematopoietic expressed: PTK9L (SEQ ID NO:22), DRAK2 (SEQ ID NO:29), AI025291 (SEQ ID NO:94)

Angiogenic or endothelial expressed: DRAK1 (SEQ ID NO:31), MAK-V (SEQ ID NO:40), TRAD (SEQ ID NO:44), MOK (SEQ ID NO:57), AA08847 (SEQ ID NO:78), HGP_66444466 (SEQ ID NO:79), RSK4 (SEQ ID NO:16).

Cell cycle regulated: AA454060 (SEQ ID NO:45), KIAA0999 (Mitotic – SEQ ID NO:32), AA579641 (Mitotic – SEQ ID NO:60), AA305176 (Mitotic – SEQ ID NO:6), AA018361 (S1 phase – SEQ ID NO:100).

VIII. Transgenic Animals.

A variety of methods are available for the production of transgenic animals associated with this invention. DNA can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (*e.g.*, the nucleus of a two-cell embryo) following the initiation of cell division (Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442, 1985). Embryos can

be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term. Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan *et al.*, *supra*). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout (Experientia 47: 897-905, 1991). Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sanford *et al.*, July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. Females are placed with males, and the mated females are sacrificed by CO₂ asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice (Hammer *et al.*, Cell 63:1099-1112, 1990).

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art (Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987).

In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, the gene encoding neomycin resistance is physically linked to the sequence(s) of the invention.

Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination (Capecchi, Science 244: 1288-1292, 1989). Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner *et al.* (Nature 338: 153-156, 1989), the teachings of which are incorporated herein in their entirety including any drawings. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science 244:1281-1288, 1989; and Simms *et al.*, Bio/Technology 6:179-183, 1988).

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding a kinase of the invention or a gene effecting the expression of the kinase. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introduction of a kinase, or regulating the expression of a kinase (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode human STE20-related kinases. Native expression in an animal may be reduced by providing an amount of anti-sense RNA or DNA effective to reduce expression of the receptor.

IX. Gene Therapy

Protein kinases of the invention, or their genetic sequences will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated

positive initial results. The basic science of gene therapy is described in Mulligan (Science 260:926-931, 1993).

In one preferred embodiment, an expression vector containing protein kinase coding sequence is inserted into cells, the cells are grown *in vitro*, and then are infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous gene encoding kinases of the invention in such a manner that the promoter segment enhances expression of the endogenous kinase gene (for example, the promoter segment is transferred to the cell such that it becomes directly linked to the endogenous kinase gene).

The gene therapy may involve the use of an adenovirus containing kinase cDNA targeted to a tumor, systemic kinase increase by implantation of engineered cells, injection with kinase-encoding virus, or injection of naked kinase DNA into appropriate tissues.

Target cell populations may be modified by introducing altered forms of one or more components of the protein complexes in order to modulate the activity of such complexes. For example, by reducing or inhibiting a complex component activity within target cells, an abnormal signal transduction event(s) leading to a condition may be decreased, inhibited, or reversed. Deletion or missense mutants of a component, that retain the ability to interact with other components of the protein complexes but cannot function in signal transduction may be used to inhibit an abnormal, deleterious signal transduction event.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, several RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (*e.g.*, cDNA) encoding recombinant kinase of the invention protein into the targeted cell population (*e.g.*, tumor cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., 1989; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y., 1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in a reconstituted system *e.g.*, liposomes or other lipid systems for delivery to target cells (*e.g.*, Felgner *et al.*, Nature 337:387-8,

1989). Several other methods for the direct transfer of plasmid DNA into cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins (Miller, *supra*).

5 In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection (Capecchi, Cell 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is
10 precipitated with CaPO_4 and taken into cells by pinocytosis (Chen *et al.*, Mol. Cell Biol. 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu *et al.*, Nucleic Acids Res. 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner *et al.*, Proc. Natl. Acad. Sci. USA. 84:7413-7417, 1987); and
15 particle bombardment using DNA bound to small projectiles (Yang *et al.*, Proc. Natl. Acad. Sci. 87:9568-9572, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The admixture of adenovirus to
20 solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene (Curiel *et al.*, Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic acid molecule into a cell. Gene transfer is commonly performed to enable the expression
25 of a particular product encoded by the gene. The product may include a protein, polypeptide, anti-sense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or
30 receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic

acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express
5 a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In another preferred embodiment, a vector having nucleic acid sequences encoding a protein kinase polypeptide of the invention is provided in which the nucleic acid
10 sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression are set forth in International Publication No. WO 93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or
15 modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, a method of gene replacement is set forth. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene that is missing or defective in the animal.

20 X. Administration of Substances

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by
25 reference in their entirety, including any drawings, figures, or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used, and the size and physiological condition of
30 the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be formulated in animal models to achieve a circulating concentration range that initially

takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors, and major organs can be also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan, and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition, and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, *Journal of American Veterinary Medical Assoc.*, 202:229-249, 1993). Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness, or toxicity. Gross abnormalities in tissue are noted, and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

EXAMPLES

10 The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of the protein kinases of the invention.

EXAMPLE 1: Isolation of cDNA clones Encoding Novel Mammalian Protein Kinases Materials and Methods Identification from cDNA databases and isolation of clones encoding novel protein kinases

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Novel kinases were identified from the public EST databases using a Hidden Markov model, abbreviated HMM (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531). The model was built with 70 mammalian and yeast kinase catalytic domain sequences. These sequences were chosen from a comprehensive collection of kinases such that no two sequences had more than 50% sequence identity. ESTs were translated in six open reading frames and were searched against the model. ESTs that had a score of at least 10 against the HMM were then masked for repetitive sequences and vectors and were clustered using MSA. The resulting contigs were searched against known kinases to identify EST clones that encode novel kinases.

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Approximately 40% of the ESTs encoding potentially novel kinases did not correspond to the correct EST upon sequence analysis. Most of these discrepancies were resolved by ordering additional clones, however, 14 remained unavailable. These 14 ESTs were amplified from a variety of single-stranded cDNA sources with primers derived from the corresponding EST entry as shown on Table 5. The PCR product was subcloned into a bluescript vector, digested to confirm the presence of a correct size insert and sequenced. Full sequencing of EST and PCR was carried out using a cycle sequencing Big-dye kit

30

with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Table 5: Primers used to clone PCR products corresponding to novel kinases

	ID#	ID#	Parent	5' primer	3' primer
sp	na	aa	Sequencec	Sequence*	Sequence*
H	33	153	2R22-5-11	GAGATCGRNTTYAARGA RTTYGA	TGTCACNCCNAGNSWCCAN AYRTT
M	81	200	5R57_10_2_ m TESK2_m	GCTGCTGGACAGTGACT TGATTTT	GAAAGCAAAGCCTTCACAC CTT
H	67	187	5R69_17_2_h	CTCTCACCTCAGGAACT GG	GCTTGCGGATCTTCTCA
H	46	166	SGK309_h	GACATCCTGCCGGCCAA CTACG	CGGCCCTGGAGCTGCATCA CTA
M	67	228	5R72_16_2_h	TGCGCGACACCATTGAC CAG	CTCAGGGCTTACATACAGA G
H	45	165	5R72_8_2_h	AAAGGAGAACTACATTT TGAAAAT	CTTCATCATCTCTAATACAT TGGTTGG
H	41	161	Z36720	CAAATTAAGATCATTGA CTTTGGG	GGAAACAAAGTCCTTGGCC TC
H	115	234	AL031652 - Pak6	GTGGACATCTGGTCCCT CG	GTAGGTCCTTCACTCTTGG AG

- degenerate oligonucleotide residue designation:

5 N= A,C,G or T

R= A or G

Y= C or T

S = C or G

W= A or T

10

Full-length sequence extension of protein kinases using cDNA and genomic databases

Extension of partial cDNA sequences to encompass the full-length open-reading frame was carried out by iterative blastn searching of the cDNA databases listed in Table 6. All blastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1. The gapped blast algorithm is described in: (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and

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PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402).

Table 6. Databases used for cDNA-based sequence extensions

Database	Database Date
LifeGold templates	Feb 2000
LifeGold compseqs	Feb 2000
LifeGold compseqs	Mar 2000
LifeGold compseqs	Apr 2000
LifeGold fl	Feb 2000
LifeGold flt	Apr 2000
NCBI human Ests	May 2000
NCBI murine Ests	May 2000
NCBI nonredundant	May 2000

Extension of partial cDNA sequences to encompass the full-length open-reading frame was also carried out by iterative searches of genomic databases. Three methods were used. The first method made use of the Smith-Waterman algorithm to carry out protein-protein searches of the closest homologue or orthologue to the partial kinase. The target databases consisted of Genescan and open-reading frame (ORF) predictions of all human genomic sequence derived from the human genome project (HGP) as well as from Celera. The complete set of genomic databases searched is shown in Table 7 below. Genomic sequences encoding potential extensions were further assessed by blastp analysis against the NCBI nonredundant to confirm the novelty of the hit. The extending genomic sequences were incorporated into the cDNA sequence after removal of potential introns using the Seqman program from DNASTar. The default parameters used for Smith-Waterman searches were as shown next. Matrix: blosum 62; gap-opening penalty: 12; gap extension penalty: 2. Genescan predictions were made using the Genescan program as detailed in (Chris Burge and Sam Karlin "Prediction of Complete Gene Structures in Human Genomic DNA", JMB (1997) 268(1):78-94). ORF predictions from genomic DNA were made using a standard 6-frame translation.

The second method for genomic sequence-based extensions made use of tBlastn searches of the homologue or orthologue to the partial kinase against the cDNA databases listed in Table 7. The recognition of significant hits in these databases made possible to identify bridging partial cDNA clones. The iterative application of the two methods made possible the assemblage of the virtual full-length sequence for a large number of the kinases presented in this application. All tblastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1.

The last method for defining cDNA extensions from genomic sequence used iterative searches of genomic databases through the Genescan program to predict exon splicing and the Genewise program (<http://www.sanger.ac.uk/Software/Wise2/>) to predict potential ORFs based on homology to the closest orthologue/homologue.

Table 7. Databases used for genomic-based sequence extensions

Database	Number of entries	Database Date
Celera v. 1-5	5,306,158	Jan 19/00
Celera v. 6-10	4,209,980	Mar 24/00
Celera v. 11-14	7,222,425	Apr 24/00
Celera v. 15	243,044	May 14/00
HGP all Genescan	25,885	Apr 04/00
HGP; Phase 0	4,944	May 04/00
HGP; Phase 1	28,478	May 05/00
HGP; Phase 2	1,508	May 04/00
HGP; Phase 3	9,971	May 05/00

Virtual Extensions

Human AA826850 (SEQ ID NO: 3, SEQ ID NO:124)

Blastn analysis of the partial AA826850 sequence revealed an extension to encompass the complete ORF in the Incyte EST 238299.1. A frame-shift correction at position 595 of this EST (marked by X in NA sequence) generated an uninterrupted ORF.

Human AA960957 (SEQ ID NO: 4, SEQ ID NO:125)

Since the initial filing of this application, the partial AA960957 sequence appeared in the public database as the full-length gene for a protein kinase encoded by a gene that maps adjacent to the evc (AJ250839) (ellis-van creveld syndrome and weyers acrodermal dysostosis) gene from 4p16.1.

5 Human 5R79-46-1_h (SEQ ID NO: 5, SEQ ID NO:126)

Blastn analysis of the partial 5R79-46-1 sequence revealed an extension to encompass the complete ORF in the Incyte EST 463894.6. Since the initial filing of this application, the full-length virtual 5R79-46-1 appeared in the public database as the full-length gene for the TANK-binding kinase (TBK1) (Pomerantz, J.L. and Baltimore, D. (1999) EMBO J. 18 (23), 6694-6704). TBK1 participates in NF- κ B activation through the formation of a signaling complex with TRAF2 and TANK.

Human AA305176 (SEQ ID NO: 6, SEQ ID NO:127)

Blastn analysis of the partial AA305176 sequence revealed an extension to encompass the complete ORF in the Incyte EST 220937.1.

15 Human AA256100 (SEQ ID NO: 8, SEQ ID NO:129)

Blastn analysis of the partial AA256100 sequence revealed an extension to encompass the complete ORF through the assembly of three partial clones: Incyte EST 480815.6, KIAA0965 (BAA76809) and AA256100.

Human AA210825 (SEQ ID NO: 9, SEQ ID NO: 130)

20 Blastn analysis of the partial AA210825 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte EST 014721.7, and the NCBI EST's AW01158 and AA210825. An insertion of two "N's" at positions 1915 and 1916 generated an uninterrupted ORF. Blastx analysis indicated the possibility of a start Met in the range of 400-450 nucleotides (i.e. compared to the closest homolog, human PKCmu (CAA53384.1). However, no Met was found in this region; rather ORF ends in an in-frame stop preceeded by the sequence
25 "RGLLAPGDPPCPPNPAPATPPSSRLPTLFSNFCDS". It is possible that part of the sequence covered by nucleotide positions 1-400 derived from AW01158 comes from an intron, explaining the absence of a start Met.

30 Human AA127299 (SEQ ID NO:10, SEQ ID NO:131)

No entries in the database extended this sequence. The 1684 bp insert of this EST contains a 1369 bp intron at the 3' end. Blastx and SW analysis of the 315 bp coding

region revealed homology to the extracatalytic C2 domain of PKC. This EST, may or may not encode a kinase.

Human AA316804 (SEQ ID NO:11, SEQ ID NO:132)

5 Since the initial filing of this application, the partial AA316804 sequence appeared in the public database as the full-length gene for the PKC family protein kinase EPK2 or PKC ϵ (AB015982).

Human H19102 (SEQ ID NO:14, SEQ ID NO:135)

10 Genewise and Genescan analyses of the partial H19102 sequence revealed an extension from the HGP phase 3 contig 3810672 to encompass the complete catalytic domain of this EST. Blastn analysis against the non-redundant database revealed that this gene is found in the cosmid AC005726 from chromosome 17. H19102 may encode a dual catalytic kinase given the homology to S6 kinase. Analysis of genomic sequence upstream of the 5' end of H19102 revealed a non-kinase gene oriented in the same polarity as H19102 suggestive of the start Met for H19102 being close to the 5' end of the H19102
15 sequence. From this analysis it is deduced that the second catalytic domain of H19102, if present, is most likely located within the 47334-185,215 bp region of the genomic sequence of AC005726.

Human AA476563 (SEQ ID NO:15, SEQ ID NO:136)

20 Since the initial filing of this application, the partial AA476563 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KC1 (NM_012424) (Zhang, H. et al Genomics (1999) 61, 314-318), which is an S6 kinase mapping to 12q12-q13.1.

Human AA626690 (SEQ ID NO:16, SEQ ID NO:137)

25 Since the initial filing of this application, the partial AA626690 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KA6 (AF184965) (Yntema, H.G et al (1999) Genomics 62, 332-343), an S6 kinase commonly deleted in patients with complex X-linked (Xq21.1) mental retardation.

Human AI215680 (SEQ ID NO: 17, SEQ ID NO:138)

30 Since the initial filing of this application, the partial AI215680 sequence appeared in the public database as the full-length gene encoding a hypothetical protein (AAD30182) from the locus AC006530.4 from chromosome 14.

Human AA887783 (SEQ ID NO:21, SEQ ID NO:142)

Blastn analysis of the partial AA887783 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte 415390R6 and the NCBI EST's AA887783 and N94726. Since the initial filing of this application, the nearly full-length virtual AA887783 sequence appeared in the public database as the full-length gene encoding SGK3 (AF169035), a serum- and glucocorticoid-induced protein kinase (Kobayashi, T. et al (1999) Biochemical J. 344, 189-197.

Human R47805 (SEQ ID NO:22, SEQ ID NO:143)

A cDNA clone encoding the full-length ORF of R47805 was isolated using R47805 as a screening probe. A full-length form for R47805 has also appeared in the public database as

PTK9L (NM_007284), an A6-related protein kinase.

Human H60215 (SEQ ID NO:23, SEQ ID NO:144)

Blastn analysis of the partial H60215 sequence revealed an extension to encompass the complete ORF in the public EST AI275726. This was confirmed through the full insert sequencing of this EST (2,310 bp) which corresponds to the sequence under SEQ ID NO:144.

A different stop codon was predicted for AI275726 compared to H60215 due to a single nucleotide insertion at position 1586 in AI275726. Evidence for the extra nucleotide comes from EST AI191922.

SGK324_h orthologue of W30246_m (SEQ ID NO:24, SEQ ID NO:145)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding to the human orthologue of murine W30246. Exons predicted from the following sequences were used for contig construction: Celera 17000189645083, 17000057549105 and 11000501939981; Incyte142404.1, HGP_7249119, Incyte 7196489H1, Celera 11000501939981, 17000028165594; Incyte 7249119_3, Celera 17000035772368, 11000502081575 and 17000140274329. The latter Celera sequence provides the N-terminus.

Human AA383293 (SEQ ID NO:26, SEQ ID NO:147)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding for AA383293. Exons predicted from the following sequences were used for contig construction: (numbers in parenthesis

refer to the aa sequence of the closest homolog (RU2S, NP_057440) used for the Smith-Waterman query): N-term from Incyte 6010175_2 (14-97), Incyte 6981981 (134-184) 7596749 (186-232) Celera 17000020789545 (243-301) CAB75619.1 (310-341)--(56-145 DCX homology) 6010175_2, Celera 17000030058129 (241-262 DCX homology).

5 Human AA021445 (SEQ ID NO:32, SEQ ID NO:152)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. Contig reconstruction was as follows: nucleotides 1-802 from KIAA0999 (AB023216); nucleotides 803-4321 from full-insert sequence of AA021445. A pairwise alignment between the AA021445 and KIAA0999 revealed three
10 inserts in the extracatalytic C-terminus of 48, 48 and 161 aminoacids. In addition, both AA021445 and KIAA0999 have 15 copies of a CAG repeat. Trinucleotide repeats are often found in genes that linked to neurodegenerative diseases.

Human 2R22-55-1 (SEQ ID NO:33, SEQ ID NO:153)

Blastn analysis revealed an extension in the Incyte EST clone 321074.1 to
15 encompass the complete ORF corresponding to 2R22-55-1.

Human orthologue of AA544838_m (SEQ ID NO:36, SEQ ID NO:156)

tBlastn analysis identified the partial human KIAA0135 (U79240) clone as the human orthologue of murine AA544838. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from
20 Incyte406786.5, KFZp430051 and KIAA0135 (U79240).

Human orthologue of AI785735_m (SEQ ID NO:38, SEQ ID NO:158)

tBlastn analysis identified the partial human KIAA0781 (AB018324) clone as the human orthologue of murine AI785735. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte
25 986123.37 KIAA0781 (AB018324).

Human AA207220 (SEQ ID NO: 39, SEQ ID NO:159)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. The full ORF was reconstructed from Incyte 402740.1 and AA207220. Frame corrections: deletion of 441 and 595 over Inc402740.1 seq based on
30 blastx to keep frame open; two n insertions 940, 941 over AA207220 to keep frame open.

Human AA426580 (SEQ ID NO:40, SEQ ID NO:160)

Since the initial filing of this application, the partial AA426580 sequence appeared in the public database as the full-length gene encoding MAK-V (AJ271722) from chromosome 21q22.1.

Human 5R79-54-1 (SEQ ID NO: 41, SEQ ID NO:161)

5 Genewise and Genescan analyses of the partial 5R79-54-1 sequence revealed an extension from genomic sequence to encode the full ORF for 5R79-54-1.

Human orthologue of AA542015_m (SEQ ID NO: 42, SEQ ID NO:162)

10 tBlastn analysis identified KIAA1297 (AB037718). Blastn extended the KIAA1297 sequence to provide the C-terminus through the Incyte 224074.1 EST. The partial ORF consists of a dual catalytic domain flanked by 6 Ig domains and 2 fibronectin repeats. Based on homology to the bt drosophila protein (AAF59316.1), the human form of AA542015 is expected to be missing 16 Ig domains.

Human R19772 (SEQ ID NO:44, SEQ ID NO:164)

15 The full-length ORF for R19772 was isolated by screening a cDNA library using a probe derived from R19772. Since the initial filing of this application, the R19772 sequence appeared in the public database as the full-length gene encoding Trio (Duet) (AB011422). CDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

20 Table 8. Isoforms for R19772

Kestrl Name	Kestrl AA Acc #	Isoform type	Source	Description*
Trad (Duet)	R19772	B	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762
		C	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762

				Deletion of 32 aa (160-191)
		D	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)
		E	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)

* reference amino acid position are with respect to sequence of Trad (AB011422)

Human AA435956 (SEQ ID NO:48, SEQ ID NO:168)

5 Blastn analysis revealed an extension to encompass the nearly complete catalytic region of AA435956. 5' end sequence extension was provided by genomic locus AC007242.3_h (range 44880-43801). Based on blastx analysis, the extended sequence encodes is full-length at the C-terminus.

Human AA397553 (SEQ ID NO: 51, SEQ ID NO:171)

10 Since the initial filing of this application, the partial AA397553 sequence appeared in the public database as the full-length gene encoding CRK7 (AF227198), a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters.

Human AA789239 (SEQ ID NO: 52, SEQ ID NO:172)

15 Since the initial filing of this application, the partial AA789239 sequence appeared in the public database as the full-length gene encoding NKIAMRE (AF130372), a novel kinase deleted in human leukemia.

Human AA631990 (SEQ ID NO:55, SEQ ID NO:175)

20 Blastn analysis revealed an extension to encompass the full-length ORF for AA631990. The full ORF was reconstructed from 253847.5 and AA631990 and AA207220. Frame corrections: delete 1 C at 1380, delete 2N's at 2033/2034.

Human AA557536 (SEQ ID NO:56, SEQ ID NO:176)

25 Blastn analysis revealed an extension to encompass full-length ORF for AA557536. The full ORF was reconstructed from AA557536, celera 11000504061899 and the Incyte 097089.1 EST. An 85bp intron was removed from AA557536.

Human N34132 (SEQ ID NO: 63, SEQ ID NO:183)

Full sequencing of EST N34132 (1.3 kb) confirmed that this cDNA encodes a novel NEK-subfamily kinase. Blast analysis against the EST database showed that four

EST sequences (AA283140, AA283140, AA282911 and N53011) extended the sequence of N34132 at the 3' end to form a 2.31 kb contig. Blast analysis of the new contig against the nonredundant public database showed that the N34132 extended contig overlapped (100% identity) over 228 bp at its 3' end with human KIAA0344 (AB002342), a 5,787 bp cDNA encoding a 1246 aa polypeptide. The 5' 790 bp of the KIAA0344 cDNA (encoding the 58 N-terminal protein sequence) were found to be divergent with respect to the extended 2.32 kb N34132 contig. Evidence that the extended N34132 contig (2.31kb) and KIAA0344 (AB002342) belong to the same gene is the following. First, blast analysis of the nucleotide sequences for N34132 and KIAA0344 against the NR database confirmed that these cDNA's are transcribed from the same genomic locus defined by two overlapping BACs (AC004765 and AC004803) from chromosome 12p13.3. Second, full sequence determination of a PCR fragment amplified from single-stranded cDNA confirmed the junction between the extended N34132 contig and KIAA0344_h (AB002342). The 462 PCR product was amplified with primers CTCCTCAACAGACAGTGCAG (5' primer) and GACATTCTACTACTCGGTCTC (3' primer) designed from the N34132 extended contig and KIAA0344 sequences, respectively. The region of N34132 containing the start Met was isolated by PCR from a testis cDNA library (Clontech).

Human 5R69-17-2 (SEQ ID NO:67, SEQ ID NO:187)

The full-length ORF for 5R69-17-2 was isolated by screening a cDNA library using a probe derived from 5R69-17-2.

Human H85811 (SEQ ID NO:68, SEQ ID NO:188)

Tblastn, Smith-Waterman and blastn analyses using cDNA databases revealed an extension to encompass full-length ORF for H85811. The full ORF was reconstructed from Incyte ESTs 202971.8, 034583.3 and 034583.1 and public ESTs H85811 and AI570599.

Human R43524 (SEQ ID NO:73, SEQ ID NO:192)

Blastn analysis revealed an extension to encompass the complete catalytic region and the C-terminus of R43524. Since the initial filing of this application, the partial R43524 sequence appeared in the public database as the full-length gene encoding the heme-regulated initiation factor 2-alpha kinase (HRI) (AF181071).

Human AA088547 (SEQ ID NO:78, SEQ ID NO:197)

Genewise and Genescan analyses of genomic databases revealed an extension to encompass the complete ORF for AA088547.

Human orthologue of AA139478_m (SEQ ID NO:80, SEQ ID NO:199)

5 Tblastn identified the Incyte 211475.1 as the potential full-length human orthologue of murine AA139478

Human AA232253 (SEQ ID NO:82, SEQ ID NO:201)

10 The full-length ORF for AA232253 was isolated by screening a cDNA library using a probe derived from AA232253. Since the initial filing of this application, the AA232253 sequence appeared in the public database as the full-length gene encoding SLK (AB011422). SLK is a stress-regulated mixed lineage kinase-like protein that activation of Rac and induction of apoptosis. cDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

15 Table 9. Isoforms for AA232253

Kestrl Name	Kestrl AA Acc #	Isoform type	Description*
MLK4	AA232253	MLK4	Substitution of C for W at 346
		MLK4B	Different Cterm (332-800); seq in MLK4B is as shown in *

* C-terminus specific to MLK4B

LPLAARMSEESYFESKTEESNSAEMSCQITATSNNGEGHGMNPSLQAMMLMGFGDI

FSMNKAGAVMHSGMQINMQAKQNSS

20 KTTSKRGRGKKVNMALGFSDFDLSEGD D D D D D D D D G E E E D N D M D N S E

Human H97685 (SEQ ID NO:84, SEQ ID NO:203)

25 Blastn analysis revealed an extension to encompass the full-length ORF for H97685. The full ORF was reconstructed from Incyte 474824.1 and the public ESTs H97685 and M62021.

Human AI052250 (SEQ ID NO:87, SEQ ID NO:206)

Blastn analysis revealed an extension to encompass the full-length ORF for AI052250. The full ORF was reconstructed from Incyte 396868.1, the public partial cDNA FLJ10074 (minus intron) and the public ESTs and the public ESTs AI052250 and H97685, AI499220 and M62021.

5 Human AA278842 (SEQ ID NO:88, SEQ ID NO:206)

A nearly full-length cDNA (FL4F12) for AA278842 was isolated by screening a cDNA library using a probe derived from AA278842. A full-length virtual ORF was generated using FL4F12 and AA278842.

Human AA599286 (SEQ ID NO:89, SEQ ID NO:208)

10 Since the initial filing of this application, the partial AA599286 sequence appeared in the public database as a full-length ORF (AK000342).

Human AA425725 (SEQ ID NO:90, SEQ ID NO:209)

Since the initial filing of this application, the partial AA425725 sequence appeared in the public database as MSSK1, a serine kinase gene located from human chromosome Xq28.

15 Human SGK022 orthologue of AA060026_m (SEQ ID NO:91, SEQ ID NO:210)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed a potential human orthologue for murine AA060026. The full-length ORF for SGK022 was reconstructed from genomic locus AC022307.

20 Human AA399669 (SEQ ID NO:93, SEQ ID NO:212)

Blastn analysis revealed an extension to encompass the full-length ORF for AA399669. The full ORF was reconstructed as follows: sequence 1-1007 from AL136295.2; sequence1008-2319 from AA399669 and Incyte 428177.1.

Human AA883975 (SEQ ID NO:95, SEQ ID NO:214)

25 Genescan and Genewise analyses of the genomic databases revealed an extension for AA883975 to encompass the full-length ORF

Human AA905446 (SEQ ID NO:96, SEQ ID NO:215)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed an extension for AA905446 to encompass the full-length ORF. For the Smith-Waterman analysis murine STK22 (NP_033462) was used as the closest orthologue. Contig formation: range 162133-163687 from HGP_h 6921333_9; removed intron (146-893) predicted from blastx analysis.

Human H29974 (SEQ ID NO: 97 SEQ ID NO:216)

Blastn analysis revealed an extension to encompass a complete catalytic ORF for AA399669. The nearly full-length ORF was reconstructed using Incyte 213829.1 and H29974.

5 Human AA215311 (SEQ ID NO:99, SEQ ID NO:218)

Blastn analysis revealed an extension to encompass the full-length ORF for AA21531. The full ORF was reconstructed from Incyte 067584.1, 022456.1, AA215311 and the reverse complement of CPG_043208.

Human AA018361 (SEQ ID NO:100, SEQ ID NO:219)

10 The full-length ORF for AA018361 was isolated by screening a cDNA library using a probe derived from AA018361. This yielded clone Sug4-30. Clone Sug4-30, like multiple, independent cDNA clones contained a 181bp intron. The existence of intron-less RNA's was confirmed by a PCR reaction that generated a product that upon sequence analysis skipped the intron region. The full-length virtual ORF for AA018361 was
15 generated through a contig between AL117482 (seq 1-367) and the sequence for clone Sug4-30.

Human orthologue of AA396601_m (SEQ ID NO:106, SEQ ID NO:225)

tBlastn and Smith-Waterman analyses of genomic sequence revealed an extension to encompass the full catalytic region for the human orthologue of AA396601. The ORF
20 was reconstructed from Incyte 018653.9 (7261449H1, 6891740J1) and genomic sequence CPG_040010.

Human orthologue of AA671275_m (SEQ ID NO:108, SEQ ID NO:227)

Since the initial filing of this application, a potential human orthologue for murine AA671275 appeared in the public database as the full-length ORF for vaccinia related
25 kinase 3 (BAA90769).

Human H05721 (SEQ ID NO:111, SEQ ID NO:230)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for H05721.

Human AI086865 (SEQ ID NO:112, SEQ ID NO:231)

30 Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AI086865. The full-length ORF was reconstructed from Celera 17000102901516, Incyte 243269.1 and public AL1377531.

Human AA836348 (SEQ ID NO:113, SEQ ID NO:232)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AA836348.

Human R86668 (SEQ ID NO:14, SEQ ID NO:233)

5 The full-length ORF for R86668 was isolated by screening a cDNA library using a probe derived from R86668. Since the initial filing of this application, the R8668 sequence appeared in the public database as the full-length gene mitogen-activated protein kinase kinase kinase 6 (MAP3K6) (NM_00467).

Human 2R41-9-4 (SEQ ID NO: 16, SEQ ID NO:235)

10 The full-length virtual ORF for 2R41-9-4 was generated using genomic sequence to provide the Nterminus for the partial ORF predicted from clone 2R41-9-4

Table 10. Sequences deleted from the provisional patent due to duplication with other genes in the patent

Prov. SEQ ID NO: (na)	Prov. SEQ ID NO: (aa)
160	196
213	214
215	216
122	126
119	123
148	184
4	20
7	23
205	206
14	30
15	31
35	56
42	63
51	72
44	65
77	91

78	92
79	93
80	94
157	193

Results

Table 1 documents the results from the analysis of the nucleic acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "ORF Start", "ORF End", "ORF Length" refer to the open reading frame range and length as calculated by standard nucleic acid translation programs such as MapDraw (DNASStar). "DNA Repeats" refers to regions of low complexity sequence or repetitive elements such as Alu, LINE, SINE, and LTR sequences. The chromosomal location (CHR localization) for 37 of the 110 novel protein kinases is shown on Table 1 (NA, not available). The methods for determining chromosomal position are outlined below, in Example 2.

Table 2 documents the results from the analysis of the amino acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "nraa Score", "ID match aa", "Identity", "Similar", "nraa Match Acc#", "Description" refer to the data obtained using a Smith-Waterman search of the amino acid sequence against the non-

redundant protein database (Matrix: Pam100; gap open/extension penalties 14/1). "Kinase Domain Start", "Kinase Domain End", "Profile Start" and "Profile End" refer to data obtained using a Hidden-Markov Model to define catalytic range boundaries. The profile has a length of 261 amino acids, corresponding to the complete protein kinase catalytic domain. Proteins in which the profile recognizes a full length catalytic domain have a "Profile Start" of 1 and a "Profile End" of 261. The boundaries of the catalytic domain within the overall protein are noted in the "Kinase Domain Start" and "Kinase Domain End" columns.

10 The following abbreviations were used for kinases:

ASK	Apoptosis signal-regulating kinase
CaMK	Ca ²⁺ /calmodulin-dependent protein kinase
CCRK	Cell cycle-related kinase
CDK	Cyclin-dependent kinase
CK	Casein kinase
DAPK	Death-associated protein kinase
DM	myotonic dystrophy kinase
Dyrk	dual-specificity-tyrosine phosphorylating-regulated kinase
GAK	Cyclin G-associated kinase
GRK	G-protein coupled receptor
GuC	Guanylate cyclase
HIPK	Homeodomain-interacting protein
IRAK	Interleukin-1 receptor-associated kin
MAPK	Mitogen activated protein kinase
MAST	Micotubule-associated STK
MLCK	Myosin-light chain kinase
MLK	Mixed lineage kinase
NIMA	NimA-related protein kinase
PKA	cAMP-dependent protein kinase
RSK	Ribosomal protein S6 kinase
RTK	Receptor tyrosine kinase

SGK	Serum and glucocorticoid-regulated kinase
STK	serine threonine kinase
ULK	UNC-51-like kinase

The following abbreviations were used for species

H	Human
M	Murine
R	Rat
FV	Fowlpox virus
MT	<i>M. thermoautotrophicum</i>
CE	<i>Caenorhabditis elegans</i>
DM	<i>Drosophila melanogaster</i>
OS	<i>Oryza sativa</i>
SP	<i>Schizosaccharomyces pombe</i>
TP	<i>Tetrahymena pyriformis</i>
PI	<i>Petunia inflata</i>
NC	<i>Neurospora crassa</i>
MSV	<i>Medicago sativa</i>
MSV	Moloney murine sarcoma virus
SA	<i>Squalus acanthias</i>
CS	<i>Cucumis sativus</i>
GM	<i>Glycine max</i>
LL	<i>Lilium longiflorum</i>
TV	<i>Trichomonas vaginalis</i>
MP	<i>Mycoplasma pneumoniae</i>
DD	<i>Dictyostelium discoideum</i>
SC	<i>Saccharomyces cerevisiae</i>
MT	<i>Methanobacterium thermoautotrophicum</i>

Domain and Motif Identification

A Hidden Markov model (HMM) (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. (1994). Hidden Markov models in computational biology: Applications to protein modeling. J. Mol. Biol., 235:1501-1531) was used to identify, both catalytic and extracatalytic domains. Table 4 shows extra-catalytic domains that were identified using the HMM program. Other domains such as coiled-coil and pest motifs were identified as described next.

Potential coiled-coil domains were identified using the COILS program (www.ch.embnet.org/software/COILS_form.html). The matrix used was MTIDK with windows of 14, 21, 28 amino acids. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region.

Protein sequences containing potential pest motifs were identified using the program PESTfind (www.at.embnet.org/embnet/tools/bio/PESTfind/). PEST regions in proteins are by definition sequences that tend to be rich in proline, glutamic or aspartic acid, arginine and histidine; they have been associated with increased protein turnover rates (Rogers S. *et al.* (1986) Science 234, 364-368. The algorithm defines PEST sequences as hydrophilic stretches of amino acids greater than or equal to 12 residues in length. Such regions contain at least one P, one E or D and one S or T. They are flanked by lysine (K), arginine (R) or histidine (H) residues, but positively charged residues are disallowed within the PEST sequence. PESTfind produces a score ranging from about -50 to +50. By definition, a score above zero denotes a possible PEST region; a value greater than +5 defines a high probability that there is a PEST domain.

Identification of potential coiled-coil domains and PEST domains in N34132

Potential coiled-coil domains were identified in N34132 (SEQ ID NO:183) using the COILS program. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region. The amino acid positions within N34231 scoring for potential coil-coil regions are shown below.

Table 11 coiled-coil domains predicted for N34132

Coiled-coil Region	Amino acid range	Length (aa)
1	124-147	24
2	437-451	15
3	495-526	32
4	1,723-1,749	27

Potential PEST domains were identified in N34132 using PESTfind, a value greater than +5 defines a high probability that there is a PEST domain. The amino acid positions within N34132 scoring for potential PEST regions are shown below.

Table 12 Potential Pest domains identified in N34132

PEST Region	Score	Amino acid range	Amino Acid Length
1	+ 4.91	54-95	42
2	+11.4	537-570	34
3	+31.08	1293-1304	12
4	+10.15	1543-1565	23
5	+ 6.17	1698-1732	35

EXAMPLE 2. Chromosomal Localization of Novel Mammalian Protein Kinases

Materials and Methods

Several sources were used to find information about the chromosomal localization of each of the genes described in this patent. First, the accession number for the nucleic acid sequence was used to query the Unigene database. The site containing the Unigene search engine is: <http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html>. Information on map position within the Unigene database is imported from several sources, including the Online Mendelian Inheritance in Man (OMIM, <http://www.ncbi.nlm.nih.gov/Omim/searchomim.html>), The Genome Database (<http://gdb.infobiogen.fr/gdb/simpleSearch.html>), and the Whitehead Institute human physical map (http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts_info?database=release). For example, searching Unigene with W56561, an EST for a MAK-like kinase, the

following information is retrieved: Chr.14, D14S65-qTEL. The location of this gene on an "ideogram" of the cytogenetic map of chromosome 14 is also provided, showing that W56561 maps to the bottom of chromosome 14, between 14q31 and 14qTel. If Unigene has not mapped the EST, then the nucleic acid for the gene of interest is used as a query against databases, such as dbsts and htgs (described at http://www.ncbi.nlm.nih.gov/BLAST/blast_databases.html) containing sequences that have been mapped already. The nucleic acid sequence is searched using BLAST-2 at NCBI (<http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast>) and is used to query either dbsts or htgs. In addition to the Whitehead and GDB sites mentioned above, Stanford University maintains a useful site for chromosomal mapping from STS data (<http://www-shgc.stanford.edu/RH/rhserverformnew.html>). Matches in htgs are often resolved immediately because the genomic region hit is annotated in the htgs entry. If an exact match match is found (defined roughly as 99% identity over a region of about 100 base pairs or longer, excluding any repetitive sequence), then the mapped position of the entry in the database is assigned to the original kinase query. Once a cytogenetic region has been identified by one of these approaches, disease association is established by searching OMIM (see above for URL) with the cytogenetic location. OMIM maintains a searchable catalog of cytogenetic map locations organized by disease. A thorough search of available literature for the cytogenetic region is also made using Medline (<http://www.ncbi.nlm.nih.gov/PubMed/medline.html>). References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123.

Results

The chromosomal location for 37 of the 110 novel protein kinases is shown on Table 1. Three of the novel protein kinases were mapped to regions associated with cancer amplicons, as shown on this table. The regions were also cross-checked with the Mendelian Inheritance in Man database, which tracks genetic information for many human diseases, including cancer. References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123. Association of these mapped regions with other diseases is

documented in the Online Mendelian Inheritance in Man (OMIM)
(<http://www.ncbi.nlm.nih.gov/htbin-post/Omim>).

EXAMPLE 3: Generation of Specific Immunoreagents

5 Materials and Methods

Peptide sequences to extra-catalytic regions of novel kinases are chosen which are not homologous to other known kinases based on a Smith Waterman homology search against the non-redundant protein database and predicted to be antigenic based on the DNASTar Protean program. These peptides are conjugated to KLH using Glutaraldehyde.

10 Rabbits are immunized with the KLH-peptide conjugates by four injections three weeks apart. The rabbits are bled ten and fourteen days following the third injection and bled out ten days after the fourth. The serum is checked against the peptide by ELISA.

Table 13. Peptides to be used as immunogens for raising antibodies

Clone Name	SEQ ID NO (aa)	Peptide Sequence	Amino Location
AA8256850	124	KSRDNSRDSSQSEND	339-353
		TEKLRKSQDLPREPLP	372-386
		RGWRPYDIHS	223-232
5R79-46-1	126	FEGPRRNKEVMYK	224-236
		KDDYNETVHKKTE	451-463
		GTHPKDRNVEKLQ	541-553
		EVSKYQEYTNELQET	643-657
AA256100	129	IDDTSNFDDFPESDI	405-419
		TEPDYKSKDWVFL	427-439
		EEKKLRRSQHARKET	61-75
AA210825	130	SNKDTLRKRHYWRLD	507-521
		RHTTRKSSTTLRE	488-500
		FQNNTTNRYEKEIPL	528-542
		GKHRKTGRDVAVK	668-680
		FPTKQESQLRNE	687-698

AA316804	132	ESHVHQEPSKRIPS	239-252
		HTKRKSSTMVKEGW	409-422
		PSDLDERDEEAVK	375-388
		SPGQGKDHKDLSTSI	543-557
R47805	143	EPVGRWDQDYDRAVL	44-58
		KPKGPGGKRGHKRLI	325-339
		PTDVAQLPSRVPRDA	219-233
AA234451	167	DPDFWEKTGNDGSLT	293-307
		HPRPQEKDVWEE	374-385
		RENTDEVFPDEQLSD	340-354
		RSEITQPDRDIPLVR	427-441
AA460132	180	LKSYSTSSKKARPVL	222-236
		KKLDEVRLRGRKRSM	237-251
		ETEKTAQGLSNLAKT	131-145
N34132	183	SGRRRRPTKSKGSKS	1848-1862
		PGTAPSKPPLTKAPV	1474-1488
		VSDTQPKAPGIDD	1365-1378
		AHSLDKTSHSSTTGL	1253-1267
5R69-17-2	187	GTTREKTDREVKST	178-190
		HSEAPELHGKIRSSN	138-152
		DETVTPPQFSIV	87-98
		QYDVKSEIYS	204-213
AA278842	206	TVDPEKSVRDQAFKA	515-529
		DSSTADRWDDWGS	637-651
		SVSEDPTQLEEVEKD	539-553
AA836348	232	NAPTKRPRSSTVTEA	323-337
		LDSEEDYYTPQKVDV	514-528
		GDKASYRQPKHVEKL	409-423

EXAMPLE 4. Expression analysis of Novel Mammalian Protein KinasesGENE EXPRESSION ANALYSIS

Tissue Arrays

“cDNA libraries” derived from a variety of sources were immobilized onto nylon
5 membranes and probed with ³²P-labeled cDNA fragments derived from the gene(s) of
interest.

Total RNA or mRNA was used as template in a reverse transcription reaction to
generate single-stranded cDNAs (ss cDNA) that were tagged with specific sequences at
each end. An oligo dT primer containing a specific sequence (CDS:

10 AAGCAGTGGTAACAACGCAGAGTACT30VN (V=A,G,C N=A,G,C,T)) anneals at
the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV
RnaseH-) transcribes the antisense strand until it reaches the end of the RNA strand when
it adds additional C residues. If a primer (SMII:

AAGCAGTGGTAACAACGCAGAGTACGCGGG or ML2G:

15 AAGTGGCAACAGAGATAACGCGTACGCGGG) ending with 3 Gs is added, it anneals
to the added Cs and the MMLV recognizes the rest of the primer sequence as template and
continues transcription. As a result, the synthesized cDNAs contain specific sequence tags
at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same
sequence (CDS and SMII) it is referred to as “symmetric.” When the 5' end is tagged
20 with a different sequence than the 3' end (CDS and ML2G) is referred to as “asymmetric”
A double-stranded “cDNA library “ is then generated by PCR amplification using the
3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT and ML2:
AAGTGGCAACAGAGATAACGCGT) that anneal to the added sequence tags.

The amplified “cDNA libraries” were manually arrayed onto nylon membranes
25 with a 384 pin replicator. The DNA was denatured by alkali treatment, neutralized and
cross-linked by UV light. The arrays were pre-hybridized with Express Hyb (Clontech)
and hybridized with ³²P labeled probes generated by random hexamer priming of cDNA
fragments corresponding to the genes of interest. After washing, the blots were exposed to
phosphorimaging cassettes and the intensity of the signal was quantified. The amount of
30 the DNA on the arrays was also quantified by treating non-denatured or denatured arrays
with Syber Green I or Syber Green II respectively (1:100,000 in 50mM Tris, pH8.0) for 2
minutes. After washing with 50mM Tris, pH8.0, the fluorescent emission was detected

with a phosphorimager (Molecular Dynamics) and quantified. The amount of the arrayed DNA was used to normalize the hybridization signal and the corrected values are tabulated in Table 3.

5 Results

The results of the microarray expression analysis of the protein kinases presented in this application is shown in Table 3. Data presentation from left to right is as follows: "Tissue": tissue type of the cDNA; "Tumor sym", indicates that the tissue is derived from a tumor, "sym" refers to the fact that the 5' and 3' primers used to make the sample are the same; "Normal Sym", indicates normal tissue was used to make the sample, with symmetric primers as described above; "Tumor 1o", indicates that primary tumor tissue was used to make the cDNA; "Tumor cells", indicates that these cDNA samples were made from cultured tumor cells; "Normal", indicates that these samples are derived from normal tissue or cell lines; "Endos", indicates that these samples are derived from endothelium-related tissue sources; "p53" refers to the status, mutant or wild-type, of the p53 gene in the source samples. Normalized expression values are presented for each gene referred to by its SEQ ID# on the subsequent columns. Genes represented in expression Table 3 are: SEQ ID NO:3 (AA826850), SEQ ID NO:5 (TBK1), SEQ ID NO:6 (AA305176), SEQ ID NO:8 (AA256100), SEQ ID NO:9 (CAB43292), SEQ ID NO:11 (EPK2), SEQ ID NO:12 (PKNbeta), SEQ ID NO:14 (H19102), SEQ ID NO:16 (RSK4), SEQ ID NO:17 (AAD30182), SEQ ID NO:20 (SGK2), SEQ ID NO:22 (PTK9L), SEQ ID NO:26 (AA383293), SEQ ID NO:29 (DRAK2), SEQ ID NO:31 (DRAK1), SEQ ID NO:032 (AA015726), SEQ ID NO:40 (MAK-V), SEQ ID NO:044 (TRAD), SEQ ID NO:044 (TRAD), SEQ ID NO:45 (AA454060), SEQ ID NO:47 (AA234451), SEQ ID NO:48 (AA436054), SEQ ID NO:49 (AA626859), SEQ ID NO:51 (KIAA0904), SEQ ID NO:52 (AA789239), SEQ ID NO:54 (CCRK), SEQ ID NO:55 (CLK4), SEQ ID NO:56 (AA557536), SEQ ID NO:57 (W56561), SEQ ID NO:60 (AA579641), SEQ ID NO:63 (NEK7), SEQ ID NO:66 (CAMKKB), SEQ ID NO:68 (HIPK2), SEQ ID NO:72 (R19609), SEQ ID NO:73 (HRI), SEQ ID NO:78 (AA088547), SEQ ID NO:79 (AA449542), SEQ ID NO:082a (MLK4), SEQ ID NO:82 (MLK4b), SEQ ID NO:84 (RIP4), SEQ ID NO:88 (AA278842), SEQ ID NO:89 (AA195964), SEQ ID NO:90 (MSSK1), SEQ ID NO:93 (TSK4), SEQ ID NO:94 (AI025291), SEQ ID NO:95

(AA948538), SEQ ID NO:96 (AA905446), SEQ ID NO:97 (H85389), SEQ ID NO:100 (AA018361), SEQ ID NO:101 (AA311714), SEQ ID NO:110 (AA452647), SEQ ID NO:111 (AA310219), SEQ ID NO:112 (AJ086865), SEQ ID NO:114 (MEKK6), and SEQ ID NO:116 (SuRTK106).

5

EXAMPLE 5. Kinase assays for Erk, JNK1 and p38 MAP kinases

293T cells were transiently transfected with HA- p38 or co-transfected with Flag-tagged wt MLK4A, kinase-dead MLK4A, wild-type MLK4B or kinase-dead MLK4B using Lipofectamine 2000 (Lifetech). Cells were lysed 36 hr post-transfection. Cell lysates normalized to contain equivalent amounts of HA-p38 were immunoprecipitated with anti-HA antibody (Mab HA-11, Babco). Immunoprecipitates were split in two portions, one portion was Western-blotted with anti- HA antibody and the other with a phospho-specific p38 antibody (Promega) to detect activated levels of p38. Activation of Erk1 and Jnk1 was measured similarly. (This example applies to AA232253 (SEQ ID NO:82, SEQ ID NO:201).)

15

Results:

In transient assays wild-type MLK4A and MLK4B (but not kinase-inactive MLK4A(K45M) or MLK4B(K45M)) activate Erk, JNK1 and p38 MAP kinases.

20 EXAMPLE 6. RAC1 guanine-exchange factor assay

293T cells were transiently transfected with HA-Rac1 or co-transfected with Flag-tagged Duet C, Duet E, Dbl and HA-Tiam-1. Cells were lysed 36 hour post-transfection. Cell lysates normalized to contain equivalent amounts of Rac1 were affinity precipitated with immobilized GST-PBD (p21-binding domain of Pak3). Bound proteins were Western blotted and probed with anti-HA antibody to detect levels of activated Rac1. ((This example applies to R199772 (Trad/Duet)(SEQ ID NO:44, SEQ ID NO:164).)

25

Results:

Duet C and Duet E both act as guanine nucleotide exchange factors on Rac1.

CONCLUSION

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

In particular, although some formulations described herein have been identified by the excipients added to the formulations, the invention is meant to also cover the final formulation formed by the combination of these excipients. Specifically, the invention includes formulations in which one to all of the added excipients undergo a reaction during formulation and are no longer present in the final formulation, or are present in modified forms.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush

group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

Other embodiments are within the following claims.

What is claimed is:

CLAIMS

1. An isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ
5 ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ
ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ
ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ
ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ
ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ
10 ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ
ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ
ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ
15 ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ
20 ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ
ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ
25 ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ
ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ
ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ
ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) is the complement of the nucleotide sequence of (a);

(c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide;

(d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(e) is the complement of the nucleotide sequence of (d);

(f) encodes a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, wherein said domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(g) is the complement of the nucleotide sequence of (f);

(h) encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID

NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, further comprising a vector or promoter effective to initiate transcription in a host cell.

4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

5. The nucleic acid molecule of claim 4, wherein said mammal is a human.

6. A nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of
5 SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,
10 SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

30

7. The probe of claim 6, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

8. A recombinant cell comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

9. The cell of claim 8, wherein said polypeptide is a fragment of a protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

10. An isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, 5 SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, 10 SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, 15 SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, 20 SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, 25 SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

12. The polypeptide of claim 10, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
5 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
10 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
15 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
20 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

13. The kinase polypeptide of claim 10, wherein said polypeptide is isolated, purified, or enriched from a mammal.

14. The kinase polypeptide of claim 13, wherein said mammal is a human.

15. The kinase polypeptide of claim 10, wherein said polypeptide is a AA144574, AA116841, AA256100, AA305176, AA210825, AA316804, AA980090, N42050, AA476563, AA626690, AA960957, H19102, AA045601, AA107515, AA109508 or AA887783 polypeptide.

16. The kinase polypeptide of claim 10, wherein said polypeptide is a H60215, AA197883, AA297313, W30246, AA172300, AA383293, AA542015, H01248, N23936, W44160, 2R22-5-11, 5R72-18-1, AA021445, AA207220, AA426580, AA544838, W90839, 5R79-54-1, AA839940, R19772 or 5R72-8-2 polypeptide.

17. The kinase polypeptide of claim 10, wherein said polypeptide is a AA234451 polypeptide.

18. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R65-16-1, AA061797, AA065538, AA124976, AA397553, AA435956, AA575635, AA626859, AA789239, AI086865, H17727, H29974, AA557536 or N28606 polypeptide.

19. The kinase polypeptide of claim 10, wherein said polypeptide is a AA631990 or W08549 polypeptide.

20. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R72-16-2, R19927 or R43524 polypeptide.

21. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R57-10-2 polypeptide.

5 22. The kinase polypeptide of claim 10, wherein said polypeptide is a AA232253 polypeptide.

23. The kinase polypeptide of claim 10, wherein said polypeptide is a AA430250, AA836348, R86668 or N34132 polypeptide.

10 24. The kinase polypeptide of claim 10, wherein said polypeptide is a AA098024 or SuRTK106 polypeptide.

25. The kinase polypeptide of claim 10, wherein said polypeptide is a R47805, AA099102, AA589241, H85811, AA013524, AA452647, AA840598, AA088547, AA139478, AA826850, R87679, W65887, H97685, W20810, AA599286, AA425725, AA103218, AA711829, AA060026, AA399669, AA758539, AA883975, AA948538, 15 AA018361, AA215311, AA311714, AA498104, 5R69-17-2, 5R69-23-3, 5R69-26-2, AA118352, AA396601, AA671275, AA278842, AA460132 or H05721 polypeptide.

26. An antibody or antibody fragment having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

27. The antibody or antibody fragment of claim 26, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
5 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
10 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
15 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
20 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID
NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID
5 NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
10 NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID
NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting
of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a
proline-rich region, a coiled-coil structure region, and a C-terminal tail.

28. A hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

29. A method for identifying a substance that modulates kinase activity comprising:

(a) contacting a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,

SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,
 SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,
 SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151,
 SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,
 5 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,
 SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,
 SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,
 SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
 SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
 10 SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
 SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
 SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
 SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
 SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
 15 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
 SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
 SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
 SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
 20 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
 SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
 and SEQ ID NO:242 with a test substance;

(b) measuring the activity of said polypeptide; and

(c) determining whether said substance modulates the activity of said

polypeptide.

30. A method for identifying a substance that modulates kinase activity in a cell comprising:

(a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID

NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID
NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID
NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
5 NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID
10 NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID
NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID
15 NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID
20 NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

- (b) adding a test substance to said cell; and
- (c) monitoring a change in cell phenotype or the interaction between
said polypeptide and a natural binding partner.

31. A method for treating a disease or disorder by administering to a patient in need of such treatment a substance that modulates the activity of a kinase selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

32. The method of claim 31, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

33. The method of claim 31, wherein said substance modulates kinase activity *in vitro*.

34. The method of claim 33, wherein said substance is a kinase inhibitor.

35. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

- (a) contacting said sample with a nucleic acid probe which hybridizes
5 under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
10 SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
15 SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
20 SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
25 SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
30 SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding said polypeptide, fragments thereof, or the complements of said sequences and fragments; and

(b) detecting the presence or amount of the probe:target region hybrid as an indication of said disease.

36. The method of claim 35, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease,
5 neurodegenerative disorders, and cancer.

37. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) comparing a nucleic acid target region encoding said kinase polypeptide in a sample, wherein said kinase polypeptide is selected from the group
10 consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ
15 ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ
20 ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ
25 ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ
30 ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ

ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding said kinase polypeptide, or one or more fragments thereof; and

- 5 (b) detecting differences in sequence or amount between said target region and said control target region, as an indication of said disease or disorder.

38. The method of claim 37, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

Table 1 (cont'd)

Gene Name	SP	Prov	Sex	D	NA	Prov	Sex	D	NA	SEQ ID # 1	SEQ ID # 2	SEQ ID # 3	Family	Group	Length NA	Length AA	ORF Start	ORF End	ORF Length	DNA Repeats	C-H Localization
BCON3 h	H									184	64	184	Other	CRC2 ca	2164	516	113	1717	1608	245-267	NA
AA111829 m	M									184	65	184	Other	CRC2 ca	1568	376	1	1717	1608	245-267	NA
AA091072 h CAMKKB	H									184	66	184	Other	CAMKKB	1787	388	1	1784	1784	95-84	12323-q14
SRBP 17.2 h	H									184	67	184	Other	CTRI	3387	241	1850	1784	1784	95-84	12323-q14
TRB811 h	H									184	68	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA02163 h DYRK3	H									184	69	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA09241 m DYRK3	M									184	70	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
SR72 16.2 h R19827 h	H									184	71	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA3324 h R1 h R19809	H									184	72	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
17000057619467 h	H									184	73	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA013524 m	M									184	74	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
17000138801187 h IRAKM	H									184	75	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA040590 m IRAKM	M									184	76	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA08547 h	H									184	77	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
HGP 0044468	H									184	78	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA44542 m	M									184	79	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
5557 10.2 m TESK2 m	M									184	80	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA33253 h	H									184	81	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA375137 h	H									184	82	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
H97865 h	H									184	83	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
W20810 m	M									184	84	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA144235 h	M									184	85	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA052250 h	H									184	86	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA278642 h	H									184	87	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA569288 h	H									184	88	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA26725 h	M									184	89	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
SGK022 h	H									184	90	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA090020 m SGK022 m	M									184	91	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA390869 h	H									184	92	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA683075 h	H									184	93	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA605448 h	H									184	94	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
H28874 h	H									184	95	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA488104 m H28874 m	M									184	96	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA215311 h	H									184	97	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA018391 h	H									184	98	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA311714 h	H									184	99	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
SGK384 h	H									184	100	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA310451 m SGK384 m	M									184	101	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
SGK071 h	H									184	102	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA118357 m SGK071 m	M									184	103	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
0186539 h	H									184	104	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA396081 m	M									184	105	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA671275 h VRK3	H									184	106	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
ST1575 m VRK3 m	M									184	107	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA442624 h VRK3 m	M									184	108	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
H3721 h	H									184	109	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA08885 h	H									184	110	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA039348 h	H									184	111	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
RA6868 h MOKB	H									184	112	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
PAK3 h 5595-20-11	H									184	113	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
SURTK106 h 2541-p4 h	H									184	114	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
AA098024 m	M									184	115	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
SGK384 h	H									184	116	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
H09650 h CORK	H									184	117	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14
NM 007170 h TESK2	H									184	118	184	Other	DYRK	3387	241	1850	1784	1784	95-84	12323-q14

Table 2

	Patent	Seq	SP ID# na	Family	Group	nraa	Length aa	match aa	ID	% Identity	% Similar	nraa	Match ACC#	Description	Kinase Domain(s) start	Kinase Domain(s) end	Profile start	Profile end
H 1	122	AGC	GRK	GRK	2.76-314	688	687	100	100	100	100	CAB45657.1	BAR22 [Homo sapiens]	Adrenic receptor kinase, beta 2 (G-protein-linked receptor kin	191	453	1	281
M 2	123	AGC	GRK	GRK	1.30E-108	378	371	98	98	98	98	NP 037029.1	Adrenic receptor kinase, beta 2 (G-protein-linked receptor kin	3	143	121	281	
H 3	124	AGC	GRK	GRK	5.80E-106	419	282	71	88	88	88	CAB78471.1	Serine/threonine protein kinase [Homo sapiens]	28	286	1	281	
H 4	125	AGC	GRK	GRK	1.40E-137	414	414	100	100	100	100	CAB78471.1	Serine/threonine protein kinase [Homo sapiens]	23	283	1	281	
H 5	126	AGC	GRK	GRK	0	729	729	100	100	100	100	NP 037388.1	TANK-binding kinase 1 [Homo sapiens]	9	304	1	281	
H 6	127	AGC	GRK	GRK	1.20E-98	329	73	46	66	66	66	BA076817.1	KIAA0973 protein [Homo sapiens]	35	310	1	281	
M 7	128	AGC	GRK	GRK	1.30E-19	84	42	48	71	71	71	AA75594.1	CG7719 gene product [Drosophila melanogaster]	24	44	242	281	
H 8	128	AGC	GRK	GRK	6.10E-181	484	483	100	100	100	100	BA07808.1	KIAA0985 protein [Homo sapiens]	90	383	1	281	
H 9	130	AGC	GRK	GRK	8.90E-100	978	615	67	80	80	80	NP 002733.1	Protein kinase C, mu [Homo sapiens]	651	907	1	281	
H 10	131	AGC	GRK	GRK	1.10E-10	105	42	42	57	57	57	P05127	Protein kinase C, BETA-1 TYPE PKC-BETA-2) [Homo sapiens]	19	24	256	281	
H 11	132	AGC	GRK	GRK	0	880	880	100	100	100	100	NP 005804.1	Protein kinase C, nu [Homo sapiens]	578	832	1	281	
H 12	133	AGC	GRK	GRK	9.4E-319	889	889	100	100	100	100	NP 037487.1	PKNbeta [Homo sapiens]	559	818	1	281	
M 13	134	AGC	GRK	GRK	1.20E-108	205	204	100	100	100	100	JC7083	Protein kinase N beta [Homo sapiens]	1	134	128	281	
H 14	135	AGC	GRK	GRK	3.80E-12	384	94	38	55	55	55	AA032485.1	Ribosomal protein S6 kinase 3 [Homo sapiens]	81	333	1	281	
H 15	136	AGC	GRK	GRK	2.80E-257	489	489	100	100	100	100	NP 036558.1	Ribosomal protein S6 kinase, 62kD, polypeptide 1 [Homo sapien	225	459	1	281	
H 16	137	AGC	GRK	GRK	7.00E-178	745	745	100	100	100	100	NP 035531.1	Ribosomal protein S6 kinase, 90kD, polypeptide 6 [Homo sapien	73 & 428	330 & 683	1	281	
H 17	138	AGC	GRK	GRK	9.80E-222	549	549	100	100	100	100	AA030182.1	Unknown [Homo sapiens]	153	539	1	281	
H 18	139	AGC	GRK	GRK	9.20E-103	431	430	100	100	100	100	AA041081.1	SGK [Homo sapiens]	98	355	1	281	
M 19	140	AGC	GRK	GRK	2.80E-157	430	429	99	99	99	99	NP 035491.1	Serum glucocorticoid regulated kinase [Mus musculus]	88	354	1	281	
M 20	141	AGC	GRK	GRK	2.00E-76	244	244	100	100	100	100	AAF12757.2	Protein kinase [Homo sapiens]	1	169	24	281	
H 21	142	AGC	GRK	GRK	4.10E-211	448	375	88	88	88	88	AAF27051.1	SGK-like protein SGK [Homo sapiens]	182	369	1	281	
H 22	143	AGC	GRK	GRK	5.80E-218	349	349	100	100	100	100	NP 009215.1	Protein tyrosine kinase 9-like (A8-related protein) [Homo sapien	10	17	253	281	
H 23	144	CAMK	DAPK	DAPK	1.40E-19	440	68	39	61	61	61	CA04119.1	Phosphatase [Homo sapiens]	40	333	1	281	
H 24	145	CAMK	DAPK	DAPK	1.50E-165	999	488	65	77	77	77	O15075	DCAMK1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1	398	625	1	281	
M 25	146	CAMK	DAPK	DAPK	1.80E-62	297	199	67	83	83	83	AAF28875.1	CPG16 [Mus musculus]	59	297	1	281	
H 26	147	CAMK	DAPK	DAPK	2.80E-48	708	181	44	60	60	60	O15075	DCAMK1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1	415	673	1	281	
M 28	148	CAMK	DAPK	DAPK	2.80E-31	806	147	55	73	73	73	AAF26975.1	CPG16 [Mus musculus]	514	771	1	281	
H 29	149	CAMK	DAPK	DAPK	3.10E-121	372	372	100	100	100	100	NP 004217.1	Death-associated protein kinase-related 2	33	293	1	281	
M 30	150	CAMK	DAPK	DAPK	7.90E-93	372	340	91	95	95	95	NP 004217.1	Death-associated protein kinase-related 2	32	293	1	281	
H 31	151	CAMK	DAPK	DAPK	1.20E-113	414	414	100	100	100	100	NP 004751.1	Death-associated protein kinase-related 1	61	321	1	281	
H 32	152	CAMK	DAPK	DAPK	5.80E-185	1311	1053	80	80	80	80	BA07843.1	KIAA0989 protein [Homo sapiens]	8	258	1	281	
H 33	153	CAMK	DAPK	DAPK	1.20E-45	438	153	51	70	70	70	T22427	Hypothetical protein F40C5.4 - [Caenorhabditis elegans]	74	325	1	281	
H 34	154	CAMK	DAPK	DAPK	1.40E-32	438	122	48	65	65	65	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	56	307	1	281	
M 35	155	CAMK	DAPK	DAPK	1.30E-184	729	728	100	100	100	100	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	56	340	1	281	
H 36	156	CAMK	DAPK	DAPK	3.50E-128	462	462	100	100	100	100	AAC33487.1	R31237.1, partial CDS [Homo sapiens]	999	1258	1	281	
M 37	157	CAMK	DAPK	DAPK	0	1330	1235	100	100	100	100	BA008484.1	KIAA0135 gene, related to pim-1 oncogene, [Homo sapiens]	20	158	23	281	
H 38	158	CAMK	DAPK	DAPK	5.10E-59	230	183	79	85	85	85	BA008484.1	KIAA0135 gene, related to pim-1 oncogene, [Homo sapiens]	1	158	23	281	
H 39	159	CAMK	DAPK	DAPK	3.00E-111	928	838	100	100	100	100	BA008484.1	KIAA0135 gene, related to pim-1 oncogene, [Homo sapiens]	20	158	23	281	
H 40	160	CAMK	DAPK	DAPK	7.30E-60	628	387	57	69	69	69	NP 055655.1	KIAA0537 gene product [Homo sapiens]	53	304	1	281	
H 41	161	CAMK	DAPK	DAPK	1.40E-244	714	714	100	100	100	100	NP 055401.1	Hormonally upregulated neu tumor-associated kinase [Homo sa	61	320	1	281	
H 42	162	CAMK	DAPK	DAPK	8.20E-76	874	211	83	80	80	80	AA073198.1	Skeletal muscle myosin light chain kinase [Homo sapien	570	825	1	281	
M 43	163	CAMK	DAPK	DAPK	0	2288	2227	100	100	100	100	AA073198.1	Skeletal muscle myosin light chain kinase [Homo sapien	820 & 1088	873 & 1356	1	281	
H 44	164	CAMK	DAPK	DAPK	7.80E-37	127	67	99	99	99	99	BA092535.1	KIAA1297 protein [Homo sapiens]	3	78	188	281	
H 45	165	CAMK	DAPK	DAPK	5.00E-20	514	114	41	63	63	63	NP 009995.1	STK with DBP- and pleckstrin homology domains [Homo sapiens]	985	1239	1	281	
H 46	166	CAMK	DAPK	DAPK	3.30E-89	508	181	53	65	65	65	P25323	MLCK [Dictyostellium discoideum]	116	381	1	281	
H 47	167	CAMK	DAPK	DAPK	8.80E-98	478	188	57	68	68	68	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	34	313	1	281	
H 48	168	CAMK	DAPK	DAPK	9.80E-39	268	138	62	79	79	79	NP 038527.1	PFTAIRE protein kinase 1 [Homo sapiens]	21	471	1	281	
H 49	169	CAMK	DAPK	DAPK	7.10E-48	247	146	59	75	75	75	NP 004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sa	1	218	23	281	

Table 2 (cont'd)

M 50	170	CMGC	CDK	2.90E-64	288	193	65	78	NP 004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	240	24	261
H 51	171	CMGC	CDK	1.10E-284	1490	1490	100	100	AAF38401.1	CDC2-related protein kinase 7 [Homo sapiens]	21	1020	1	261
H 52	172	CMGC	CDK	9.20E-101	534	377	82	82	AAF38509.1	NKIATRE [Homo sapiens]	4	385	1	261
M 53	173	CMGC	CDK	1.40E-128	337	225	92	92	AAF34871.1	NKIATRE alpha [Rattus norvegicus]	1	28	235	261
M 54	174	CMGC	CDK	3.00E-48	211	159	79	84	NP 038251.1	Cell cycle related kinase [Homo sapiens]	1	183	134	261
H 55	175	CMGC	CLK	1.50E-242	499	438	91	83	NP 031740.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	177	493	1	261
H 56	176	CMGC	RCK	9.10E-89	544	343	57	84	AAD12719.1	Extracellular signal-regulated kinase 7: ERK7 [Rattus norvegicus]	13	305	1	261
H 57	177	CMGC	RCK	2.30E-189	419	419	100	100	NP 055041.1	Renal tumor antigen [Homo sapiens]	4	285	1	261
H 58	178	CMGC	RCK	1.50E-180	832	832	100	100	AAF37278.1	Intestinal cell kinase [Homo sapiens]	4	284	1	261
H 59	179	CMGC	RCK	1.80E-79	413	198	60	77	P20969	MLCK [Rattus norvegicus]	109	364	1	261
H 60	180	Microb	PK	2.50E-45	253	102	46	67	AAF50799.1	CG10873 gene product [Drosophila melanogaster]	101	187	85	147
H 61	181	Other	C28C2	2.30E-158	509	258	100	100	CAB70864.1	Hypothetical protein [Homo sapiens]	2	187	1	261
M 62	182	Other	C28C2	1.60E-152	281	243	94	98	CAB70864.1	Hypothetical protein [Homo sapiens]	59	86	235	261
H 63	183	Other	C28C2	6.70E-300	1952	1193	99	99	NP 056635.1	KIAA0344 gene product [Homo sapiens]	221	479	1	261
H 64	184	Other	C28C2	1.10E-254	535	535	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	73	327	1	261
M 65	185	Other	C28C2	2.50E-208	378	372	98	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	170	85	261
H 66	186	Other	CAMKK	3.80E-148	588	588	100	100	AAD31507.1	Ca2+/calmodulin-dependent protein kinase beta [Homo sapiens]	165	448	1	261
H 67	187	Other	CTRI	9.90E-24	287	87	33	52	QJ1743	Hypothetical 33.5K protein - rab5 fibrona virus	24	285	1	261
H 68	188	Other	DYRK	0	1171	1137	97	98	AAD32568.1	Nuclear body associated kinase 1a [Mus musculus]	199	527	1	261
H 69	189	Other	DYRK	2.10E-280	563	553	100	100	NP 035773.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	174	467	1	261
M 70	190	Other	DYRK	2.30E-95	168	149	90	98	NP 035773.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	76	103	235	261
H 71	191	Other	EIFK	0	1649	1493	90	96	NP 038747.1	GCN2 eIF2alpha kinase [Mus musculus]	280 & 590	539 & 1001	1	261
H 72	192	Other	EIFK	1.50E-220	630	630	100	100	NP 055228.1	Heme-regulated initiation factor 2-alpha kinase [Homo sapiens]	167	583	1	261
M 73	193	Other	Endop	2.50E-45	253	102	46	67	AAF50799.1	CG10873 gene product [Drosophila melanogaster]	101	187	85	147
M 74	194	Other	Endop	3.70E-45	216	100	45	94	AAF50799.1	CG10873 gene product [Drosophila melanogaster]	116	150	116	147
M 75	195	Other	IRAK	0	596	596	100	100	NP 009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	185	443	1	261
H 76	196	Other	IRAK	1.20E-170	392	293	75	85	NP 009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	1	239	19	261
H 77	197	Other	IRE	1.5e-323	922	746	82	89	NP 036148.1	Irf1, inhibitor-requirement 1 gene [Mus musculus]	516	777	1	261
H 78	198	Other	KYK2	8.70E-40	225	102	45	62	AAF48758.1	CG8173 gene product [Drosophila melanogaster]	32	318	1	261
M 79	199	Other	KYK2	5.90E-32	280	109	32	50	AAF48758.1	CG8173 gene product [Drosophila melanogaster]	12	268	1	261
M 80	200	Other	LINK	2.90E-17	41	37	92	95	NP 009101.1	Irf1a-specific kinase 2 [Homo sapiens]	12	39	101	128
H 81	201	Other	MLK	2.50E-282	800	799	100	100	AAD63490.1	Mixed lineage kinase [Homo sapiens]	16	259	1	261
H 82	202	Other	MLK	8.60E-251	835	835	100	100	AAD29632.1	Puative protein-tyrosine kinase [Homo sapiens]	463	723	1	261
H 83	203	Other	RIP	2.20E-158	634	385	100	100	BAA32317.1	KIAA0472 protein [Homo sapiens]	357	620	1	261
M 84	204	Other	RIP	5.30E-158	289	288	100	100	AAF03133.1	Receptor interacting protein 3 [Mus musculus]	7	27	181	202
H 85	205	Other	SCY1	0	688	688	100	100	CAB55300.1	Hypothetical protein [Homo sapiens]	57	83	50	76
H 86	206	Other	SCY1	1.70E-209	505	354	98	98	BAA9298.1	KIAA1360 protein [Homo sapiens]	32	327	1	261
H 87	207	Other	SLOB7	2.20E-157	808	398	45	61	AAF58933.1	CG1973 gene product [Drosophila melanogaster]	85	131	47	116
H 88	208	Other	SLOB7	7.40E-188	849	849	100	100	BAA91097.1	Unnamed protein product [Homo sapiens]	230	305	81	143
H 89	209	Other	SRPK	5.80E-252	533	533	100	100	NP 055185.1	Serine/threonine kinase 22A [Homo sapiens]	10	285	1	261
H 90	210	Other	STK22A	3.80E-53	268	122	46	70	NP 033481.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	25	280	1	261
H 91	211	Other	STK22	2.70E-52	268	122	46	68	NP 033481.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	12	272	1	261
H 92	212	Other	STK22A	4.80E-16	292	112	45	64	NP 033481.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	12	272	1	261
H 93	213	Other	STK22A	5.10E-123	358	322	90	96	NP 033481.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	25	280	1	261
H 94	214	Other	TSK	2.10E-33	273	122	46	62	NP 033481.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	12	272	1	261
H 95	215	Other	TSK	2.50E-32	216	93	41	58	NP 033481.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	1	213	7	261
H 96	216	Other	UNC	0.000082	333	57	36	56	AAD32787.1	Puative protein kinase [Arabidopsis thaliana]	1	329	1	261
H 97	217	Other	UNC	0.002492	412	53	37	52	BAA77341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	80	408	1	261
H 98	218	Other	UNC	0.001098	341	50	36	58	BAA77341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	8	340	1	261
H 99	219	Other	UNC	1.90E-88	480	247	100	100	T17265	Hypothetical protein DKF2p343C131.1 - human (fragment)	57	313	1	261
H 100	220	Other	UNC	1.80E-208	565	468	96	96	BAA81270.1	Unnamed protein product [Homo sapiens]	4	265	1	261
H 101	221	Other	Unique	6.70E-10	39	27	59	80	AAD00575.1	Serum-inducible kinase [Homo sapiens]	1	39	84	124

Table 2 (cont'd)

M 103	222	Other	Unique	0.000022	349	38	30	50	CAA18118.1	Serine/threonine protein kinase like protein [Arabidopsis thaliana]	80	159	1	88
H 104	223	Other	Unique	0.000128	704	54	30	45	BAA8578.1	KIAA1284 protein [Homo sapiens]	1	248	25	261
M 105	224	Other	Unique	0.007385	640	25	42	81	AAF4751A.1	The gene product [Drosophila melanogaster]	9	104	198	261
H 106	225	Other	Unique	0.31334	540	52	30	42	P1G162	SALIVARY PROLINE-RICH PROTEIN PO [ALLELE K] [Homo sapiens]	1	272	18	73
M 107	226	Other	Unique	0.022848	355	25	34	57	NP_006276.1	testis-specific kinase 1 [Homo sapiens]	68	66	42	71
H 108	227	Other	VRK	3.10E-263	474	474	100	100	BAA90769.1	Vaccinia related kinase 3 [Homo sapiens]	247	316	63	136
M 109	228	Other	VRK	1.20E-111	234	191	82	90	BAA90769.1	(AB031052) vaccinia related kinase 3 [Homo sapiens]	7	78	63	136
H 110	229	Other	YPL236.ac	7.40E-144	305	304	100	100	AAC28337.1	MPK [Homo sapiens]	20	290	1	261
H 111	230	Other	YQ09.c9	5.10E-49	581	135	43	83	AAF46188.1	CG4523 gene product [Drosophila melanogaster]	156	507	1	261
H 112	231	STE	NEK	3.30E-30	698	122	48	67	P01954	NEK1 (NIMA-RELATED PROTEIN KINASE 1) [Mus musculus]	4	261	1	261
H 113	232	STE	NEK	2.70E-119	836	357	88	86	AAD31839.1	(AC007055) unknown [Homo sapiens]	52	308	1	261
H 114	233	STE	STE11	1.10E-291	1011	1011	100	100	NP_004663.1	mitogen-activated protein kinase kinase kinase 6 [Homo sapiens]	376	629	6	261
H 115	234	STE	STE20-02	7.70E-177	719	719	100	100	BAA94194.1	(AB040812) protein kinase PAK5 [Homo sapiens]	449	700	1	261
H 116	235	TK	RTK-20	4.90E-24	495	77	38	56	AAA98465.1	(U40427) protein tyrosine kinase [Mus musculus]	187	453	1	261
M 117	236	TK	RTK-20	5.30E-18	183	53	39	57	NP_032036.1	fibroblast growth factor receptor 3 [Mus musculus]	8	143	123	261
H 118	237	AGC	SGK	6.30E-112	367	367	100	100	AAF12757.2	SGK2alpha protein kinase [Homo sapiens]	35	292	1	261
H 120	238	CMGC	CDK	2.80E-137	452	452	100	100	NP_039251.1	Cell cycle related kinase [Homo sapiens]	4	287	1	261
H 121	239	Other	LIMK	6.50E-233	555	555	100	100	NP_009101.1	Testis-specific kinase 2 [Homo sapiens]	62	293	5	261

164
Table 3[illegible]

165
Table 3 (cont'd)[illegible]

166
Table 3 (cont'd)[illegible]

167
Table 3 (cont'd)[illegible]

168
Table 3 (cont'd)

Trans	Trans-type	Normal-type	Trans - to	Trans - from	Normal	Ends	JSI	SEQ 07 AA	SEQ 20 BB	SEQ 22 CC	SEQ 23 DD	SEQ 24 EE	SEQ 25 FF	SEQ 26 GG	SEQ 27 HH	SEQ 28 II	SEQ 29 JJ	SEQ 30 KK	SEQ 31 LL	SEQ 32 MM	SEQ 33 NN	SEQ 34 OO	SEQ 35 PP	SEQ 36 QQ	SEQ 37 RR	SEQ 38 SS	SEQ 39 TT	SEQ 40 UU	SEQ 41 VV	SEQ 42 WW	SEQ 43 XX	SEQ 44 YY	SEQ 45 ZZ	SEQ 46 AA	SEQ 47 BB	SEQ 48 CC	SEQ 49 DD	SEQ 50 EE	SEQ 51 FF	SEQ 52 GG	SEQ 53 HH	SEQ 54 II	SEQ 55 JJ	SEQ 56 KK	SEQ 57 LL	SEQ 58 MM	SEQ 59 NN	SEQ 60 OO	SEQ 61 PP	SEQ 62 QQ	SEQ 63 RR	SEQ 64 SS	SEQ 65 TT	SEQ 66 UU	SEQ 67 VV	SEQ 68 WW	SEQ 69 XX	SEQ 70 YY	SEQ 71 ZZ	SEQ 72 AA	SEQ 73 BB	SEQ 74 CC	SEQ 75 DD	SEQ 76 EE	SEQ 77 FF	SEQ 78 GG	SEQ 79 HH	SEQ 80 II	SEQ 81 JJ	SEQ 82 KK	SEQ 83 LL	SEQ 84 MM	SEQ 85 NN	SEQ 86 OO	SEQ 87 PP	SEQ 88 QQ	SEQ 89 RR	SEQ 90 SS	SEQ 91 TT	SEQ 92 UU	SEQ 93 VV	SEQ 94 WW	SEQ 95 XX	SEQ 96 YY	SEQ 97 ZZ	SEQ 98 AA	SEQ 99 BB	SEQ 100 CC	SEQ 101 DD	SEQ 102 EE	SEQ 103 FF	SEQ 104 GG	SEQ 105 HH	SEQ 106 II	SEQ 107 JJ	SEQ 108 KK	SEQ 109 LL	SEQ 110 MM	SEQ 111 NN	SEQ 112 OO	SEQ 113 PP	SEQ 114 QQ	SEQ 115 RR	SEQ 116 SS	SEQ 117 TT	SEQ 118 UU	SEQ 119 VV	SEQ 120 WW	SEQ 121 XX	SEQ 122 YY	SEQ 123 ZZ	SEQ 124 AA	SEQ 125 BB	SEQ 126 CC	SEQ 127 DD	SEQ 128 EE	SEQ 129 FF	SEQ 130 GG	SEQ 131 HH	SEQ 132 II	SEQ 133 JJ	SEQ 134 KK	SEQ 135 LL	SEQ 136 MM	SEQ 137 NN	SEQ 138 OO	SEQ 139 PP	SEQ 140 QQ	SEQ 141 RR	SEQ 142 SS	SEQ 143 TT	SEQ 144 UU	SEQ 145 VV	SEQ 146 WW	SEQ 147 XX	SEQ 148 YY	SEQ 149 ZZ	SEQ 150 AA	SEQ 151 BB	SEQ 152 CC	SEQ 153 DD	SEQ 154 EE	SEQ 155 FF	SEQ 156 GG	SEQ 157 HH	SEQ 158 II	SEQ 159 JJ	SEQ 160 KK	SEQ 161 LL	SEQ 162 MM	SEQ 163 NN	SEQ 164 OO	SEQ 165 PP	SEQ 166 QQ	SEQ 167 RR	SEQ 168 SS	SEQ 169 TT	SEQ 170 UU	SEQ 171 VV	SEQ 172 WW	SEQ 173 XX	SEQ 174 YY	SEQ 175 ZZ	SEQ 176 AA	SEQ 177 BB	SEQ 178 CC	SEQ 179 DD	SEQ 180 EE	SEQ 181 FF	SEQ 182 GG	SEQ 183 HH	SEQ 184 II	SEQ 185 JJ	SEQ 186 KK	SEQ 187 LL	SEQ 188 MM	SEQ 189 NN	SEQ 190 OO	SEQ 191 PP	SEQ 192 QQ	SEQ 193 RR	SEQ 194 SS	SEQ 195 TT	SEQ 196 UU	SEQ 197 VV	SEQ 198 WW	SEQ 199 XX	SEQ 200 YY	SEQ 201 ZZ	SEQ 202 AA	SEQ 203 BB	SEQ 204 CC	SEQ 205 DD	SEQ 206 EE	SEQ 207 FF	SEQ 208 GG	SEQ 209 HH	SEQ 210 II	SEQ 211 JJ	SEQ 212 KK	SEQ 213 LL	SEQ 214 MM	SEQ 215 NN	SEQ 216 OO	SEQ 217 PP	SEQ 218 QQ	SEQ 219 RR	SEQ 220 SS	SEQ 221 TT	SEQ 222 UU	SEQ 223 VV	SEQ 224 WW	SEQ 225 XX	SEQ 226 YY	SEQ 227 ZZ	SEQ 228 AA	SEQ 229 BB	SEQ 230 CC	SEQ 231 DD	SEQ 232 EE	SEQ 233 FF	SEQ 234 GG	SEQ 235 HH	SEQ 236 II	SEQ 237 JJ	SEQ 238 KK	SEQ 239 LL	SEQ 240 MM	SEQ 241 NN	SEQ 242 OO	SEQ 243 PP	SEQ 244 QQ	SEQ 245 RR	SEQ 246 SS	SEQ 247 TT	SEQ 248 UU	SEQ 249 VV	SEQ 250 WW	SEQ 251 XX	SEQ 252 YY	SEQ 253 ZZ	SEQ 254 AA	SEQ 255 BB	SEQ 256 CC	SEQ 257 DD	SEQ 258 EE	SEQ 259 FF	SEQ 260 GG	SEQ 261 HH	SEQ 262 II	SEQ 263 JJ	SEQ 264 KK	SEQ 265 LL	SEQ 266 MM	SEQ 267 NN	SEQ 268 OO	SEQ 269 PP	SEQ 270 QQ	SEQ 271 RR	SEQ 272 SS	SEQ 273 TT	SEQ 274 UU	SEQ 275 VV	SEQ 276 WW	SEQ 277 XX	SEQ 278 YY	SEQ 279 ZZ	SEQ 280 AA	SEQ 281 BB	SEQ 282 CC	SEQ 283 DD	SEQ 284 EE	SEQ 285 FF	SEQ 286 GG	SEQ 287 HH	SEQ 288 II	SEQ 289 JJ	SEQ 290 KK	SEQ 291 LL	SEQ 292 MM	SEQ 293 NN	SEQ 294 OO	SEQ 295 PP	SEQ 296 QQ	SEQ 297 RR	SEQ 298 SS	SEQ 299 TT	SEQ 300 UU	SEQ 301 VV	SEQ 302 WW	SEQ 303 XX	SEQ 304 YY	SEQ 305 ZZ	SEQ 306 AA	SEQ 307 BB	SEQ 308 CC	SEQ 309 DD	SEQ 310 EE	SEQ 311 FF	SEQ 312 GG	SEQ 313 HH	SEQ 314 II	SEQ 315 JJ	SEQ 316 KK	SEQ 317 LL	SEQ 318 MM	SEQ 319 NN	SEQ 320 OO	SEQ 321 PP	SEQ 322 QQ	SEQ 323 RR	SEQ 324 SS	SEQ 325 TT	SEQ 326 UU	SEQ 327 VV	SEQ 328 WW	SEQ 329 XX	SEQ 330 YY	SEQ 331 ZZ	SEQ 332 AA	SEQ 333 BB	SEQ 334 CC	SEQ 335 DD	SEQ 336 EE	SEQ 337 FF	SEQ 338 GG	SEQ 339 HH	SEQ 340 II	SEQ 341 JJ	SEQ 342 KK	SEQ 343 LL	SEQ 344 MM	SEQ 345 NN	SEQ 346 OO	SEQ 347 PP	SEQ 348 QQ	SEQ 349 RR	SEQ 350 SS	SEQ 351 TT	SEQ 352 UU	SEQ 353 VV	SEQ 354 WW	SEQ 355 XX	SEQ 356 YY	SEQ 357 ZZ	SEQ 358 AA	SEQ 359 BB	SEQ 360 CC	SEQ 361 DD	SEQ 362 EE	SEQ 363 FF	SEQ 364 GG	SEQ 365 HH	SEQ 366 II	SEQ 367 JJ	SEQ 368 KK	SEQ 369 LL	SEQ 370 MM	SEQ 371 NN	SEQ 372 OO	SEQ 373 PP	SEQ 374 QQ	SEQ 375 RR	SEQ 376 SS	SEQ 377 TT	SEQ 378 UU	SEQ 379 VV	SEQ 380 WW	SEQ 381 XX	SEQ 382 YY	SEQ 383 ZZ	SEQ 384 AA	SEQ 385 BB	SEQ 386 CC	SEQ 387 DD	SEQ 388 EE	SEQ 389 FF	SEQ 390 GG	SEQ 391 HH	SEQ 392 II	SEQ 393 JJ	SEQ 394 KK	SEQ 395 LL	SEQ 396 MM	SEQ 397 NN	SEQ 398 OO	SEQ 399 PP	SEQ 400 QQ	SEQ 401 RR	SEQ 402 SS	SEQ 403 TT	SEQ 404 UU	SEQ 405 VV	SEQ 406 WW	SEQ 407 XX	SEQ 408 YY	SEQ 409 ZZ	SEQ 410 AA	SEQ 411 BB	SEQ 412 CC	SEQ 413 DD	SEQ 414 EE	SEQ 415 FF	SEQ 416 GG	SEQ 417 HH	SEQ 418 II	SEQ 419 JJ	SEQ 420 KK	SEQ 421 LL	SEQ 422 MM	SEQ 423 NN	SEQ 424 OO	SEQ 425 PP	SEQ 426 QQ	SEQ 427 RR	SEQ 428 SS	SEQ 429 TT	SEQ 430 UU	SEQ 431 VV	SEQ 432 WW	SEQ 433 XX	SEQ 434 YY	SEQ 435 ZZ	SEQ 436 AA	SEQ 437 BB	SEQ 438 CC	SEQ 439 DD	SEQ 440 EE	SEQ 441 FF	SEQ 442 GG	SEQ 443 HH	SEQ 444 II	SEQ 445 JJ	SEQ 446 KK	SEQ 447 LL	SEQ 448 MM	SEQ 449 NN	SEQ 450 OO	SEQ 451 PP	SEQ 452 QQ	SEQ 453 RR	SEQ 454 SS	SEQ 455 TT	SEQ 456 UU	SEQ 457 VV	SEQ 458 WW	SEQ 459 XX	SEQ 460 YY	SEQ 461 ZZ	SEQ 462 AA	SEQ 463 BB	SEQ 464 CC	SEQ 465 DD	SEQ 466 EE	SEQ 467 FF	SEQ 468 GG	SEQ 469 HH	SEQ 470 II	SEQ 471 JJ	SEQ 472 KK	SEQ 473 LL	SEQ 474 MM	SEQ 475 NN	SEQ 476 OO	SEQ 477 PP	SEQ 478 QQ	SEQ 479 RR	SEQ 480 SS	SEQ 481 TT	SEQ 482 UU	SEQ 483 VV	SEQ 484 WW	SEQ 485 XX	SEQ 486 YY	SEQ 487 ZZ	SEQ 488 AA	SEQ 489 BB	SEQ 490 CC	SEQ 491 DD	SEQ 492 EE	SEQ 493 FF	SEQ 494 GG	SEQ 495 HH	SEQ 496 II	SEQ 497 JJ	SEQ 498 KK	SEQ 499 LL	SEQ 500 MM	SEQ 501 NN	SEQ 502 OO	SEQ 503 PP	SEQ 504 QQ	SEQ 505 RR	SEQ 506 SS	SEQ 507 TT	SEQ 508 UU	SEQ 509 VV	SEQ 510 WW	SEQ 511 XX	SEQ 512 YY	SEQ 513 ZZ	SEQ 514 AA	SEQ 515 BB	SEQ 516 CC	SEQ 517 DD	SEQ 518 EE	SEQ 519 FF	SEQ 520 GG	SEQ 521 HH	SEQ 522 II	SEQ 523 JJ	SEQ 524 KK	SEQ 525 LL	SEQ 526 MM	SEQ 527 NN	SEQ 528 OO	SEQ 529 PP	SEQ 530 QQ	SEQ 531 RR	SEQ 532 SS	SEQ 533 TT	SEQ 534 UU	SEQ 535 VV	SEQ 536 WW	SEQ 537 XX	SEQ 538 YY	SEQ 539 ZZ	SEQ 540 AA	SEQ 541 BB	SEQ 542 CC	SEQ 543 DD	SEQ 544 EE	SEQ 545 FF	SEQ 546 GG	SEQ 547 HH	SEQ 548 II	SEQ 549 JJ	SEQ 550 KK	SEQ 551 LL	SEQ 552 MM	SEQ 553 NN	SEQ 554 OO	SEQ 555 PP	SEQ 556 QQ	SEQ 557 RR	SEQ 558 SS	SEQ 559 TT	SEQ 560 UU	SEQ 561 VV	SEQ 562 WW	SEQ 563 XX	SEQ 564 YY	SEQ 565 ZZ	SEQ 566 AA	SEQ 567 BB	SEQ 568 CC	SEQ 569 DD	SEQ 570 EE	SEQ 571 FF	SEQ 572 GG	SEQ 573 HH	SEQ 574 II	SEQ 575 JJ	SEQ 576 KK	SEQ 577 LL	SEQ 578 MM	SEQ 579 NN	SEQ 580 OO	SEQ 581 PP	SEQ 582 QQ	SEQ 583 RR	SEQ 584 SS	SEQ 585 TT	SEQ 586 UU	SEQ 587 VV	SEQ 588 WW	SEQ 589 XX	SEQ 590 YY	SEQ 591 ZZ	SEQ 592 AA	SEQ 593 BB	SEQ 594 CC	SEQ 595 DD	SEQ 596 EE	SEQ 597 FF	SEQ 598 GG	SEQ 599 HH	SEQ 600 II	SEQ 601 JJ	SEQ 602 KK	SEQ 603 LL	SEQ 604 MM	SEQ 605 NN	SEQ 606 OO	SEQ 607 PP	SEQ 608 QQ	SEQ 609 RR	SEQ 610 SS	SEQ 611 TT	SEQ 612 UU	SEQ 613 VV	SEQ 614 WW	SEQ 615 XX	SEQ 616 YY	SEQ 617 ZZ	SEQ 618 AA	SEQ 619 BB	SEQ 620 CC	SEQ 621 DD	SEQ 622 EE	SEQ 623 FF	SEQ 624 GG	SEQ 625 HH	SEQ 626 II	SEQ 627 JJ	SEQ 628 KK	SEQ 629 LL	SEQ 630 MM	SEQ 631 NN	SEQ 632 OO	SEQ 633 PP	SEQ 634 QQ	SEQ 635 RR	SEQ 636 SS	SEQ 637 TT	SEQ 638 UU	SEQ 639 VV	SEQ 640 WW	SEQ 641 XX	SEQ 642 YY	SEQ 643 ZZ	SEQ 644 AA	SEQ 645 BB	SEQ 646 CC	SEQ 647 DD	SEQ 648 EE	SEQ 649 FF	SEQ 650 GG	SEQ 651 HH	SEQ 652 II	SEQ 653 JJ	SEQ 654 KK	SEQ 655 LL	SEQ 656 MM	SEQ 657 NN	SEQ 658 OO	SEQ 659 PP	SEQ 660 QQ	SEQ 661 RR	SEQ 662 SS	SEQ 663 TT	SEQ 664 UU	SEQ 665 VV	SEQ 666 WW	SEQ 667 XX	SEQ 668 YY	SEQ 669 ZZ	SEQ 670 AA	SEQ 671 BB	SEQ 672 CC	SEQ 673 DD	SEQ 674 EE	SEQ 675 FF	SEQ 676 GG	SEQ 677 HH	SEQ 678 II	SEQ 679 JJ	SEQ 680 KK	SEQ 681 LL	SEQ 682 MM	SEQ 683 NN	SEQ 684 OO	SEQ 685 PP	SEQ 686 QQ	SEQ 687 RR	SEQ 688 SS	SEQ 689 TT	SEQ 690 UU	SEQ 691 VV	SEQ 692 WW	SEQ 693 XX	SEQ 694 YY	SEQ 695 ZZ	SEQ 696 AA	SEQ 697 BB	SEQ 698 CC	SEQ 699 DD	SEQ 700 EE	SEQ 701 FF	SEQ 702 GG	SEQ 703 HH	SEQ 704 II	SEQ 705 JJ	SEQ 706 KK	SEQ 707 LL	SEQ 708 MM	SEQ 709 NN	SEQ 710 OO	SEQ 711 PP	SEQ 712 QQ	SEQ 713 RR	SEQ 714 SS	SEQ 715 TT	SEQ 716 UU	SEQ 717 VV	SEQ 718 WW	SEQ 719 XX	SEQ 720 YY	SEQ 721 ZZ	SEQ 722 AA	SEQ 723 BB	SEQ 724 CC	SEQ 725 DD	SEQ 726 EE	SEQ 727 FF	SEQ 728 GG	SEQ 729 HH	SEQ 730 II	SEQ 731 JJ	SEQ 732 KK	SEQ 733 LL	SEQ 734 MM	SEQ 735 NN	SEQ 736 OO	SEQ 737 PP	SEQ 738 QQ	SEQ 739 RR	SEQ 740 SS	SEQ 741 TT	SEQ 742 UU	SEQ 743 VV	SEQ 744 WW	SEQ 745 XX	SEQ 746 YY	SEQ 747 ZZ	SEQ 748 AA	SEQ 749 BB	SEQ 750 CC	SEQ 751 DD	SEQ 752 EE	SEQ 753 FF	SEQ 754 GG	SEQ 755 HH	SEQ 756 II	SEQ 757 JJ	SEQ 758 KK	SEQ 759 LL	SEQ 760 MM	SEQ 761 NN	SEQ 762 OO	SEQ 763 PP	SEQ 764 QQ	SEQ 765 RR	SEQ 766 SS	SEQ 767 TT	SEQ 768 UU	SEQ 769 VV	SEQ 770 WW	SEQ 771 XX	SEQ 772 YY	SEQ 773 ZZ	SEQ 774 AA	SEQ 775 BB	SEQ 776 CC	SEQ 777 DD	SEQ 778 EE	SEQ 779 FF	SEQ 780 GG	SEQ 781 HH	SEQ 782 II	SEQ 783 JJ	SEQ 784 KK	SEQ 785 LL	SEQ 786 MM	SEQ 787 NN	SEQ 788 OO	SEQ 789 PP	SEQ 790 QQ	SEQ 791 RR	SEQ 792 SS	SEQ 793 TT	SEQ 794 UU	SEQ 795 VV	SEQ 796 WW	SEQ 797 XX	SEQ 798 YY	SEQ 799 ZZ	SEQ 800 AA	SEQ 801 BB	SEQ 802 CC	SEQ 803 DD	SEQ 804 EE	SEQ 805 FF	SEQ 806 GG	SEQ 807 HH	SEQ 808 II	SEQ 809 JJ	SEQ 810 KK	SEQ 811 LL	SEQ 812 MM	SEQ 813 NN	SEQ 814 OO	SEQ 815 PP	SEQ 816 QQ	SEQ 817 RR	SEQ 818 SS	SEQ 819 TT	SEQ 820 UU	SEQ 821 VV	SEQ 822 WW	SEQ 823 XX	SEQ 824 YY	SEQ 825 ZZ	SEQ 826 AA	SEQ 827 BB	SEQ 828 CC	SEQ 829 DD	SEQ 830 EE	SEQ 831 FF	SEQ 832 GG	SEQ 833 HH	SEQ 834 II	SEQ 835 JJ	SEQ 836 KK	SEQ 837 LL	SEQ 838 MM	SEQ 839 NN	SEQ 840 OO	SEQ 841 PP	SEQ 842 QQ	SEQ 843 RR	SEQ 844 SS	SEQ 845 TT	SEQ 846 UU	SEQ 847 VV	SEQ 848 WW	SEQ 849 XX	SEQ 850 YY	SEQ 851 ZZ	SEQ 852 AA	SEQ 853 BB	SEQ 854 CC	SEQ 855 DD	SEQ 856 EE	SEQ 857 FF	SEQ 858 GG	SEQ 859 HH	SEQ 860 II	SEQ 861 JJ	SEQ 862 KK	SEQ 863 LL	SEQ 864 MM	SEQ 865 NN	SEQ 866 OO	SEQ 867 PP	SEQ 868 QQ	SEQ 869 RR	SEQ 870 SS	SEQ 871 TT	SEQ 872 UU	SEQ 873 VV	SEQ 874 WW	SEQ 875 XX	SEQ 876 YY	SEQ 877 ZZ	SEQ 878 AA	SEQ 879 BB	SEQ 880 CC	SEQ 881 DD	SEQ 882 EE	SEQ 883 FF	SEQ 884 GG	SEQ 885 HH	SEQ 886 II	SEQ 887 JJ	SEQ 888 KK	SEQ 889 LL	SEQ 890 MM	SEQ 891 NN	SEQ 892 OO	SEQ 893 PP	SEQ 894 QQ	SEQ 895 RR	SEQ 896 SS	SEQ 897 TT	SEQ 898 UU	SEQ 899 VV	SEQ 900 WW	SEQ 901 XX	SEQ 902 YY	SEQ 903 ZZ	SEQ 904 AA	SEQ 905 BB	SEQ 906 CC	SEQ 907 DD	SEQ 908 EE	SEQ 909 FF	SEQ 910 GG	SEQ 911 HH	SEQ 912 II	SEQ 913 JJ	SEQ 914 KK	SEQ 915 LL	SEQ 916 MM	SEQ 917 NN	SEQ 918 OO	SEQ 919 PP	SEQ 920 QQ	SEQ 921 RR	SEQ 922 SS	SEQ 923 TT	SEQ 924 UU	SEQ 925 VV	SEQ 926 WW	SEQ 927 XX	SEQ 928 YY	SEQ 929 ZZ	SEQ 930 AA	SEQ 931 BB	SEQ 932 CC	SEQ 933 DD	SEQ 934 EE	SEQ 935 FF	SEQ 936 GG	SEQ 937 HH	SEQ 938 II	SEQ 939 JJ	SEQ 940 KK	SEQ 941 LL	SEQ 942 MM	SEQ 943 NN	SEQ 944 OO	SEQ 945 PP	SEQ 946 QQ	SEQ 947 RR	SEQ 948 SS	SEQ 949 TT	SEQ 950 UU	SEQ 951 VV	SEQ 952 WW	SEQ 953 XX	SEQ 954 YY	SEQ 955 ZZ	SEQ 956 AA	SEQ 957 BB	SEQ 958 CC	SEQ 959 DD	SEQ 960 EE	SEQ 961 FF	SEQ 962 GG	SEQ 963 HH	SEQ 964 II	SEQ 965 JJ	SEQ 966 KK	SEQ 967 LL	SEQ 968 MM	SEQ 969 NN	SEQ 970 OO	SEQ 971 PP	SEQ 972 QQ	SEQ 973 RR	SEQ 974 SS	SEQ 975 TT	SEQ 976 UU	SEQ 977 VV	SEQ 978 WW	SEQ 979 XX	SEQ 980 YY	SEQ 981 ZZ	SEQ 982 AA	SEQ 983 BB	SEQ 984 CC	SEQ 985 DD	SEQ 986 EE	SEQ 987 FF	SEQ 988 GG	SEQ 989 HH	SEQ 990 II	SEQ 991 JJ	SEQ 992 KK	SEQ 993 LL	SEQ 994 MM	SEQ 995 NN	SEQ 996 OO	SEQ 997 PP	SEQ 998 QQ	SEQ 999 RR	SEQ 1000 SS
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Table 3 (cont'd)

Threat	Tumor-ary	Normal-ary	Tumor - 1a	Tumor code	Normal	Endos	p33	SEQ 34	SEQ 41	SEQ 47	SEQ 48	SEQ 49	SEQ 50	SEQ 51	SEQ 52	SEQ 53	SEQ 54	SEQ 55	SEQ 56	SEQ 57	SEQ 58	SEQ 59	SEQ 60	SEQ 61	SEQ 62	SEQ 63	SEQ 64	SEQ 65	SEQ 66	SEQ 67	SEQ 68	SEQ 69	SEQ 70	SEQ 71	SEQ 72	SEQ 73	SEQ 74	SEQ 75	SEQ 76	SEQ 77	SEQ 78	SEQ 79	SEQ 80	SEQ 81	SEQ 82	SEQ 83	SEQ 84	SEQ 85	SEQ 86	SEQ 87	SEQ 88	SEQ 89	SEQ 90	SEQ 91	SEQ 92	SEQ 93	SEQ 94	SEQ 95	SEQ 96	SEQ 97	SEQ 98	SEQ 99	SEQ 100	SEQ 101	SEQ 102	SEQ 103	SEQ 104	SEQ 105	SEQ 106	SEQ 107	SEQ 108	SEQ 109	SEQ 110	SEQ 111	SEQ 112	SEQ 113	SEQ 114	SEQ 115	SEQ 116	SEQ 117	SEQ 118	SEQ 119	SEQ 120	SEQ 121	SEQ 122	SEQ 123	SEQ 124	SEQ 125	SEQ 126	SEQ 127	SEQ 128	SEQ 129	SEQ 130	SEQ 131	SEQ 132	SEQ 133	SEQ 134	SEQ 135	SEQ 136	SEQ 137	SEQ 138	SEQ 139	SEQ 140	SEQ 141	SEQ 142	SEQ 143	SEQ 144	SEQ 145	SEQ 146	SEQ 147	SEQ 148	SEQ 149	SEQ 150	SEQ 151	SEQ 152	SEQ 153	SEQ 154	SEQ 155	SEQ 156	SEQ 157	SEQ 158	SEQ 159	SEQ 160	SEQ 161	SEQ 162	SEQ 163	SEQ 164	SEQ 165	SEQ 166	SEQ 167	SEQ 168	SEQ 169	SEQ 170	SEQ 171	SEQ 172	SEQ 173	SEQ 174	SEQ 175	SEQ 176	SEQ 177	SEQ 178	SEQ 179	SEQ 180	SEQ 181	SEQ 182	SEQ 183	SEQ 184	SEQ 185	SEQ 186	SEQ 187	SEQ 188	SEQ 189	SEQ 190	SEQ 191	SEQ 192	SEQ 193	SEQ 194	SEQ 195	SEQ 196	SEQ 197	SEQ 198	SEQ 199	SEQ 200	SEQ 201	SEQ 202	SEQ 203	SEQ 204	SEQ 205	SEQ 206	SEQ 207	SEQ 208	SEQ 209	SEQ 210	SEQ 211	SEQ 212	SEQ 213	SEQ 214	SEQ 215	SEQ 216	SEQ 217	SEQ 218	SEQ 219	SEQ 220	SEQ 221	SEQ 222	SEQ 223	SEQ 224	SEQ 225	SEQ 226	SEQ 227	SEQ 228	SEQ 229	SEQ 230	SEQ 231	SEQ 232	SEQ 233	SEQ 234	SEQ 235	SEQ 236	SEQ 237	SEQ 238	SEQ 239	SEQ 240	SEQ 241	SEQ 242	SEQ 243	SEQ 244	SEQ 245	SEQ 246	SEQ 247	SEQ 248	SEQ 249	SEQ 250	SEQ 251	SEQ 252	SEQ 253	SEQ 254	SEQ 255	SEQ 256	SEQ 257	SEQ 258	SEQ 259	SEQ 260	SEQ 261	SEQ 262	SEQ 263	SEQ 264	SEQ 265	SEQ 266	SEQ 267	SEQ 268	SEQ 269	SEQ 270	SEQ 271	SEQ 272	SEQ 273	SEQ 274	SEQ 275	SEQ 276	SEQ 277	SEQ 278	SEQ 279	SEQ 280	SEQ 281	SEQ 282	SEQ 283	SEQ 284	SEQ 285	SEQ 286	SEQ 287	SEQ 288	SEQ 289	SEQ 290	SEQ 291	SEQ 292	SEQ 293	SEQ 294	SEQ 295	SEQ 296	SEQ 297	SEQ 298	SEQ 299	SEQ 300	SEQ 301	SEQ 302	SEQ 303	SEQ 304	SEQ 305	SEQ 306	SEQ 307	SEQ 308	SEQ 309	SEQ 310	SEQ 311	SEQ 312	SEQ 313	SEQ 314	SEQ 315	SEQ 316	SEQ 317	SEQ 318	SEQ 319	SEQ 320	SEQ 321	SEQ 322	SEQ 323	SEQ 324	SEQ 325	SEQ 326	SEQ 327	SEQ 328	SEQ 329	SEQ 330	SEQ 331	SEQ 332	SEQ 333	SEQ 334	SEQ 335	SEQ 336	SEQ 337	SEQ 338	SEQ 339	SEQ 340	SEQ 341	SEQ 342	SEQ 343	SEQ 344	SEQ 345	SEQ 346	SEQ 347	SEQ 348	SEQ 349	SEQ 350	SEQ 351	SEQ 352	SEQ 353	SEQ 354	SEQ 355	SEQ 356	SEQ 357	SEQ 358	SEQ 359	SEQ 360	SEQ 361	SEQ 362	SEQ 363	SEQ 364	SEQ 365	SEQ 366	SEQ 367	SEQ 368	SEQ 369	SEQ 370	SEQ 371	SEQ 372	SEQ 373	SEQ 374	SEQ 375	SEQ 376	SEQ 377	SEQ 378	SEQ 379	SEQ 380	SEQ 381	SEQ 382	SEQ 383	SEQ 384	SEQ 385	SEQ 386	SEQ 387	SEQ 388	SEQ 389	SEQ 390	SEQ 391	SEQ 392	SEQ 393	SEQ 394	SEQ 395	SEQ 396	SEQ 397	SEQ 398	SEQ 399	SEQ 400	SEQ 401	SEQ 402	SEQ 403	SEQ 404	SEQ 405	SEQ 406	SEQ 407	SEQ 408	SEQ 409	SEQ 410	SEQ 411	SEQ 412	SEQ 413	SEQ 414	SEQ 415	SEQ 416	SEQ 417	SEQ 418	SEQ 419	SEQ 420	SEQ 421	SEQ 422	SEQ 423	SEQ 424	SEQ 425	SEQ 426	SEQ 427	SEQ 428	SEQ 429	SEQ 430	SEQ 431	SEQ 432	SEQ 433	SEQ 434	SEQ 435	SEQ 436	SEQ 437	SEQ 438	SEQ 439	SEQ 440	SEQ 441	SEQ 442	SEQ 443	SEQ 444	SEQ 445	SEQ 446	SEQ 447	SEQ 448	SEQ 449	SEQ 450	SEQ 451	SEQ 452	SEQ 453	SEQ 454	SEQ 455	SEQ 456	SEQ 457	SEQ 458	SEQ 459	SEQ 460	SEQ 461	SEQ 462	SEQ 463	SEQ 464	SEQ 465	SEQ 466	SEQ 467	SEQ 468	SEQ 469	SEQ 470	SEQ 471	SEQ 472	SEQ 473	SEQ 474	SEQ 475	SEQ 476	SEQ 477	SEQ 478	SEQ 479	SEQ 480	SEQ 481	SEQ 482	SEQ 483	SEQ 484	SEQ 485	SEQ 486	SEQ 487	SEQ 488	SEQ 489	SEQ 490	SEQ 491	SEQ 492	SEQ 493	SEQ 494	SEQ 495	SEQ 496	SEQ 497	SEQ 498	SEQ 499	SEQ 500	SEQ 501	SEQ 502	SEQ 503	SEQ 504	SEQ 505	SEQ 506	SEQ 507	SEQ 508	SEQ 509	SEQ 510	SEQ 511	SEQ 512	SEQ 513	SEQ 514	SEQ 515	SEQ 516	SEQ 517	SEQ 518	SEQ 519	SEQ 520	SEQ 521	SEQ 522	SEQ 523	SEQ 524	SEQ 525	SEQ 526	SEQ 527	SEQ 528	SEQ 529	SEQ 530	SEQ 531	SEQ 532	SEQ 533	SEQ 534	SEQ 535	SEQ 536	SEQ 537	SEQ 538	SEQ 539	SEQ 540	SEQ 541	SEQ 542	SEQ 543	SEQ 544	SEQ 545	SEQ 546	SEQ 547	SEQ 548	SEQ 549	SEQ 550	SEQ 551	SEQ 552	SEQ 553	SEQ 554	SEQ 555	SEQ 556	SEQ 557	SEQ 558	SEQ 559	SEQ 560	SEQ 561	SEQ 562	SEQ 563	SEQ 564	SEQ 565	SEQ 566	SEQ 567	SEQ 568	SEQ 569	SEQ 570	SEQ 571	SEQ 572	SEQ 573	SEQ 574	SEQ 575	SEQ 576	SEQ 577	SEQ 578	SEQ 579	SEQ 580	SEQ 581	SEQ 582	SEQ 583	SEQ 584	SEQ 585	SEQ 586	SEQ 587	SEQ 588	SEQ 589	SEQ 590	SEQ 591	SEQ 592	SEQ 593	SEQ 594	SEQ 595	SEQ 596	SEQ 597	SEQ 598	SEQ 599	SEQ 600	SEQ 601	SEQ 602	SEQ 603	SEQ 604	SEQ 605	SEQ 606	SEQ 607	SEQ 608	SEQ 609	SEQ 610	SEQ 611	SEQ 612	SEQ 613	SEQ 614	SEQ 615	SEQ 616	SEQ 617	SEQ 618	SEQ 619	SEQ 620	SEQ 621	SEQ 622	SEQ 623	SEQ 624	SEQ 625	SEQ 626	SEQ 627	SEQ 628	SEQ 629	SEQ 630	SEQ 631	SEQ 632	SEQ 633	SEQ 634	SEQ 635	SEQ 636	SEQ 637	SEQ 638	SEQ 639	SEQ 640	SEQ 641	SEQ 642	SEQ 643	SEQ 644	SEQ 645	SEQ 646	SEQ 647	SEQ 648	SEQ 649	SEQ 650	SEQ 651	SEQ 652	SEQ 653	SEQ 654	SEQ 655	SEQ 656	SEQ 657	SEQ 658	SEQ 659	SEQ 660	SEQ 661	SEQ 662	SEQ 663	SEQ 664	SEQ 665	SEQ 666	SEQ 667	SEQ 668	SEQ 669	SEQ 670	SEQ 671	SEQ 672	SEQ 673	SEQ 674	SEQ 675	SEQ 676	SEQ 677	SEQ 678	SEQ 679	SEQ 680	SEQ 681	SEQ 682	SEQ 683	SEQ 684	SEQ 685	SEQ 686	SEQ 687	SEQ 688	SEQ 689	SEQ 690	SEQ 691	SEQ 692	SEQ 693	SEQ 694	SEQ 695	SEQ 696	SEQ 697	SEQ 698	SEQ 699	SEQ 700	SEQ 701	SEQ 702	SEQ 703	SEQ 704	SEQ 705	SEQ 706	SEQ 707	SEQ 708	SEQ 709	SEQ 710	SEQ 711	SEQ 712	SEQ 713	SEQ 714	SEQ 715	SEQ 716	SEQ 717	SEQ 718	SEQ 719	SEQ 720	SEQ 721	SEQ 722	SEQ 723	SEQ 724	SEQ 725	SEQ 726	SEQ 727	SEQ 728	SEQ 729	SEQ 730	SEQ 731	SEQ 732	SEQ 733	SEQ 734	SEQ 735	SEQ 736	SEQ 737	SEQ 738	SEQ 739	SEQ 740	SEQ 741	SEQ 742	SEQ 743	SEQ 744	SEQ 745	SEQ 746	SEQ 747	SEQ 748	SEQ 749	SEQ 750	SEQ 751	SEQ 752	SEQ 753	SEQ 754	SEQ 755	SEQ 756	SEQ 757	SEQ 758	SEQ 759	SEQ 760	SEQ 761	SEQ 762	SEQ 763	SEQ 764	SEQ 765	SEQ 766	SEQ 767	SEQ 768	SEQ 769	SEQ 770	SEQ 771	SEQ 772	SEQ 773	SEQ 774	SEQ 775	SEQ 776	SEQ 777	SEQ 778	SEQ 779	SEQ 780	SEQ 781	SEQ 782	SEQ 783	SEQ 784	SEQ 785	SEQ 786	SEQ 787	SEQ 788	SEQ 789	SEQ 790	SEQ 791	SEQ 792	SEQ 793	SEQ 794	SEQ 795	SEQ 796	SEQ 797	SEQ 798	SEQ 799	SEQ 800	SEQ 801	SEQ 802	SEQ 803	SEQ 804	SEQ 805	SEQ 806	SEQ 807	SEQ 808	SEQ 809	SEQ 810	SEQ 811	SEQ 812	SEQ 813	SEQ 814	SEQ 815	SEQ 816	SEQ 817	SEQ 818	SEQ 819	SEQ 820	SEQ 821	SEQ 822	SEQ 823	SEQ 824	SEQ 825	SEQ 826	SEQ 827	SEQ 828	SEQ 829	SEQ 830	SEQ 831	SEQ 832	SEQ 833	SEQ 834	SEQ 835	SEQ 836	SEQ 837	SEQ 838	SEQ 839	SEQ 840	SEQ 841	SEQ 842	SEQ 843	SEQ 844	SEQ 845	SEQ 846	SEQ 847	SEQ 848	SEQ 849	SEQ 850	SEQ 851	SEQ 852	SEQ 853	SEQ 854	SEQ 855	SEQ 856	SEQ 857	SEQ 858	SEQ 859	SEQ 860	SEQ 861	SEQ 862	SEQ 863	SEQ 864	SEQ 865	SEQ 866	SEQ 867	SEQ 868	SEQ 869	SEQ 870	SEQ 871	SEQ 872	SEQ 873	SEQ 874	SEQ 875	SEQ 876	SEQ 877	SEQ 878	SEQ 879	SEQ 880	SEQ 881	SEQ 882	SEQ 883	SEQ 884	SEQ 885	SEQ 886	SEQ 887	SEQ 888	SEQ 889	SEQ 890	SEQ 891	SEQ 892	SEQ 893	SEQ 894	SEQ 895	SEQ 896	SEQ 897	SEQ 898	SEQ 899	SEQ 900	SEQ 901	SEQ 902	SEQ 903	SEQ 904	SEQ 905	SEQ 906	SEQ 907	SEQ 908	SEQ 909	SEQ 910	SEQ 911	SEQ 912	SEQ 913	SEQ 914	SEQ 915	SEQ 916	SEQ 917	SEQ 918	SEQ 919	SEQ 920	SEQ 921	SEQ 922	SEQ 923	SEQ 924	SEQ 925	SEQ 926	SEQ 927	SEQ 928	SEQ 929	SEQ 930	SEQ 931	SEQ 932	SEQ 933	SEQ 934	SEQ 935	SEQ 936	SEQ 937	SEQ 938	SEQ 939	SEQ 940	SEQ 941	SEQ 942	SEQ 943	SEQ 944	SEQ 945	SEQ 946	SEQ 947	SEQ 948	SEQ 949	SEQ 950	SEQ 951	SEQ 952	SEQ 953	SEQ 954	SEQ 955	SEQ 956	SEQ 957	SEQ 958	SEQ 959	SEQ 960	SEQ 961	SEQ 962	SEQ 963	SEQ 964	SEQ 965	SEQ 966	SEQ 967	SEQ 968	SEQ 969	SEQ 970	SEQ 971	SEQ 972	SEQ 973	SEQ 974	SEQ 975	SEQ 976	SEQ 977	SEQ 978	SEQ 979	SEQ 980	SEQ 981	SEQ 982	SEQ 983	SEQ 984	SEQ 985	SEQ 986	SEQ 987	SEQ 988	SEQ 989	SEQ 990	SEQ 991	SEQ 992	SEQ 993	SEQ 994	SEQ 995	SEQ 996	SEQ 997	SEQ 998	SEQ 999	SEQ 1000
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Table 3 (cont'd)

[illegible]

Table 3 (cont'd)

Trans	Trans-cym	Normal-cym	Trans - To	Trans-cym	Normal	Endos	pt3	SEQ 17	AN	SEQ 20	SEQ 22	PT	SEQ 24	AN	SEQ 28	DR	SEQ 31	DR	SEQ 32	AN	SEQ 40	MA	SEQ 44	T
MA-EXT								48043	143	118114	7208	2366	887	9245	0	269								
MA-F-MAONES	153							48043	0	0	20411	721	387	0	15558	0	856							
MA-7	151							53048	804	30804	11824	2950	218	13820	0	0								
MA-8	148							63383	371	22286	15825	2725	257	4104	875	73								
MA-9	145							38900	1000	72538	4818	111	0	32383	0	311								
MA-10	147							27441	0	7895	282	886	74	8820	384	281								
MA-11	144							20851	71	10240	1482	2016	634	4083	178	264								
MA-12	143							58220	0	12483	3318	644	1206	1427	1605	0								
MA-13	140							28381	0	137176	1884	110	280	18800	480	134								
MA-14	138							30982	207	8823	2828	5	85	1287	0	259								
MA-15	136							30577	0	50884	3528	827	485	10563	0	188								
MA-16	134							54738	445	25382	2780	1572	207	8868	542	0								
MA-17	132							46800	1489	88489	4322	243	294	12794	226	451								
MA-18	130							57726	423	10862	2548	485	0	5756	0	174								
MA-19	128							28810	0	181758	1512	880	562	25226	246	624								
MA-20	126							38849	437	28279	730	283	188	8406	375	164								
MA-21	124							43827	88	18876	1718	883	282	7085	72	48								
MA-22	122							32489	345	18778	1178	0	458	3812	721	68								
MA-23	120							34175	0	27823	0	534	157	6538	667	14								
MA-24	118							62382	734	17290	0	188	238	5881	0	641								
MA-25	116							28880	330	81788	1363	817	333	4048	75	226								
MA-26	114							35282	32	80887	3008	188	487	8286	819	4								
MA-27	112							40444	285	82881	3148	2477	2041	28824	478	0								
MA-28	110							37777	0	8182	5152	140	480	16854	0	0								
MA-29	108							36257	321	81153	9431	88	527	22488	888	180								
MA-30	106							37880	0	80288	7587	1172	141	28803	156	0								
MA-31	104							38104	0	108217	4214	0	1885	2825	423	884								
MA-32	102							32576	727	8124	2880	2182	425	13014	0	0								
MA-33	100							36277	85	84277	138	1473	182	23838	0	331								
MA-34	98							38448	888	2014	0	325	771	707	884	380								
MA-35	96							28329	732	17195	881	532	1023	4838	0	0								
MA-36	94							23273	0	42226	1888	337	1585	8852	588	71								
MA-37	92							54213	542	18849	2178	302	122	5444	0	0								
MA-38	90							42988	1500	108842	5320	2238	2543	8231	1226	1110								
MA-39	88							38120	878	108822	2781	831	470	41880	0	0								
MA-40	86							32817	544	4788	1242	958	363	7048	2442	0								
MA-41	84							38885	88	14822	2625	0	360	18280	0	252								
MA-42	82							18878	5	84820	1545	1188	880	7728	0	100								
MA-43	80							46247	287	17888	388	708	1184	3288	417	637								
MA-44	78							47438	0	78287	1648	488	383	17119	1514	0								
MA-45	76							30245	84	66487	272	185	75	12447	482	144								
MA-46	74							44511	0	81828	585	813	278	8838	0	84								
MA-47	72							54878	433	48828	372	124	716	17927	888	0								
MA-48	70							38888	388	78178	438	485	883	12488	888	152								
MA-49	68							41884	0	17812	482	486	388	4792	884	318								
MA-50	66							48837	88	10250	2888	4827	481	28338	746	0								
MA-51	64							88854	442	13823	1417	431	2844	3284	166	825								
MA-52	62							833	833	5072	2288	1231	886	18338	743	88								
MA-53	60							33178	0	18888	2841	522	200	18881	243	81								
MA-54	58							3481	0	8416	4782	146	283	28888	0	481								
MA-55	56							41888	442	11180	3881	228	383	11348	0	0								
MA-56	54							28817	0	14573	1822	0	642	34177	0	8								
MA-57	52							21188	0	7828	48	101	187	8382	11	8								
MA-58	50							32880	0	18882	1074	288	486	12782	482	180								
MA-59	48							32880	0	8173	1588	5270	341	401	200	184								
MA-60	46							30837	184	0	2185	0	130	0	883	127								
MA-61	44							28128	88	23481	1117	0	82	10270	344	0								
MA-62	42							22853	783	18828	7310	88	120	5677	1204	131								
MA-63	40							0	0	0	348	1138	4288	412	571	0								
MA-64	38							0	0	0	831	124	4878	538	1033	0								
MA-65	36							0	0	0	0	0	1284	7888	0	880	0							
MA-66	34							0	0	0	0	416	8888	141	0	0								
MA-67	32							0	0	0	0	813	8824	787	0	0								
MA-68	30							0	0	0	0	1340	3420	8820	475	2338	0							
MA-69	28							0	0	0	0	2888	4210	2881	338	180	0							
MA-70	26							0	0	0	0	1888	4881	0	705	0								
MA-71	24							0	0	0	0	284	1112	8847	137	0								
MA-72	22							0	0	0	0	0	0	7483	887	0								
MA-73	20							0	0	0	0	483	881	3344	155	0								
MA-74	18							0	0	0	0	18	3448	2887	482	0								
MA-75	16							0	0	0	0	878	827	1028	218	1386	0							
MA-76	14							0	0	0	0	1191	2831	4828	0	288	0							
MA-77	12							0	0	0	0	588	433	887	420	184								
MA-78	10							0	0	0	0	2736	2737	4888	2888	0								
MA-79	8							0	0	0	0	1148	3482	4838	1088	0								
MA-80	6							0	0	0	0	112	0	2812	881	0								
MA-81	4							0	0	0	0	482	2288	882	0	0								
MA-82	2							0	0	0	0	2811	2888	1838	888	488	0							
MA-83	0							0	0	0	0	0	7795	2846	588	1831	0							
MA-84	0							0	0	0	0	888	8888	8820	181	0								
MA-85	0							0	0	0	0													

172
Table 3 (cont'd)

Tissue	Tumor type	Normal type	Tumor - to	Tumor cells	Normal	Endoth	p53	SEQ 17	AA SEQ 26	30	SEQ 21	PIRSEQ 25	AA SEQ 25	DN SEQ 31	DN SEQ 32	AA SEQ 33	AA SEQ 34	T
DuPang-7								0	0	0	21804	8478	31595	2728	1224	0	0	0
DuPang-8								0	0	0	10005	55431	17854	1880	1078	0	0	0
DuPang-11								0	0	0	9122	1868	25873	1318	494	0	0	0
DuPang-12								0	0	0	7501	8218	14361	1857	889	0	0	0
DuPang-10								0	0	0	3487	3285	16748	1828	0	0	0	0
DuPang-1								0	0	0	3841	12536	8797	832	17952	0	0	0
DuPang-2								0	0	0	3679	10380	6327	148	88625	0	0	0
DuPang-3								0	0	0	4784	2948	2782	3307	4770	0	0	0
DuPang-4								0	0	0	1944	4721	87	4274	803	0	0	0
DuPang-5								0	0	0	1170	2028	327	1917	2183	0	0	0
DuPang-6								0	0	0	12057	5345	0	2639	1453	0	0	0
AS40 - 8								0	0	0	1464	8852	0	427	0	0	0	0
PRVX - 8								0	0	0	1513	7153	8436	580	17	0	0	0
HCT-116 - 7								0	0	0	742	2507	3043	5499	819	0	0	0
HCT-116 - 8								0	0	0	514	8117	2207	761	0	0	0	0
HT29 - 1								0	0	0	420	3056	3122	891	0	0	0	0
HT29 - 7								0	0	0	444	150	8	0	151	0	0	0
HT29 - 8								0	0	0	1051	2808	2178	0	1148	0	0	0
SP-208 - 7								0	0	0	8143	2843	1875	208	0	0	0	0
SP-208 - 8								0	0	0	88	16246	2922	982	0	0	0	0
SP-208 - 9								0	0	0	771	8891	2712	1188	1864	0	0	0
OVCA4-7								0	0	0	1149	8034	4832	384	0	0	0	0
OVCA4-8								0	0	0	0	1284	8383	0	0	0	0	0
OVCA4-9								0	0	0	3258	3109	12809	585	3736	0	0	0
OVCA4-10								0	0	0	0	857	21830	0	0	0	0	0
MC7-7 - 8								0	0	0	89	2843	7100	2503	0	0	0	0
ADR-RES - 8								0	0	0	0	3539	1521	0	180	0	0	0
SW620 - 7								0	0	0	485	8172	3211	8	0	0	0	0
SW620 - 8								0	0	0	1629	225	4785	1618	0	0	0	0
SW620 - 9								0	0	0	246	841	4842	8	1427	0	0	0
HT29 - 8								0	0	0	0	470	4328	0	1168	0	0	0
C3A - 7								0	0	0	1406	4731	2916	298	45	0	0	0
C3A - 8								0	0	0	0	3062	2718	1002	837	0	0	0
U2OS - 7								0	0	0	0	9543	451	805	0	0	0	0
U2OS - 8								0	0	0	3225	4849	3018	877	1215	0	0	0
Hs6 - 7								0	0	0	311	4440	8018	0	0	0	0	0
Hs6 - 8								0	0	0	1028	345	3185	144	0	0	0	0
WT38 - 8								0	0	0	1446	1183	3374	1882	0	0	0	0
Hs6 modulate RNA								0	0	0	1470	0	2514	0	455	0	0	0
CSL1572 - 31788								37888	0	4415	210	280	1447	8182	18	58	0	0
Row-4								25584	878	738	543	4685	27	579	18	58	0	0
HT29								36078	0	0	487	3221	1952	0	238	0	0	0
HT29								32554	0	0	7887	21100	3572	28	0	381	0	0
HT29								37558	0	388	842	2890	2874	0	0	0	0	0
HT29								18122	0	0	14370	8858	1350	318	0	0	0	0
Row-4								27182	851	0	0	35229	1183	185	873	574	0	0
Row-4								38821	38	0	0	1854	1018	78	178	0	0	0
Row-8								18890	0	0	0	311	80	0	171	10	0	0
Hs6 modulate RNA								177	0	142	393	0	843	0	418	110	0	0
HT29								8327	0	0	3240	546	48	0	178	0	0	0
HT29								44182	257	0	245	733	2244	408	0	0	0	0
Hs6 modulate RNA								80088	0	0	1378	3582	0	0	0	0	0	0
Hs6 modulate RNA								44374	88	0	0	4910	70	0	281	0	0	0
Hs6 modulate RNA								20025	7	0	0	5212	14	0	0	0	0	0
Hs6 modulate RNA								24878	239	1275	3582	3701	1721	1048	0	0	0	0
Hs6 modulate RNA								27047	0	0	18785	8881	874	0	0	0	0	0
Hs6 modulate RNA								32124	0	281	12889	10412	478	1982	383	483	0	0
Hs6 modulate RNA								0	0	0	11	1788	4488	297	241	483	0	0
Hs6 modulate RNA								0	0	0	0	3318	7870	113	0	0	0	0
Hs6 modulate RNA								0	0	0	1789	1889	2247	0	0	0	0	0
Hs6 modulate RNA								0	0	0	588	2878	7815	287	243	0	0	0
Hs6 modulate RNA								0	0	0	0	2261	52	0	282	0	0	0
Hs6 modulate RNA								0	0	0	148	8824	7875	1143	813	0	0	0
Hs6 modulate RNA								0	0	0	0	1842	2378	0	436	0	0	0
Hs6 modulate RNA								0	0	0	1238	323	3534	181	0	0	0	0
Hs6 modulate RNA								0	0	0	1070	3808	3887	0	383	0	0	0
Hs6 modulate RNA								0	0	0	0	2090	8878	800	0	0	0	0
Hs6 modulate RNA								0	0	0	1283	1813	11868	870	1055	0	0	0
Hs6 modulate RNA								0	0	0	708	8721	708	0	586	0	0	0
Hs6 modulate RNA								0	0	0	899	3034	13756	1758	3848	0	0	0
Hs6 modulate RNA								0	0	0	813	16878	2575	211	284	0	0	0
Hs6 modulate RNA								0	0	0	1288	11033	1872	158	748	0	0	0
Hs6 modulate RNA								0	0	0	0	1883	2226	0	108	0	0	0
Hs6 modulate RNA								0	0	0	846	1202	2280	414	0	0	0	0
Hs6 modulate RNA								0	0	0	588	6480	0	840	908	0	0	0
Hs6 modulate RNA								0	0	0	1647	8487	7120	0	111	0	0	0
Hs6 modulate RNA								0	0	0	0	3700	2419	28	400	0	0	0
Hs6 modulate RNA								0	0	0	236	288	1833	13	0	0	0	0
Hs6 modulate RNA								0	0	0	838	2525	2787	433	0	0	0	0
Hs6 modulate RNA								0	0	0	0	1654	2858	84	718	0	0	0
Hs6 modulate RNA								0	0	0	1387	1884	4781	128	182	0	0	0
Hs6 modulate RNA								0	0	0	389	0	372	0	0	0	0	0
Hs6 modulate RNA								0	0	0	858	3540	283	2588	0	0	0	0
Hs6 modulate RNA								0	0	0	0	377	3878	502	1084	0	0	0
Hs6 modulate RNA								0	0	0	2315	1278	4244	300	14325	0	0	0
Hs6 modulate RNA								0	0	0	1782	1828	4535	80	1577	0	0	0
Hs6 modulate RNA								0	0	0	0	1863	0	0	288	0	0	0
Hs6 modulate RNA								0	0	0	72	775	451	0	808	0	0	0
Hs6 modulate RNA								0	0	0	0	5487	8	0	0	0	0	0
Hs6 modulate RNA								0	0	0	0	10	2127	0	0	0	0	0
Hs6 modulate RNA								0	0	0	578	411	1477	381	284	0	0	0
Hs6 modulate RNA								0	0	0	1430	11836	8021	10003	5163	0	0	0
Hs6 modulate RNA								0	0	0	1198	8148	5884	9918	2043	0	0	0
Hs6 modulate RNA								0	0	0	1755	8146	2388	0	3289	0	0	0
Hs6 modulate RNA								0	0	0	606	17887	319	507	219	0	0	0
Hs6 modulate RNA								0	0	0	1828	2318	2948	388	0	0	0	0
Hs6 modulate RNA								0	0	0	2401	8487	7121	105	529	0	0	0
Hs6 modulate RNA								0	0	0	2780	1182	2086	1817	0	0	0	0
Hs6 modulate RNA								0	0	0	1194	1180	8451	0	0	0	0	0
Hs6 modulate RNA								0	0	0	1417	2882	4751	1874	22	0	0	

Thru	Trans-ysn	Normal-ysn	Trans-1-6	Trans-ends	Normal	Ends	ps3	REQ	44	REQ	45	ANISO	46	ANISO	47	ANISO	48	ANISO	49	ANISO	50	ANISO	51	ANISO	52	ANISO	53	ANISO	54	ANISO	55	ANISO	56	ANISO	57	ANISO	58	ANISO	59	ANISO	60	ANISO	61	ANISO	62	ANISO	63	ANISO	64	ANISO	65	ANISO	66	ANISO	67	ANISO	68	ANISO	69	ANISO	70	ANISO	71	ANISO	72	ANISO	73	ANISO	74	ANISO	75	ANISO	76	ANISO	77	ANISO	78	ANISO	79	ANISO	80	ANISO	81	ANISO	82	ANISO	83	ANISO	84	ANISO	85	ANISO	86	ANISO	87	ANISO	88	ANISO	89	ANISO	90	ANISO	91	ANISO	92	ANISO	93	ANISO	94	ANISO	95	ANISO	96	ANISO	97	ANISO	98	ANISO	99	ANISO	100	ANISO	101	ANISO	102	ANISO	103	ANISO	104	ANISO	105	ANISO	106	ANISO	107	ANISO	108	ANISO	109	ANISO	110	ANISO	111	ANISO	112	ANISO	113	ANISO	114	ANISO	115	ANISO	116	ANISO	117	ANISO	118	ANISO	119	ANISO	120	ANISO	121	ANISO	122	ANISO	123	ANISO	124	ANISO	125	ANISO	126	ANISO	127	ANISO	128	ANISO	129	ANISO	130	ANISO	131	ANISO	132	ANISO	133	ANISO	134	ANISO	135	ANISO	136	ANISO	137	ANISO	138	ANISO	139	ANISO	140	ANISO	141	ANISO	142	ANISO	143	ANISO	144	ANISO	145	ANISO	146	ANISO	147	ANISO	148	ANISO	149	ANISO	150	ANISO	151	ANISO	152	ANISO	153	ANISO	154	ANISO	155	ANISO	156	ANISO	157	ANISO	158	ANISO	159	ANISO	160	ANISO	161	ANISO	162	ANISO	163	ANISO	164	ANISO	165	ANISO	166	ANISO	167	ANISO	168	ANISO	169	ANISO	170	ANISO	171	ANISO	172	ANISO	173	ANISO	174	ANISO	175	ANISO	176	ANISO	177	ANISO	178	ANISO	179	ANISO	180	ANISO	181	ANISO	182	ANISO	183	ANISO	184	ANISO	185	ANISO	186	ANISO	187	ANISO	188	ANISO	189	ANISO	190	ANISO	191	ANISO	192	ANISO	193	ANISO	194	ANISO	195	ANISO	196	ANISO	197	ANISO	198	ANISO	199	ANISO	200	ANISO	201	ANISO	202	ANISO	203	ANISO	204	ANISO	205	ANISO	206	ANISO	207	ANISO	208	ANISO	209	ANISO	210	ANISO	211	ANISO	212	ANISO	213	ANISO	214	ANISO	215	ANISO	216	ANISO	217	ANISO	218	ANISO	219	ANISO	220	ANISO	221	ANISO	222	ANISO	223	ANISO	224	ANISO	225	ANISO	226	ANISO	227	ANISO	228	ANISO	229	ANISO	230	ANISO	231	ANISO	232	ANISO	233	ANISO	234	ANISO	235	ANISO	236	ANISO	237	ANISO	238	ANISO	239	ANISO	240	ANISO	241	ANISO	242	ANISO	243	ANISO	244	ANISO	245	ANISO	246	ANISO	247	ANISO	248	ANISO	249	ANISO	250	ANISO	251	ANISO	252	ANISO	253	ANISO	254	ANISO	255	ANISO	256	ANISO	257	ANISO	258	ANISO	259	ANISO	260	ANISO	261	ANISO	262	ANISO	263	ANISO	264	ANISO	265	ANISO	266	ANISO	267	ANISO	268	ANISO	269	ANISO	270	ANISO	271	ANISO	272	ANISO	273	ANISO	274	ANISO	275	ANISO	276	ANISO	277	ANISO	278	ANISO	279	ANISO	280	ANISO	281	ANISO	282	ANISO	283	ANISO	284	ANISO	285	ANISO	286	ANISO	287	ANISO	288	ANISO	289	ANISO	290	ANISO	291	ANISO	292	ANISO	293	ANISO	294	ANISO	295	ANISO	296	ANISO	297	ANISO	298	ANISO	299	ANISO	300	ANISO	301	ANISO	302	ANISO	303	ANISO	304	ANISO	305	ANISO	306	ANISO	307	ANISO	308	ANISO	309	ANISO	310	ANISO	311	ANISO	312	ANISO	313	ANISO	314	ANISO	315
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174
Table 3 (cont'd)

Tissue	Tumor-typ	Normal-typ	Tumor - 1a	Tumor cells	Normal	Endo	μ33	SEQ 844	TRE6	48	AN	SEQ 47	AN	SEQ 48	AN	SEQ 31	HA	SEQ 32	AN	SEQ 33	EQ	SEQ 35	CL
Adip			108					0	0	47	88	4012	0	164	258	8448							
Adip			108					4917	0	0	912	7888	48	0	21583	20805							
Adip			171					0	0	0	26	4438	773	256	5531	7187							
Adip			181					0	0	0	162	1646	274	0	0	261							
Adip			181					0	0	0	162	1380	120	383	162	0							
Adip			181					0	0	0	31	867	0	1	212	410							
Adip			181					0	0	0	135	1053	25	52	2111	7693							
Adip			181					0	0	0	0	3637	0	84	341	3781							
Adip			181					0	0	0	0	2832	208	171	9142	3184							
Adip			181					0	0	0	131	1290	0	0	1277	1270							
Adip			181					0	0	0	36	7	1207	0	0	1238	1028						
Adip			181					0	0	0	171	22	0	0	0	0	0	0	0	0	0	0	0
Adip			181					0	0	0	0	742	0	0	0	0	0	0	0	0	0	0	0
Adip			181					0	0	0	0	7127	0	0	0	0	0	0	0	0	0	0	0
Adip			181					0	0	0	0	141	1104	0	0	0	0	0	0	0	0	0	0
Adip			181					0	0	0	0	2120	0	0	0	0	0	0	0	0	0	0	0
Adip			181					0	0	0	0	896	0	0	0	0	0	0	0	0	0	0	0
Adip			181					0	0	0	0	2236	320	0	0	0	0	0	0	0	0	0	0
Adip			181					0	0	0	0	178	0	0	0	0	0	0	0	0	0	0	0
Adip			181					0	0	0	0	1184	272	0	0	0	0	0	0	0	0	0	0
Adip			181					0	0	0	0	1198	128	0	0	0	0	0	0	0	0	0	0
Adip			181					0	0	0	0	129	2740	138	217	2810	2440						
Adip			181					0	0	0	0	2832	307	814	1488	10317							
Adip			181					0	0	0	0	2628	3413	241	2562	8358							
Adip			181					0	0	0	0	2938	0	0	0	0	0	0	0	0	0	0	0
Adip			181					0	0	0	0	2108	1910	33	281	2208							
Adip			181					0	0	0	0	2481	0	415	163	244							
Adip			181					0	0	0	0	1567	263	648	1361	0							

Table 3 (cont'd)

Tissue	Tumor type	Normal type	Tumor - to	Tumor cells	Normal	Endoth	p53	SEF 444	TRF5	45	AN	SEF 47	AN	SEF 48	AN	SEF 51	KH5E	32	AN	SEF 54	CG	SEF 55	CL
h. 528T		153						4199	0	0	84	0	4775	0	670	1535	18395						
hCT-TRACRES		153						0	0	0	188	3752	0	110	1947	4826							
MCF7		153						3532	0	0	181	0	7951	0	16021	0	27225						
MH		149						0	0	150	0	3887	1881	6927	0	1425							
UACC-257		147						0	0	0	0	6325	506	0	812	14838							
UACC-42		145						0	0	0	0	0	0	0	0	0							
SK-MEL-20		144						0	0	0	47	45	3386	319	64	1253	4601						
UO-31		143						869	0	0	107	0	4289	199	22	96	8368						
SK-MEL-5		142						755	0	0	0	0	8124	1944	426	0	5065						
KAL-12		141						895	0	14	0	4762	979	484	1913	8211							
SK-MEL-2		140						1090	0	0	29	2880	290	437	868	1786							
HCT-15		138						0	0	4	0	3883	389	177	1587	18258							
h. 528T		138						0	0	0	0	6162	0	285	370	16981							
CCQ-D 205		137						1858	0	0	0	0	4847	25	311	1087	8770						
LOX-BV1		136						2752	0	222	329	5648	0	0	0	0	5235						
SW-420		135						8430	0	0	181	2535	895	93	0	11410							
TK-10		134						1038	0	27	0	2084	1187	304	859	3486							
HCT-116		133						1885	0	0	10	2528	1063	344	895	11184							
786-0		132						519	0	107	104	3883	1088	180	0	4887							
HOC-2688		131						2791	0	7	119	3530	0	370	374	8885							
ADH1		130						1271	0	0	0	8532	767	281	770	7943							
PC-3		129						0	0	0	0	104	4586	527	102	880	8837						
ROF-363		128						0	0	0	0	3699	619	250	246	9009							
DU-145		127						3343	0	11	212	3357	0	268	982	16947							
C461		126						455	0	0	83	3437	231	81	0	2441							
SK		125						0	0	132	180	4852	0	285	487	7704							
A498		124						1045	0	2	0	3878	0	0	620	7915							
hCT-TRACRES		123						2386	0	126	305	4461	0	732	4011	12161							
SM-12		122						0	0	0	84	3952	1414	162	8477	5650							
h. 40		121						0	0	0	288	4346	1782	350	11461	10454							
MOLT-4		120						0	0	0	144	2636	0	263	0	1405							
OVCA9-6		119						501	0	24	0	3217	509	83	3253	4967							
h. 40		118						875	0	86	30	4878	0	86	4265	7605							
OVCA9-4		117						0	0	0	0	7270	0	372	2107	843							
OVCA9-3		116						1705	0	0	0	8428	2262	352	4352	13504							
CCRF-CEM		115						618	0	70	0	3041	1813	180	852	14584							
OVCA9-3		114						2526	0	86	0	3837	0	180	281	5828							
HOP-62		113						841	0	2	0	3052	613	0	183	489							
SP-385		112						327	0	0	189	3630	204	25	811	14252							
ASU-ATCC		111						679	0	9	710	8431	2145	387	1058	10818							
SP-385		110						1174	0	0	183	9631	1777	634	1289	11838							
MDA-M22		108						883	0	0	152	2841	432	107	1883	5808							
U251		107						0	0	21	0	8381	1671	402	863	8185							
MDA-M22		106						1887	0	0	474	4657	640	321	1215	7924							
MDA-M22		105						284	0	271	41	4586	651	346	0	8432							
MDA-M22		104						883	0	78	3	2647	633	330	0	8105							
MDA-M22		103						0	0	0	26	2880	134	348	0	8695							
MDA-M22		102						0	0	82	0	0	2171	1079	491	2088	4580						
MDA-M22		101						4486	0	0	0	7047	19	0	284	1818	1584						
MDA-M22		100						842	0	58	0	3732	2010	825	0	11644							
MDA-M22		99						209	0	142	0	3780	1389	492	1750	6447							
MDA-M22		98						783	0	0	0	4188	1610	786	0	4385							
MDA-M22		97						0	0	14	187	2052	79	46	151	2651							
MDA-M22		96						0	0	72	385	2056	29	46	151	2651							
MDA-M22		95						0	0	0	108	2888	1247	54	445	4824							
MDA-M22		94						1188	0	0	123	3977	1635	86	1335	2848							
MDA-M22		93						2288	0	112	0	4184	0	36	742	4423							
MDA-M22		92						1043	0	0	328	3112	734	278	0	2314							
MDA-M22		91						0	0	115	8	2362	7026	256	311570	3115							
MDA-M22		90						407	0	48	37	0	0	0	0	0							
MDA-M22		89						317	0	105	0	0	0	0	0	0							
MDA-M22		88						0	0	26	153	0	0	0	0	0							
MDA-M22		87						321	0	109	82	0	0	0	0	0							
MDA-M22		86						0	0	128	46	0	0	0	0	0							
MDA-M22		85						3881	0	2138	265	0	0	0	0	0							
MDA-M22		84						2147	0	841	0	0	0	0	0	0							
MDA-M22		83						2885	0	0	0	0	0	0	0	0							
MDA-M22		82						1030	0	0	0	0	0	0	0	0							
MDA-M22		81						0	0	1627	0	0	0	0	0	0							
MDA-M22		80						0	0	0	0	0	0	0	0	0							
MDA-M22		79						403	0	0	46	0	0	0	0	0							
MDA-M22		78						150	0	115	0	0	0	0	0	0							
MDA-M22		77						3124	0	0	0	0	0	0	0	0							
MDA-M22		76						846	0	0	0	0	0	0	0	0							
MDA-M22		75						0	0	1818	125	0	0	0	0	0							
MDA-M22		74						3024	0	280	0	0	0	0	0	0							
MDA-M22		73						4797	0	279	128	0	0	0	0	0							
MDA-M22		72						626	0	572	84	0	0	0	0	0							
MDA-M22		71						768	0	381	11	0	0	0	0	0							
MDA-M22		70						0	0	0	0	0	0	0	0	0							
MDA-M22		69						2518	0	51	178	0	0	0	0	0							
MDA-M22		68						1849	0	80	0	0	0	0	0	0							
MDA-M22		67						0	0	0	0	0	0	0	0	0							
MDA-M22		66						3088	0	37	0	0	0	0	0	0							
MDA-M22		65						812	0	43	0	0	0	0	0	0							
MDA-M22		64						0	0	388	0	0	0	0	0	0							
MDA-M22		63																					

176
Table 3 (cont'd)[illegible]

177
Table 3 (cont'd)

Theme	Tumor type	Normal type	Tumor - to	Tumor path	Normal	Endoth	p32	SEQ 35	AN SEQ 37	WT SEQ 40	AA SEQ 43	MS SEQ 46	CA SEQ 48	PM SEQ 51	RS SEQ 53	MS SEQ 55	MS SEQ 57
RA-10T	145							0	41445	547	1888	3442	2075	2567	8305	55874	
RA-10T-RES	153							2258	18577	3302	2910	488	22338	1888	3602	84013	
RA-10T	151							3884	30995	160	1589	2844	11806	3485	22510	81758	
RA-10T	149							776	18792	0	704	437	6274	3888	4621	88088	
RA-10T-RES	147							156	14876	1834	7205	183	8887	2195	17873	61725	
RA-10T-RES	145							880	8415	0	2146	776	9453	1589	4231	41289	
RA-10T-RES	144							40	12812	4898	577	574	1071	2990	56831		
RA-10T-RES	143							448	8859	1716	824	88	14005	2232	3634	105681	
RA-10T-RES	142							1152	27382	1004	1844	2808	13115	1215	8895	42911	
RA-10T-RES	141							325	5237	3812	104	0	1081	1517	54	48888	
RA-10T-RES	140							1987	14488	3221	795	1827	7440	1378	3478	56571	
RA-10T-RES	138							746	12275	771	857	856	4827	2887	7421	71198	
RA-10T-RES	136							1725	28340	2545	3991	2563	10072	2838	7321	42597	
RA-10T-RES	134							2484	8189	2785	438	1040	12401	1881	2407	96315	
RA-10T-RES	132							303	37237	332	3101	4339	32433	822	8951	13734	
RA-10T-RES	130							838	8511	0	1807	1808	10151	1185	2780	38389	
RA-10T-RES	128							448	8427	1217	1508	1082	23888	1771	11381	42220	
RA-10T-RES	126							1818	7388	0	148	413	11784	3813	1488	38995	
RA-10T-RES	124							888	8219	827	1162	847	28089	1870	7153	41882	
RA-10T-RES	122							1790	8388	0	387	1115	8212	1884	3256	74985	
RA-10T-RES	120							819	8838	1426	1253	845	21377	1488	7825	48824	
RA-10T-RES	118							577	18302	0	33	88	14288	1450	3111	48870	
RA-10T-RES	116							1087	12823	1508	4327	377	28088	1884	13038	43831	
RA-10T-RES	114							1200	8843	100	128	178	8882	2174	3856	48304	
RA-10T-RES	112							881	12878	581	2888	324	4888	1833	15823	42879	
RA-10T-RES	110							0	8755	0	1254	2308	3627	1724	4070	44877	
RA-10T-RES	108							8113	18848	351	295	0	14129	2475	10880	48887	
RA-10T-RES	106							0	3481	0	1	112	588	3030	8708	88175	
RA-10T-RES	104							0	17323	0	2522	124	6784	2447	10872	72884	
RA-10T-RES	102							303	4211	441	118	280	1254	2857	2880	58884	
RA-10T-RES	100							225	4495	2178	551	811	5501	1313	7213	70188	
RA-10T-RES	98							108	12544	8273	2442	877	15121	388	32878	49584	
RA-10T-RES	96							1244	4813	2234	588	4278	1771	8528	58838		
RA-10T-RES	94							2174	13887	4188	240	1640	14315	14888	21344	44825	
RA-10T-RES	92							1888	31473	388	4834	681	4841	1490	7738	58882	
RA-10T-RES	90							588	8888	2282	1091	178	3448	1421	78844	42801	
RA-10T-RES	88							1113	7238	0	688	834	18312	1247	4255	41078	
RA-10T-RES	86							0	6288	2082	5356	887	18788	890	24881	25387	
RA-10T-RES	84							203	7284	304	1651	2776	8731	878	18884	47318	
RA-10T-RES	82							1371	14738	0	3748	2445	1303	1303	88884	51884	
RA-10T-RES	80							1320	11508	0	3388	1084	18314	1090	8820	32884	
RA-10T-RES	78							335	19129	1948	3385	1283	17962	2884	15385	42885	
RA-10T-RES	76							1814	8800	2187	874	1811	28919	2228	10888	53842	
RA-10T-RES	74							1881	11884	2128	5788	878	15224	1585	32838	58888	
RA-10T-RES	72							252	7383	127	538	25	20030	1090	1588	48388	
RA-10T-RES	70							3883	13887	3336	3517	473	11088	2186	28883	88284	
RA-10T-RES	68							0	7540	1418	588	329	14888	2884	8129	52719	
RA-10T-RES	66							822	18881	1882	2847	212	17882	4414	12488	103882	
RA-10T-RES	64							0	18857	871	740	482	5154	2748	8302	51778	
RA-10T-RES	62							872	18836	1788	8827	716	1781	3128	28827	58481	
RA-10T-RES	60							878	18881	3817	885	685	2286	3272	72820	58878	
RA-10T-RES	58							0	8488	388	3388	317	4888	2878	21182	43870	
RA-10T-RES	56							347	7233	2832	887	874	8834	1048	48884	48884	
RA-10T-RES	54							474	12857	2387	3887	782	12852	2285	31301	58838	
RA-10T-RES	52							0	1888	880	2436	215	28788	1814	5385	18888	
RA-10T-RES	50							37	3414	0	477	88	28787	1484	18148	72828	
RA-10T-RES	48							4753	10827	0	2520	7044	18844	1178	5181	72878	
RA-10T-RES	46							888	12882	15	3818	701	3828	2428	1814	81038	
RA-10T-RES	44							0	2886	527	12188	0	5878	321	14888	38882	
RA-10T-RES	42							0	3588	0	383	0	217	214	3847	10181	
RA-10T-RES	40							0	2888	0	1888	0	523	157	11425	18882	
RA-10T-RES	38							0	4433	0	212	0	488	242	15448	12882	
RA-10T-RES	36							0	3415	0	178	0	1883	281	12482	28821	
RA-10T-RES	34							0	7816	218	10485	0	2388	882	27484	14820	
RA-10T-RES	32							0	8888	0	7480	0	3883	1083	78184	18451	
RA-10T-RES	30							0	4185	0	8233	0	342	387	7118	14820	
RA-10T-RES	28							0	2882	442	1804	0	2888	781	18820	27888	
RA-10T-RES	26							0	8308	1484	40	0	1233	1386	5215	28818	
RA-10T-RES	24							0	2888	0	3885	0	388	287	11222	18811	
RA-10T-RES	22							0	4304	0	2710	0	177	321	18788	14247	
RA-10T-RES	20							0	2871	852	287	0	707	191	10884	15880	
RA-10T-RES	18							0	4888	0	212	0	80	24367	14888		
RA-10T-RES	16							0	2815	0	341	0	388	118	8734	14350	
RA-10T-RES	14							0	12125	0	4888	0	1132	881	48882	43288	
RA-10T-RES	12							0	7885	384	1843	0	883	715	8378	15827	
RA-10T-RES	10							0	3513	812	78	0	1047	838	10884	22884	
RA-10T-RES	8							0	1814	0	8874	0	572	118	18218	11885	
RA-10T-RES	6							0	8037	0	1518	0	438	319	8884	17885	
RA-10T-RES	4							0	11884	0	1743	0	488	814	23888	11870	
RA-10T-RES	2							0	18888	317	2832	0	2774	777	23788	13274	
RA-10T-RES	0							0	8781	0	184	0	2888	788	28888	14888	
RA-10T-RES	0							0	8853	0	1887	0	1877	780	8808	17883	
RA-10T-RES	0							0	1191	481	887	0	888	1033	12882	13882	
RA-10T-RES	0							0	2872	1045	125	0	783	381	88881	12885	
RA-10T-RES	0							0	8135	388	2880	0	288	388	18837	12211	
RA-10T-RES	0							0	1882	787	1330	0	383	819	11388	10788	
RA-10T-RES	0							0	8774	348	2888	0	2120	834	38287	18512	
RA-10T-RES	0							0	8823	0	1884	0	1873	880	18878	78187	
RA-10T-RES	0							0	8732	0	1888	0	488	788	12288	13288	
RA-10T-RES	0							0	7888	0	3838	0	581	547	4848	14887	
RA-10T-RES	0							0	11878	0	3883	0	1887	567	32388	15825	
RA-10T-RES	0							0	3388	0	2880	0	1547	552	8875	17847	
RA-10T-RES	0							0	8748	82	3847	0	8				

178
Table 3 (cont'd)

Trans	Trans-sym	Harmon-sym	Trans-to	Trans-calc	Harmon	Endus	p53	SEQ 8	AA	SEQ 37	WT	SEQ 46	AA	SEQ 47	ME	SEQ 56	CA	SEQ 64	ME	SEQ 73	ME	SEQ 78	AA
Dufang-2								0	80728	3124	2203	0	2725	1021	16539	11848							
Dufang-8								0	35261	84	3297	0	3819	949	23470	14551							
Dufang-11								0	28319	0	4208	0	4247	714	53757	12234							
Dufang-12								0	46458	0	8822	0	3724	1096	48305	13175							
Dufang-10								0	19274	0	1652	0	2814	892	58843	11887							
Dufang-2								0	18815	0	1364	0	4270	801	24045	11421							
Dufang-4								0	11239	0	21443	0	2076	1022	20201	22149							
Dufang-4								0	9371	0	13705	0	1528	783	15252	18150							
Dufang-5								0	6955	1171	810	0	17445	882	20143	25155							
Dufang-5								0	4880	0	810	0	17445	882	20143	25155							
Dufang-5								0	3723	0	216	0	1618	648	3831	12544							
ASAP-8								0	38584	0	1873	0	485	682	1829	8561							
ERVL-8								0	4018	537	1873	0	2260	386	18512	13823							
ACT-116-7								0	6748	0	8061	0	4381	807	24266	14185							
ACT-116-8								0	28415	507	80	0	812	478	6413	12863							
HT28-1								0	5165	3418	889	0	352	281	11432	18800							
HT28-7								0	2474	0	1484	0	451	28515	21737								
HT28-8								0	1063	0	54	0	307	206	9185	13162							
SP329-7								0	4333	0	2262	0	709	594	16287	19784							
SP329-7								0	5165	3418	889	0	352	281	11432	18800							
SP329-7								0	6910	1880	709	0	1318	1088	13408	17889							
SP329-7								0	8805	0	150	0	896	211	14376	8028							
OVCA4-7								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-7								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	211	14376	8028							
OVCA4-8								0	6910	1880	709	0	1318	1088	13408	17889							
OVCA4-8								0	8805	0	150	0	896	21									

[illegible]

180
Table 3 (cont'd)[illegible]

181
Table 3 (cont'd)[illegible]

Table 3 (cont'd)

[illegible]

184
Table 3 (cont'd)

Accession	Transcript	Normal	Transcript	Transcript	Normal	Ends	p33	SEQ 95	Δ SEQ 10	Δ SEQ 17	Δ SEQ 27	Δ SEQ 37	Δ SEQ 47	Δ SEQ 57	Δ SEQ 67	Δ SEQ 77	Δ SEQ 87	Δ SEQ 97	Δ SEQ 107	Δ SEQ 117	Δ SEQ 127	Δ SEQ 137	Δ SEQ 147
1-70	188							377	308	131	1114	713	82	360									
1-70	188							220	38	43	61721	9018	0	1086									
1-70	188							0	152	14	104	580	1079	0	780								
1-70	188							0	3	150	85	0	538	0	530								
1-70	188							31	447	0	1	61	747	0	583								
1-70	188							0	203	303	0	123	81	258	0	303							
1-70	188							0	263	278	1030	237	0	448	0								
1-70	188							0	131	138	163	260	0	474	0								
1-70	188							0	118	437	1048	6815	0	583	0								
1-70	188							0	64	1808	1327	167	0	808	0								
1-70	188							0	76	137	0	167	138	172	0								
1-70	188							0	624	846	0	73	1428	156	0	431	0						
1-70	188							0	886	0	0	23	134	0	157	0							
1-70	188							0	173	1711	0	251	368	0	858	0							
1-70	188							0	151	680	27	188	0	0	452	0							
1-70	188							0	186	0	111	20	115	0	306	0							
1-70	188							0	90	138	41	322	0	477	0								
1-70	188							0	80	0	8	42	212	194	0								
1-70	188							0	140	181	117	100	0	172	0								
1-70	188							0	173	284	31	88	0	582	0								
1-70	188							0	197	155	365	88	0	86	0								
1-70	188							0	173	804	3918	787	0	624	204	0							
1-70	188							0	202	302	16	379	2736	230	378	0							
1-70	188							0	272	53	330	0	0	18	0								
1-70	188							0	524	424	2576	183	0	0	0								
1-70	188							0	430	847	148	1617	0	0	480	0							
1-70	188							0	212	837	249	0	0										
1-70	188							0	122	226	281	825	0	425	0								
1-70	188							0	1127	321	3876	467	215	306	770	0							
1-70	188							0	425	54	448	1543	531	382	484	8882							
1-70	188							0	84	421	79	463	453	0	186	0							
1-70	188							0	207	62	34	0	0	1	0								
1-70	188							0	815	0	73	8728	1336	0	351	305							
1-70	188							0	890	309	1602	0	1446	389	452	687	0						
1-70	188							0	753	0	18	133	243	0	275	0							
1-70	188							0	841	454	732	2188	814	367	703	0							
1-70	188							0	880	864	458	1887	369	188	638	0							
1-70	188							0	212	0	65	47	348	0	204	0							
1-70	188							0	872	0	624	448	415	683	0								
1-70	188							0	291	0	0	1528	323	0	453	0							
1-70	188							0	252	0	158	2049	1651	0	1121	0							
1-70	188							0	883	0	132	1007	0	0									
1-70	188							0	730	287	473	91	33	544	302								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483	0								
1-70	188							0	0	70	2108	303	0	483									

Table 3 (cont'd)

[illegible]

Table 3 (cont'd)

Flavor	Tennery-nm	Normal-nm	Tennery - 1e	Tennery-nm	Normal	Errors	g23	SEQ 36	ANSEQ 36	ANSEQ 37	HSEQ 140	ANSEQ 141	ANSEQ 146	ANSEQ 147	ANSEQ 148	ANSEQ 149	ANSEQ 150	ANSEQ 151	ANSEQ 152	ANSEQ 153	ANSEQ 154
DefPump-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DefPump-28	0	0	0	0																	

187
Table 3 (cont'd)

Tissue	Tumor-type	Human-tissue	Tumor - to	Tumor code	Normal	Endoc	p13	SEQ ID NO
adrenal gland - h		1						634
lymph node - h		2						822
thymus - h		3						6
pancreas - h		4						2091
prostate - h		5						236
colon - h		6						688
carotid artery - h		7						227
adipose tissue - h		8						2718
testis - h		9						1303
kidney - h		10						717
prostate - h		11						762
testis - h		12						637
adipose tissue - h		13						648
testis - h		14						410
adipose tissue - h		15						0
heart - h		16						184
small intestine - h		17						614
kidney - h		18						262
normal cord - h		19						259
heart - h		20						81
stomach - h		21						167
stomach - h		22						496
stomach - h		23						894
stomach - h		24						89
stomach - h		25						141
stomach - h		26						322
stomach - h		27						0
stomach - h		28						188
stomach - h		29						3124
stomach - h		30						91
stomach - h		31						198
stomach - h		32						189
stomach - h		33						0
stomach - h		34						179
stomach - h		35						71
stomach - h		36						1629
stomach - h		37						102
stomach - h		38						146
stomach - h		39						123
stomach - h		40						627
stomach - h		41						140
stomach - h		42						0
stomach - h		43						0
stomach - h		44						0
stomach - h		45						0
stomach - h		46						0
stomach - h		47						1282
stomach - h		48						1237
stomach - h		49						85
stomach - h		50						0
stomach - h		51						0
stomach - h		52						0
stomach - h		53						0
stomach - h		54						0
stomach - h		55						0
stomach - h		56						0
stomach - h		57						0
stomach - h		58						0
stomach - h		59						0
stomach - h		60						0
stomach - h		61						0
stomach - h		62						0
stomach - h		63						0
stomach - h		64						0
stomach - h		65						0
stomach - h		66						0
stomach - h		67						0
stomach - h		68						0
stomach - h		69						0
stomach - h		70						0
stomach - h		71						0
stomach - h		72						0
stomach - h		73						0
stomach - h		74						0
stomach - h		75						0
stomach - h		76						0
stomach - h		77						0
stomach - h		78						0
stomach - h		79						0
stomach - h		80						0
stomach - h		81						0
stomach - h		82						0
stomach - h		83						0
stomach - h		84						0
stomach - h		85						0
stomach - h		86						0
stomach - h		87						0
stomach - h		88						0
stomach - h		89						0
stomach - h		90						0
stomach - h		91						0
stomach - h		92						0
stomach - h		93						0
stomach - h		94						0
stomach - h		95						0
stomach - h		96						0
stomach - h		97						0
stomach - h		98						0
stomach - h		99						0
stomach - h		100						0
stomach - h		101						0
stomach - h		102						0
stomach - h		103						0
stomach - h		104						0
stomach - h		105						0
stomach - h		106						0
stomach - h		107						0
stomach - h		108						0
stomach - h		109						0
stomach - h		110						0
stomach - h		111						0
stomach - h		112						0
stomach - h		113						0
stomach - h		114						0
stomach - h		115						0
stomach - h		116						0
stomach - h		117						0
stomach - h		118						0
stomach - h		119						0
stomach - h		120						0
stomach - h		121						0
stomach - h		122						0
stomach - h		123						0
stomach - h		124						0
stomach - h		125						0
stomach - h		126						0
stomach - h		127						0
stomach - h		128						0
stomach - h		129						0
stomach - h		130						0
stomach - h		131						0
stomach - h		132						0
stomach - h		133						0
stomach - h		134						0
stomach - h		135						0
stomach - h		136						0
stomach - h		137						0
stomach - h		138						0
stomach - h		139						0
stomach - h		140						0
stomach - h		141						0
stomach - h		142						0
stomach - h		143						0
stomach - h		144						0
stomach - h		145						0
stomach - h		146						0
stomach - h		147						0
stomach - h		148						0
stomach - h		149						0
stomach - h		150						0
stomach - h		151						0
stomach - h		152						0
stomach - h		153						0
stomach - h		154						0
stomach - h		155						0
stomach - h		156						0
stomach - h		157						0
stomach - h		158						0
stomach - h		159						0
stomach - h		160						0
stomach - h		161						0
stomach - h		162						0
stomach - h		163						0
stomach - h		164						0

188
Table 3 (cont'd)

Therapy	Tumor-yes	Normal-yes	Tumor - 10	Tumor cells	Normal	Examine	p33	SEQ 116 3
Cell-1				188				0
FB-4				188				0
T-470				188				0
Kan-3				177				72
CR1 1411 RNA 870				181				0
HT11 untreated + DFluor				183				188
KB poly A+				184				47
HES poly A+				186				9
ACR4				188				52
UACC-62				200				0
MCF-7ADRI-RES				202				86
UTCC (Normal) poly A+				204				0
W121 (Colony) poly A+				206				36
488 antibody RNA				208				280
COL 127 RNA 32198				218				0
W1-30 T2n 8.9ALPES, 201 10% PBS				219				0
CR1 1411 + TPA (Gib) 829				220				242
Kan-1				221				84
Kan-2				222				79
Kan-3				222				0
H20A2				241				0
MOL-1				242				0
BRVX				243				0
SL-40				244				0
MDA-MB-13				245				0
HPM 8226				248				60
ASBMTCC				249				241
SR				249				0
OVCA-3				249				86
HCT-15				250				0
OVCA-4				251				0
MDA-3				252				0
OVCA-5				253				240
SH12C				254				0
OVCA-6				255				0
LOX NBT				256				0
HBLN1				257				0
SK-MEL-2				258				152
SK-OV-3				258				0
SK-MEL-5				260				0
BP-538				261				0
SK-MEL-28				262				0
K-562				263				22
UACC-257				264				33
MDA				265				0
MDA-MB-135				267				48
MDA-MB-135				268				188
HT279				278				0
MDA-N				271				0
MDA-MB-135				273				0
MDA-MB-135				280				26
HT279 2nd TPA RNA 922				308				147
HES-A-EXP-01188				313				83
HT279 on RNA				342				0
HT279				353				0
MDA-MB-135				354				126
MDA-MB-135				355				0
MDA-MB-135				357				0
MDA-MB-135				358				61
MDA-MB-135				359				0
MDA-MB-135				360				0
MDA-MB-135				361				0
MDA-MB-135				362				480
MDA-MB-135				363				0
MDA-MB-135				365				363
MDA-MB-135				367				241
MDA-MB-135				368				0
MDA-MB-135				369				312
MDA-MB-135				370				0
MDA-MB-135				371				0
MDA-MB-135				372				0
MDA-MB-135				373				0
MDA-MB-135				374				0
MDA-MB-135				375				0
MDA-MB-135				376				0
MDA-MB-135				377				0
MDA-MB-135				378				0
MDA-MB-135				379				0
MDA-MB-135				380				0
MDA-MB-135				381				0
MDA-MB-135				382				0
MDA-MB-135				383				0
MDA-MB-135				384				0
MDA-MB-135				385				0
MDA-MB-135				386				0
MDA-MB-135				387				0
MDA-MB-135				388				0
MDA-MB-135				389				0
MDA-MB-135				390				0
MDA-MB-135				391				0
MDA-MB-135				392				0
MDA-MB-135				393				0
MDA-MB-135				394				0
MDA-MB-135				395				0
MDA-MB-135				396				0
MDA-MB-135				397				0
MDA-MB-135				398				0
MDA-MB-135				399				0
MDA-MB-135				400				0
MDA-MB-135				401				0
MDA-MB-135				402				0
MDA-MB-135				403				0
MDA-MB-135				404				0
MDA-MB-135				405				0
MDA-MB-135				406				0
MDA-MB-135				407				0
MDA-MB-135				408				0
MDA-MB-135				409				0
MDA-MB-135				410				0
MDA-MB-135				411				0
MDA-MB-135				412				0
MDA-MB-135				413				0
MDA-MB-135				414				0
MDA-MB-135				415				0
MDA-MB-135				416				0
MDA-MB-135				417				0
MDA-MB-135				418				0
MDA-MB-135				419				0
MDA-MB-135				420				0
MDA-MB-135				421				0
MDA-MB-135				422				0
MDA-MB-135				423				0
MDA-MB-135				424				0
MDA-MB-135				425				0
MDA-MB-135				426				0
MDA-MB-135				427				0
MDA-MB-135				428				0
MDA-MB-135				429				0
MDA-MB-135				430				0
MDA-MB-135				431				0
MDA-MB-135				432				0
MDA-MB-135				433				0
MDA-MB-135				434				0
MDA-MB-135				435				0
MDA-MB-135				436				0
MDA-MB-135				437				0
MDA-MB-135				438				0
MDA-MB-135				439				0
MDA-MB-135				440				0
MDA-MB-135				441				0
MDA-MB-135				442				0
MDA-MB-135				443				0
MDA-MB-135				444				0
MDA-MB-135				445				0
MDA-MB-135				446				0
MDA-MB-135				447				0
MDA-MB-135				448				0
MDA-MB-135				449				0
MDA-MB-135				450				0
MDA-MB-135				451				0
MDA-MB-135				452				0
MDA-MB-135				453				0
MDA-MB-135				454				0
MDA-MB-135				455				0
MDA-MB-135				456				0
MDA-MB-135				457				0
MDA-MB-135				458				0
MDA-MB-135				459				0
MDA-MB-135				460				0
MDA-MB-135				461				0
MDA-MB-135				462				0
MDA-MB-135				463				0
MDA-MB-135				464				0
MDA-MB-135				465				0
MDA-MB-135				466				0
MDA-MB-135				467				0
MDA-MB-135				468				0
MDA-MB-135				469				0
MDA-MB-135				470				0
MDA-MB-135				471				0
MDA-MB-135				472				0
MDA-MB-135				473				0
MDA-MB-135				474				0
MDA-MB-135				475				0
MDA-MB-135				476				0
MDA-MB-135				477				0
MDA-MB-135				478				0
MDA-MB-135				479				0
MDA-MB-135				480				0
MDA-MB-135				481				0
MDA-MB-135				482				0
MDA-MB-135				483				0
MDA-MB-135				484				0
MDA-MB-135				485				0
MDA-MB-135				486				0
MDA-MB-135				487				0
MDA-MB-135				488				0
MDA-MB-135				489				0
MDA-MB-135				490				0
MDA-MB-135				491				0
MDA-MB-135				492				0
MDA-MB-135				493				0
MDA-MB-135				494				0
MDA-MB-135				495				0
MDA-MB-135				496				0
MDA-MB-135				497				0
MDA-MB-135				498				0
MDA-MB-135				499				0
MDA-MB-135				500				0

Table 3¹⁸⁹
(cont'd)

Tissue	Tissue type	Normal type	Tumor - 1a	Tumor code	Normal	Endo	p33	SE0 118 2
HA-SBT	154							0
MACF-TACR-RES	153							0
MACF-7	151							0
MA	148							7
UACC-257	147							22
UACC-62	145							0
SK-MEL-28	144							33
UO-31	143							0
SK-MEL-5	142							91
MA-12	141							4
SK-MEL-2	140							263
TYCT-15	138							328
Melan-3M	138							181
CCLO-306	137							259
LCX-BM	136							0
SR-428	135							0
TK-10	134							0
HCT-116	133							0
786-S	132							56
HCC-2098	131							78
ACHN	130							276
PC-3	129							0
RF-303	128							338
DA-145	127							80
Csk-1	126							276
SR	125							0
A-48	124							127
RFW-8228	123							8
SH-22	122							120
HL-60	121							118
MC-1-4	120							0
OVCA-5	119							0
K-562	118							30
OVCA-4	117							542
CCRF-CEM	116							888
OVCA-3	115							191
SF-539	114							87
HOP-62	113							0
SK-295	112							161
AS46MTC	111							110
BF-288	110							120
NCI-H92	109							0
U251	108							204
NCI-H160	107							0
SW-637	106							30
NCI-H122M	105							439
SW-637	104							70
NCI-H92	103							62
SK-OV-3	102							6
NCI-H102	101							777
SK-OV-1	100							0
SK-OV-2	99							54
OVCA-8	98							8
NCI-H92	97							43
h. Nucleosome 30182 812	48							148
h. Nucleosome 3021402 817	47							210
h. Nucleosome 302482 819	46							125
TCOP	38							0
ASB-1						wt		0
ASB-2						wt		379
ASB-4						wt		456
ASB-5						wt		3477
ASB-7						wt		724
ERVX-1						mutant		91
ERVX-4						mutant		200
ERVX-3						mutant		0
ERVX-5						mutant		481
ERVX-7						mutant		877
MC7-7-1						wt		0
MC7-7-3						wt		585
MC7-7-4						wt		216
MC7-7-5						wt		0
MC7-7-7						wt		0
ADR-RES-1						mutant		3049
ADR-RES-3						mutant		150
ADR-RES-4						mutant		79
ADR-RES-5						mutant		18
ADR-RES-7						mutant		30
WI-38-1						wt		0
WI-38-3						wt		263
WI-38-4						wt		589
WI-38-5						wt		589
WI-38-7						wt		0
HLA-1						HPV ES		0
HLA-2						HPV ES		55
HLA-4						HPV ES		585
HLA-5						HPV ES		304
HLA-7						HPV ES		105
HI298-1						mutant		0
HI298-3						mutant		0
HI298-4						mutant		0
HI298-5						mutant		0
HI298-7						mutant		0
ASB-2						mutant		120
ERVX-2						mutant		9
MCT-116-1						wt		0
MCT-116-2						wt		130
HT29-2						mutant		86
SF-303-1						wt		0
SF-303-2						wt		0
SF-303-3						mutant		200
SF-303-4						mutant		631
OVCA-4-1						wt		0
OVCA-4-2						wt		0
OVCA-5-1						mutant		523
OVCA-5-2						mutant		209
MC7-7-2						wt		86
ADR-RES-2						mutant		221
HLA-3						HPV ES		172
SW-637-1						mutant		0
SW-637-2						mutant		191
HI298-2						mutant		1003
CD3A-1						mutant		0
CD3A-2						mutant		0
LRUS-1						mutant		271
LRUS-2						mutant		877
hsp8-1						wt		0
hsp8-2						wt		24
WI-38-2						wt		204
Mel-1								5
Mel-2								0
Mel-3								0
Mel-4								14529
Mel-5								562
Mel-6								0
Mel-7								0
Mel-8								0
Mel-9								0

Table 4

Gene Name	SPID#	na	ID#	aa	Family	Group	Length_AA	Extra-Catalytic Domains (Amino acid positions)
X69117_h_beta_adrenergic	H	1	122	AGC	GRK	GRK	688	Regulator of G protein signalling domain 54-175; PH domain 559-652
AA144574_m	M	2	123	AGC	GRK	GRK	378	PH domain 249-337
AA210925_h	H	9	130	AGC	PKC	PKC	978	Phorbol esters/diacylglycerol binding domain (C1 domain) 238-287; PH domain 497-577
AA318604_h	H	11	132	AGC	PKC	PKC	890	Phorbol esters/diacylglycerol binding domain (C1 domain) 155-204 and 272-321; PH domain 417-532
AA887783_h	H	21	142	AGC	SGK	SGK	448	PX domain 13-120
AA021445_h3	H	32	152	CAMK	EMK	EMK	1311	Vitamin K-dependent carboxylation/gamma-carboxyglutamic (GLA) domain 1072-1113
R31237_1_h_AAC3348	H	34	154	CAMK	EMK	EMK	728	UBA domain 327-365
408786.5_h	H	36	156	CAMK	EMK	EMK	1330	PAS domain 133-198, 247-280, 354-388
Z38720_h	H	41	161	CAMK	MLCK	MLCK	874	WD domain, G-beta repeat 874-711
SGK088_h	H	42	162	CAMK	Trk	Trk	2287	Immunoglobulin domain 1-62, 97-153, 221-277, 518-578, 1817-1878; Fibronectin type III domain 301-390, 1897-1779
R19772_h	H	44	164	CAMK	Trk	Trk	1287	Immunoglobulin domain 1-62, 97-153, 221-277, 518-578, 1817-1878; Fibronectin type III domain 301-390, 1897-1779
17000139801197_h_IRA	H	76	195	Other	IRAK	IRAK	598	RhoGEF domain 235-405; Fibronectin type III domain 870-955; Immunoglobulin domain 788-851; PH domain 418-528
AA088547_h	H	78	197	Other	IRE	IRE	922	Death domain 28-108
AA232253_h	H	82	201	Other	MLK	MLK	800	PQQ enzyme repeat 39-76
AA589286_h	H	89	208	Other	SLOB	SLOB	649	SAM domain (Sterile alpha motif) 337-408
AA836348_h	H	113	232	STE	NEK	NEK	836	PX domain 18-122
PAK6_h	H	115	234	STE	STE20-02	STE20-02	719	Regulator of chromosome condensation (RCC1) 387-427, 427-480, 483-532, 598-650
								P21-Rho-binding domain 11-69

FIGURE 1A

SEQ ID NO: 122_X69117_H BARK2_H
 MADLEAVLADVSYLMAMEKSKATPAARASKRIVLPEPSIRSVMQKYLAERNEITFDKIFN
 QKIGFLLFKDFCLNEINEAVPQVKFYEEIKEYEKL DNEEDRLCRSRQIYDAYIMKELLSC
 SHPFSKQAVEHVQSHLSKKQVTSTLFPYIEEICESLRGDI FQKFMESDKFTRFCQWKNV
 ELNIHLTMNEFSVHRIIGRGGFGEVYGCRA DTGKMYAMKCLDKKRIKMKQGETLALNER
 IMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYATE
 IILGLEHVHNRFFVYRDLKPANILLDEHGHARISDLGLACDFS KKKPHASVGTHGYMAPE
 VLQKGTAYDSSADWFSLGCM LFKLLRGHSPFRQHKT DKHEIDRMTLT VNVELPDTFSPE
 LKSLLEGLLQRDVSKRLGCHGGGSQEVKEHSFFKGVDWQH VYLQKYPPPLIPPRGEVNAA
 DAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERWQQEVTETVYEAVNADTDKIEARK
 RAKNKQLGHEEDYALGKDCIMHGYMLKLG NPFLTQWQRRYFYLF PNRLEWRGEGESRQNL
 LTMEQILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKKE LNETFKEAQRLLRR
 APKFLNKPRSGTVELPKPSLCHRSNGL

SEQ ID NO: 123_AA144574_M BARK2_M
 CFVVYRDLKPANILLDEYGHVRI SDLGLACDFS KKKPHASVGTHGYMAPEVLQKGT CYDS
 SADWFSLGCM LFKLLRGHSPFRQHKT DKHEIDRMTLT VNVELPDAFSP ELRSLLEGLLQ
 RDVSQRLGCGGGGARELKEHIFFKGIDWQH VYLRYKYPPLIPPRGEVNAA DAFDIGSFDE
 EDTKGIKLLDCDQDLYKNFPLVISERWQQE VVETIYDAVNADTDKIEARKKAKNKQLGQE
 EDYAMGKDCIMHGYMLKLG NPFLTQWQRRYFYLF PNRLEWRGEGESRQSLTMEQIMSVE
 ETQIKDRKCILLRIKGGKQFVLQCESDPEFAQWLKELTCTFNEAQRLLRRAPKFLNKPR
 AILEFSKPPLCHRNSSGL

SEQ ID NO: 124_AA826850_H
 MGSSMSAATARRPVFDDKEDVNFDFH FQILRAIGKGSFGKVCIVQKRDTEKMYAMKYM NKQ
 QCIERDEVNRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQ
 FSEDVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIATIIKDG ERA
 TALAGTKPYMAPEIFXS FVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLV
 QLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVE
 PGFVPNGRLHCDPTFELEEMILES RPLHKKKKRLAKNKS RDNSRDSSQSENDYLQDCLD
 AIQQDFVIFNREKLKRSQDLPREPLPAPE SRDAAEPVEDEAERSALPMCGPICPSAGSG

SEQ ID NO: 125_AA960957_H
 MGGNHSKPPVFDENEEVNFDFH FQILRAIGKGSFGKVCIVQKRDTEKMYAMKYM NKQKCI
 ERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFTE
 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATVVKGAE RASSM
 AGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEIH SVTPIDEILNMF
 KVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWD AVFKKALMPGF
 VPKGRNLNCDPTFELEEMILES KPLHKKKKRLAKNRSRDGT KDSCPLNGHLQHCL ETVRE
 EFIIFNREKLRRQGGQGSQLLDTSRGGGQAQSKLQDGCNNNLLTHTCTRGCSS

SEQ ID NO: 126_TBK1_H
 MQSTSNHLWLLSDILGQGATANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMREFEVLK
 KLNHNKIVKLFAIEEETTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDVV
 GGMNHLRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQFVSLYGT EEYL
 HPDMYERAVLRKD HQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV MYKIITG
 KPSGAISGVQKAENGPIDWSGDMPVSCSLSRGLQVLLTPVLANILEADQEK CWGFDQFFA
 ETSDILHRMVIHVFSLQOMTAHKIYIHSYNTATIFHEL VYKQTKIISSNQELIYEGRR LV
 LEPGRLAQHFPKTT EENPIFVVSREPLNTIGLIYEKISLPKVHPRYDLDGDASMAKAITG
 VVCYACRIASTLLLYQELMRKGIRWLI ELIKDDYNETVHKKTEVVITLDFCIRNIEKTVK

FIGURE 1B

VYEKLMKINLEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSLADAWAHQE
GTHPKDRNVEKLQVLLNCMTEIYYQFKKDKAERRLAYNEEQIHKFDKQKLYYHATKAMTH
FTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDIEEEVSKYQEYTNELQETLPQ
KMFTASSGIKHTMTPIYPSSNTLVEMTLGMKKLKEEMEGVVKELAENNHILERFGSLTMD
GGLRNVDCI

SEQ ID NO: 127_AA305176_H

MDPTAGSKKEPGGGAATEEGVNRIAVPKPPSIEEFSIVKPISRGAFGKVYLQKGKGLYA
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIGDVK
LLHIYGYFDEEMAVKYISEVALALDYLRHGI IHRDLKPDNMLI SNEGHI KLTDFGLSKV
TLNRDINMMDILTTSPMAKPRQDYSRTPGQVLSLISSLGFNTPIAEKNQDPANILSACLS
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS
SASSQSHTFISSVESECHSSPKWEKDCQV

SEQ ID NO: 128_AA116841_M

TRPIWPWEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFV
PQPDDTDTSYFEARNNAQHLTVSGFSL

SEQ ID NO: 129_AA256100_H

MAMTAGTTTTFPMSNHTRERVTVAKLTLENFYSLNLIQHEERETRQKKLEVAMEEEGLAD
EEKLRRSQHARKETEFRLRLKTRLGLDDFESLKVIGRGAFGEVRLVQKKTGHIYAMKI
LRKSDMLEKEQVAHIRAERDILVEADGAWVVKMFYSFQDKRNLYLIMEFLPGGDMMTLLM
KKDTLTTEEETQFYISETVLAIDAIHQLGFIHRDIKPDNLLDAGHVKLSDFGLCTGLKK
AHRTEFYRNLTHNPPSDFSQNMNSKRKAETWKKNRRLAYSTVGTPDYIAPEVFMQTGY
NKLCDWWSLGVIMYEMLI GYPPFCSETPQETYRKVMNWKETLVFPPEVPISEKAKDLILR
FCIDSENRI GNSGV EIKGHPFFEGVDWEHIRERPAAPIEIKSIDDTSNFD DFPESDIL
QPVPNTTEPDYKSKDWVFLNYTYKRFEGLTQRGSIPTYMKAGKL

SEQ ID NO: 130_AA210825_H

DSLLPTPALGTPLPIWPVGLRTPLSLESTRSPTQRLLPSTPKDPAILRSPPPARSFLG
SPLSHLLTRSRGSRTOGPPGPPGGSRVGSRRVAVPGLPPWPPPPHYAGLPSPGPGSP
PPGGLELQSPPLLPQIPAPGSGVSFHIQIGLTREFVLLPAASELAHVQQLACSIVDQKF
PECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQEGDLVEVLSASATFEDFQIRPHAL
TVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCLNYHKRCAFSIPNNCSGARKRRLSSTSL
ASGHSVRLGTSES LPTAEELSRSTTELLPRRPSSSSSSSSASSYTGRPIELDKMLLSKV
KVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDCKFNCHKRCATRVPNDCLEALIN
GDVPMEEATDFSEADKSALMDESEDSGVI PGSHSENALHASEEEEEGEGGKAQSSSLGYIPL
MRVVQSVRHTTRKSS TTLREGWVVHYSNKD TLRKRHYWRLDCKCITLFQNNTTNRYYKEI
PLSEILTVEAQNFSLVPPGTNPHCFEIVTANATYFVGEMPGGTGGPSGQGAEEAARGLX
ETAIRQALMPVILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSG
QFGVVYGGKHKRKTGRDVAVKVIDKLRFP TKQESQLRNEVAILQSLRHPGIVNLECMFETP
EKV FVVM EKLHGDMLEMILSSEKGR LPERLT KFLITQILVALRHLHFKNIVHCDLKPEN
VLLASADFPFQVKLCDFGFARI IGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVGVI
MYVSLSGTFPFNEDEDINDQIQNAAFMYPASPSHI SAGAI DLINLLQVKMRKRYSDVK
SLSHPWLQEQYQTWLDLRELEGKMGERYI THESDDARWEQFAAEHPLPGSGLP TDRDLGGA
CPPQDHDMQGLAERISVL

SEQ ID NO: 131_AA127299_H

IQFIIVGAKDLLAMDSNGLSDPYIKITNLSQKTKVIKKTLTPTWNETFFVHFPEKTTLEL
ECWDHDTFSDDFIGKASISLAEIPALAEVDMWIDMKTKKGEFAGK

FIGURE 1C

SEQ ID NO: 132_AA316804_H

MSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSARLSNGSFSAPSILTNSRGSVHTV
SFLQIGLTRESVTIEAQELSLSAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSEN
ILQLITSADIEHGEDLVEVLSALATVEDFQIRPHTLYVHSYKAPTFCDYCGEMLWGLVR
QGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSNVSLPGPGLSVPRPLQPEYVALPSEES
HVVHQEPSKRIPSWSGRPIWMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGM
QCKDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDNNDINSDSSRGLDDT
EESPSPEDKMFFLDPSDLDERDEEAVKTISPSTSNNIPLMRVQSIKHTKRKSSTMVKE
GWMVHYTSRDNLRKRHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNISQG
SNPHCFEIIITDMVYFVGENNGDSSHNPLAATGVGLDVAQSWEKAIRQALMPVTPQASV
CTSPGQGDHKDLSTSISVSNCQIQENVDISTVYQIFADEVLGSGQFGIVYGGKHKRTGR
DVAIKVIDKMRFPKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVMEKLHGDML
EMILSSEKSRLEPERITKFMVTQILVALRNLHFKNIVHCDLKPENVLLASAEFPQVKLCD
FGFARIIGEKSFRRSVVGTPAYLAPEVLRSGYNRSLDMWSVGVIYVSLSGTFPFNEDE
DINDQIQNAAFMYPNPWREISGEAIDLINLLQVKMRKRYSDKSLSHPWLQDYQTWLD
LREFETRIGERYITHESDDARWEIHAYTHNLVYPKHFIMAPNPDDMEEDP

SEQ ID NO: 133_PKNBETA_H

MEEGAPRQPGPSQWPPPEDEKEVIRRAIQKELKIKEGVENLRRVATDRRHLLGHVQQLLRSS
NRRLEQLHGELRELHARILLPGPGPGAEPVASGPRPWAEQLRARHLEALRRQLHVELKV
KQGAENMTHTCASGTPKERKLLAAQQMLRDSQLKVALLRMKISSLEASGSPEPGPELLA
EELQHRLHVEAAVAEGAKNVVKLLSSRRTQDRKALAEQAQLQESSQKLDLLRLALEQLL
EQLPPAHLRSRVTRRELRAAVPGYPQPSGTPVKPTALTGTQLQVRLGCEQLLTAVPGRSP
AAALASSPSEGWLRTKAKHQGRGELASEVLAVLKVDNRVVGQTGWGQVAEQSWDQTFVI
PLERARELEIGVHWRDWRQLCGVAFLRLEDFLDNACHQLSLSLVPQGLLFAQVTFCDPVI
ERRPRLQRQERIFSKRRGQDFLRRSQMNLGMAAWGRLVMNLLPPCSPSTISPPKGCPR
PTTLREASDPATPSNFLPKKTPLEEMTPPPKPPRLYLPQEPTSEETPRTKRPHMEPRTR
RGPSPPASPTRKPPRLQDFRCLAVLGRGHFGKVLVQFKGTGKYAIAKALKKQEVLSRDE
IESLYCEKRILEAVGCTGHPFLSLLVCFQTSSHARFVTEFVPGDLMMQIHEDVFPEPQ
ARFYVACVVLGLQFLHEKKIYRDLKLDNLLLDAAQGFLKIADFGLCKEGIGFGDRTSTFC
GTPEFLAPEVLTQEAYTQAVDWWALGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPG
FLSVQGLEFIQKLLQKCPEKRLGAGEQDAEEIKVQPPFRITTNWQALLARTIQPPFVPTLC
GPADLRYFEGEFTGLPPALTPPAPHSLLTARQQAARDFDFVSERFLEP

SEQ ID NO: 134_AI021023_M_PKNBETA_M

LKWDNLLLDAAQGFLKIADFGLCKEGIGFGDRTSTFCGTPEFLAPEVLTQEAYTRAVDWWG
LGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPGFLSVQGLEFIQKLLQKCPEKRLGA
GEQDAEEIKVQPPFRITTNWQALLARTIQPPFVPTLCGPADLRYFEGEFTGLPPALTPPAP
HSLLTARQQAARDFDFVSERFLEP

SEQ ID NO: 135_H19102_H

GGNIRGPWARGWKSLSWTGLGTIRSDLEELWELRGHHYHQLHESLKPAFVLVEKPLPEWVVP
QFINLFLPEFPPIRPIRGQQQLKILGLVAKGSFGTVLKVLDCTQKAVFAVKVVPKVVLQR
DTVROCKEEVSIQRQINHPFVHSLGDSWQGRHLFIMCSYICSTDLYSLSAVGCFPEASI
RLFAAELVLVLCYLHDLGIMHRDVKMENILLDERGHLKLTDFGLSRHVPQGAQAYTICGT
LQYMAPEVLSGGPYNHAADWWSLGVLLFSLATGKFPVAAERDHSVAMLASVTHSDSEIPAS
LNQGLSLLLHELLECNPLHRLRYLHHFQVHPFFRGVAFDPELLQKQPVNFVTETQATQPS
SAETMPFDDFDCDLESFLLYPIPA

FIGURE 1D

SEQ ID NO: 136_AA476563_H

MEFFRIDSKDSASELLGLDFGEKLYSLKSEPLKPFFTLPDGDSASRSFNTSESKVEFKAQ
DTISRGSDSVFVIFSKDAAFDDVSGTDEGRPDLLVNLPGELESTREAAAMGPTKFTQTN
IGIIEINKLLEAPDVLCLRLSTEQCOAHEEKGIEELSDPSGPKSYSITEKHYAQEDPRMLF
VAAVDHSSSGDMSLLPSSDPKFQGLGVVESAVTANNTESLFRICSPLSGANEYIASTDT
LKTEEVLLFTDQTDLLAKEEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALAS
RFYIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHIQLTYFSRWSEVEDS
CSDDAIERMYCAPEVGAITEETEACDWWSLGAVLFELLTGKTLVECHPAGINTHTTLNMP
ECVSEEARSLIQQLLQFNPLERLGAGVAGVEDIKSHPFFTPVDWAEELMR

SEQ ID NO: 137_AA626690_H

MLPFAPQDEPDREMEVFSGGGASSGEVNGLMVDEPMEEGEADSCHDEGVVKEIPITHH
VKEGYEKADPAQFELLKVLGQGSFGKVFLVRKKTGPDAGQLYAMKVLKKASLKVRDRVRT
KMERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGDVFTRLSKEVLFTEEDVKFYLA
ELALALDHLHLQGLIVYRDLKPENILLDEIGHIKLTDGFLSKESVDQEKKAYSFCGTVEYM
APEVVNRRGHSQSADWWSYGVLMFEMLTGTLPFQKDRNETMNMILKAKLGMPQFLSAEA
QSLRLMLFKRNPANRLGSEGVVEIKRHLFFANIDWDKLYKREVQPPFKPASGKPDFTFCF
DPEFTAKTPKDSPLPASANAHQLFKGFSFVATSIAEYKITPITSANVLPVQINGNAA
QFGEVYELKEDIGVGSYSVCKRCIHATTNMEFAVKIIDKSKRDPSEEIEILMRYGQHPNI
ITLKDVFDDGRYVYLVTDLMKGGELLDRIKQKCFEREASDILYVISKTVDYLHCQGVV
HRDLKPSNILYMDESASADSIRICDFGFAKQLRGENGILLTPCYTANFVAPEVLMQQGYD
AACDIWSLGVLFYTMLAGYTPFANGPNDTPEEILLRIGNGKFSLSGGNWDNISDGAKDLL
SHMLHMDPHQRYTAEQILKHSWITHRDQLPNDQPKRNDVSHVVKGAMVATYSALTHKTFQ
PVLEPVAASSLAQRRSMKKRTSTGL

SEQ ID NO: 138_AA215680_H

MSLVACECLPSPGLEPEPCSRARSQAHVYLEQIRNRVALGVPDMTKRDYLVDAATQIRLA
LERDVSEDYEAFFNHQNGVDVLLRGIVDPNKKERREAVKLKITKYLRAEEIFNCHLQR
PLSSGASPSAGFSSRLRLPIRTLSSAVEQLRGCRVVGVIKVLQVQDPATGGTFVVKSLP
RCHMVSRERLTIIPHGVPMYTKLLRYFVSEDSIFLHLEHVQGGTLWSHLLSQAHSRHSGL
SSGSTQERMKAQLNPHLNLTPARLPSGHAPGQDRIALEPRTSPNLLLAGEAPSTRPQR
EAEGETARTSTSGSSDLPKAPGGHLHLQARRAGQNSDAGPPRGLTWVPEGAGPVLGGCG
RGMDQSCLSADGAGRGCGRATWSVREEQVKQWAAEMLVALEALHEQGVLCRDLHPGNLLL
DQAGHIRLTYFGQWSEVEPQCCGEAVDNLISAPEVGGISELTEACDWWFSGSLLYELLTG
MALSQSHPSGIAHTQLQLPEWLSRPAASLLTELLQFEPTRRLGMGEGGVSKLKSHPFFS
TIQWSKLVG

SEQ ID NO: 139_SGK_H

MTVKTEAAKGTLYSRMRGMVAILIAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKI
SQPQPELMNANPSPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA
EVFYAVKVLQKAILKKKEEKHIMSERVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
FGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSR
NTAEMYDNILNKPLQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINW
DDLINKKITPPFNPVSGPNELRHFDPEFTEEPVPNSIGKSPDSVLVTASVKEAAEAFLG
FSYAPPTDSFL

SEQ ID NO: 140_AA107515_M

MTVKAEAAARSTLYSRMRGMVAILIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSILKM
SHPQPELMNANPSPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA

FIGURE 1E

EVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIYRDLKPENILLDSQGHIVLTD
XFQLRRIEHNGTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSRN
TAEMYDNILNKPLQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHIFFSLINWD
DLINKKITPPFNPVSGPSDLRHFDPFTEEPVPSSIGRSPDSILVTASVKEAAEAFLGF
SYAPPVDSFL

SEQ ID NO: 141_AA109508_M

HLQRERRFLEPRARFYAAEVASAIIGYLHSLNIYRDLKPENILLDCQGHVVLTDFGLCKE
GVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDVSQMY
ENILHQPLQIPGGRTVAACDLLQSLHKKQQRQLGSKADFLEIKNHVFFSPINWDDLYHK
RLTPPFNPVNTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDD
ILDC

SEQ ID NO: 142_AA887783_H

MQRDHTMDYKESCPVXIPSSDEHREKKKRFTVYKVLVSVGRSEWFVFRRYAEFDKLYNT
LKKQFPAXALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMD
SPKHQSDPSEDEDERSSQKLHSTSONINLGPSPHAKPTDFDFLKVIGKGSFGKVLLAK
RKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVL
DFVNGGEGHVLTDFGLCKEGIAISDTTTFCTGTPEYLAPEVIRKQPYDNTVDWWCLGAV
LYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSIIEELLEKDRQNLGAKEDF
LEIQNHPPFESLSWADLVQKKIPPPFNPVAGPDDIRNFDTAFTEETVPYSVCVSSDYSI
VNASVLEADDAFVGFSYAPPSDELFL

SEQ ID NO: 143_R47805_H

MAHQGTGIHATEELKEFFAKARAGSVRLIKVVIEDEQLVLGASQEPVGRWDQDYDRAVLPL
LDAQQPCYLLYRLDSQNAQGFELFLAWS PDNSPVRLKMLYAATRATVKKEFGGGHIKDE
LFGTVKDDLSFAGYQKHLSSCAAPAPLTS AERELQQIRINEVKTEISVESKHQTLQGLAF
PLQPEAQRALQQLKQKMVNYIQMKLDLERETIELVHTEPTDVAQLPSRVPRDAARYHFFL
YKHTHEGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIAKKIEIGDG
AELTAEFLYDEVHPKQHAFKQAFAPKPGGKRGHKRLIRGPGENGDDS

SEQ ID NO: 144_H60215_H

MSKLRMKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSTVQCLAR
KDGTDDFYQLKILTLEERGQDQIESQEERQGMILLHTEYSLLSLHTQDGVVHHHGLFQD
RTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFSDKTADLINLQHYVIKEKRLSERETV
VIFYDVVRVVEALHQKNIVHRDLKLGNMVLNKRTHRITITNFC LGKHLVSEGDLLKDQRG
SPAYISPDVLSGRPYRGKPSDMWALGVVLTMLYGGFPFYDSIPQELFRKIKAAEYTIPE
DGRVSENTVCLIRKLLVLDPPQRLAAADVLEALSIIASWQSLSSLSGPLQVVPDIDDQM
SNADSSQEAKVTEECQYEFENYMRQQLLLAEKSSIHDTRSWVPKRQFGSAPPVRLGH
DAQPMTSLDTAILAQRYLK

SEQ ID NO: 145_SGK324_H

MASTRSIELEHFEERDKRPRPGSRRGAPSSSGSSSGPKGNGLIPSPAHSAHCSFYRTR
TLQALSSEKKAKKARFYRNGDRYFKGLVFAISSDRFRSFDALLIELTRSLSDNVNLPQGV
RTIYTIDGSRKVTSLDELLEGESYVCASNEPFRKVDYTKNINPNWSVNIKGGTSRALAAA
SSVKSEVKESKDFIKPKLVTVIRSGVKPRKAVRILLNKKTAHSFEQVLT DITEAIKXASG
VVKRLCTLDGKQVRVTCVHLPDFFGDDDVFIACGPEKFRYAQDDFVLDHSECRVLKSSYS
RSSAVKYSGSKSPGSRSSQISAHGRSSSNVNGGPELDRCISPEGVNGNRCSESSTLLEK
YKIGKVIKVGDNFAVVKECIDRSTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNII

FIGURE 1F

MLVEEMETATELFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHGLSIVH
RDIKPENLLVCEYDPGDKSLKLGDFGLATVVEGPLYTVCGTPTYVAPXIIAETGYGLKVD
IWAAGVITYILLCGFPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQ
VNVEARCTAGQILSHPWVSDDASQENMQAEVTGKLGKQHFNNALPKQNSTTTGVSVIMVS
GRRQVWPDCGAGLEVFEGLSRELPSHGSWCLP

SEQ ID NO: 146_W30246_M SGK324_M

TKSSSSSPTSPGSFRGLKISAQGRSSSNVNGGPELDRCLSPGVNGNRCSESFPLEKYR
IGKVI GDNFAVVKECVDRTYGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNIIML
VEEMETATDLFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHSLSIVHRD
IKPENLLVCEYDPGDKSLKLGDFGLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDVW
AAGVITYILLCGFPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSPCVCFRKCL

SEQ ID NO: 147_AA383293_H

PAAKRVVVRNGDPFFPGSQLVVTQRRFPTMEAFCEVTSAVQAPLAVRALYTPCHGHPV
TNLADLKNRGQYVAAGFERFHKLPYQAFCLSVFRNGDLVSPFSLKLSQAASQDWETVL
KLLTEKVKLQSGAVRLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDLPPALSTRGLLAA
GNEAHLRSGVGTAVGSPKPLGRKAKKETCLIVTLTKYQQSETSRDQSFPSGVI GYGA
PHRRKETAGALEVADDEDTQTEEPDQRAAQIVEQVTCLODFGDDDDVFIACGPEKFRYA
QDDFVLDHSRRLLREHQAGFEKLRRTRGEEKEAEKEKKPCMSGGRMTLRDDQPAKLEK
EPKTRPEENKPERPSGRKPRPMGI IANVEKHYETGRVIGDGNFAVVKECRHRRETRQAYA
MKIIDKSRLKGKEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYLILEYVQGGDLFDAI
IESVKFPEPDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNEDKSTTLKLADFGLA
KHVVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPFRSPXXGDQDE
LFNIIQLGHFEFLPPYWDNISDAKDLVSRLLVDPKKRYTAHQVLQHPWIETAGKTNTV
KRQKQVSPSSDGHFRSQHKRVVEQVS

SEQ ID NO: 148_AA197883_M

MPTAPVLRPPPPATPAPPAPSRPAPP I P GHRGPCDHSLKCLSSKISERKLPGPWLPAGR
GPLEKPVLGPRGAVMPLFSPQSSLSHVAEHSPLKPRVTVVKLGQPLRKATLLLNRRS
VQTFEQLLSDISEALGFPRWKNDVRKLF TLKGREVKSVSDFFREGDAFIAMGKEPLTLK
SIQLAMEELYPKNRALALAPHSRVPSRLRSRLPSKLLKGSHRCGEAGSYSAEMESKAVS
RHQGKTSTVLAPEDKARAQKWVRGKQSESEPGGPPSPGAATQEETHASGEKHLGVEIEKTS
GEIVRCEKCKRERELQLGLQREPCPLGTSELDLGRAQKRDSEKLVRTKSCRPSKAKFTD
GEEGWKGD SHRGSPRDPPQEMRRPNSNSDKKEIRGSESQDSYPQAPKAQKDFVEGPPAV
EEGPIDMRREDRHTCRSKHAAWLRREQQAEPPLPRTRGEEKQAEHEKKPGGLGERRAPE
KESKRKLEEKPERPSGRKPRPKGIISADVEKHYDIGGVI GDNFATVKECRHRETKQAY
AMKMIDKSQKLGKEDIVDSEILIIQSLSHPNIVKLHEVYETEAEIYLIMEYVQGGDLFDA
IVENVKFPEPEAAVMITDLCKAFVHMHDKNIVHRDVKPENLLVQRNEDKSITLKLADFGL
AKYVVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPFRSPERDQDE
LFNIIQVQGFEFLSPYWDNISDAKDLVRNLLVDPKKRYTAEQVLQHPWIEMVGHNTG
NSQKEESPNSLGHFQSQHKKVAEQMP

SEQ ID NO: 149_DRAK2_H

MSRRRFDCRSISGLLTTPQIPIKMFNNFYILTSKELGRGKFAVVRQCI SKSTGQEYA
AKFLKKRRRGQDCRAEILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFS
LCLPELAEMVSENDVIRLIKQILEGVYYLHQNNIVHLDLKPQNILLSSIYPLGDIKIVDF
GMSRKIGHACELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYLNISQVNVYDSEETFSSVSQLATDFIQSLLVKNPEKRPTAEICLSHSLWQQWDFEN

FIGURE 1G

LFHPEETSSSSQTQDHSVRSSSEDKTSKSSCNGTCGDREDKENIPEDSSMVSKRFRFDDSL
PNPHELVSDDLCC

SEQ ID NO: 150_W44160_M DRAK2_M
MSRRRFDRCRSVSGLLTTTPQTPIKTENFNNFYTLTPKELGRGKFAVVRQCISKSTGQEYA
AKSLKKRRRGQDCRAEILHEIAVLELARSCPHVINLHEVYENATEIILVLEYAAGGEIFN
LCLPELAEMVSENDVIRLIKQILEGVHYLHQNNIVHLDLKPQNILLSSIYPLGDIKIVDF
GMSRKIGNASELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYNISQVNVVDYSEEMFSSVSQLATDFIQSLLVKNPEKRPTAESCLSHSWLQQWDFGS
LFHPEETSGSSQIQDLTLRSSEKTSKSSCNGSCGAREDKENIPEDGSLVSKRFRFDDSL
PSPHELVPDLFC

SEQ ID NO: 151_H01248_H, DRAK1_H
MIPLEKPGSGGSSPGATSGSGRAGRGLSGPCRPPPPQARGLLTEIRAVVRTEPFQDGYS
LCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKRRKGQDCRMEIIEIAVLELAQDNPW
VINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEKDVQRLMRQILEGVHFLHTR
DVVHLDLKPQNILLTSESPGDIKIVDFGLSRILKNSEELREIMGTPEYVAPEILSYDPI
SMATDMWSIGVLTYYMLTGISPFLGNDKQETFLNISQMNLSYSEEEFDVLSESAVIDFIRT
LLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEANALQEGHSVPEINSDDTKSE
TEESIVTEELIVVTSYTLGQCRQSEKEKMEQKAIKSRFKFEEPLLQEIPGEFIY

SEQ ID NO: 152_AA021445_H
MPARIGYYEIDRTIGKGNFAVVRATHLVTKAKVAIKIIDKTQLDEENLKKIFREVQIMK
MLCHPHIIRLYQVMETERMIYLVTEYASGGEIFDHLVAHGRMAEKEARRKFQIVTAVYF
CHCRNIVHRDLKAENLLLDANLNIAKIDFGFSNLFPTGQLLKTWCGSPPYAAPELFEGKE
YDGPVKDIWSLGVVLYVLVCGALPFDGSTLQNLRLARVLSGKFRI PPFMSTECEHLIRHML
VLDPNKRLSMEQICKHKWMKLGADPNFDRLIAECQQLKEERQVDPLNEDVLLAMEDMGL
DKEQTLQSLRSDAYDHYSAIYSLLCDRHKRHKTLLRLGALPSMPRALAFQAPVNIQAEQAG
TAMNISVPQVQLINPENQIVEPDGTLNLDSDGEPEPSPEALVRYLSMRRTVGVADPRT
VMEDLQKLLPGFPVNPQAPFLQVAPNVNFMHNLPMQNLQPTGQLEYKEQSLQPPPTLQ
LLNGMGPLGRRASDGGANIQLHAQQLLKRPRGPSPLVTMTPAVPAVTPVDEESSDGEPOQ
EAVQRYLANRSKRHTLAMTNPTAEIPPDQRLQGLQPPFRSRVWPPHLPDQHRSTYKDSN
TLHLPTERFSPVRRFSDGAASIQAFAHLEKMGNNSSIKQLQCECEQLQKMYGGQIDERT
LEKTQQQHMLYQQEQHHQILQQQIQDSICPPQPSPLQAACENQALLTHQLRLRIQPS
SPPNHPNNHLFRQPSNSPPPMSSAMIQPHGAASSSQFQGLPSRSAIFQQQPENCSSPPN
VALTCLGMQPPAQSQQVTIQVQEPVDMLSNMPGTAAGSSGRGISISPSAGQMOMQHRTNL
MATLSYGHRPLSKQLSADSAEAHSLNVNRFSPANYDQAHLPPLFSDQSRGSPSSYSPST
GVGFSPQTQALKVPPLDQFPTFPFSAHQPPHYTTSALQQALLSPTPPDYTRHQQVPHILO
GLLSRPHSLTGHSDIRLPPTFEAQLIKRQQQORQQQQQQQQQEQEYQELFRHMNQGDAGSL
APSLGGQSMTERQALSQYQADSYHHHTSPQHLLQIRAQECVSQASSPTPPHGYAHQPALM
HSESMEEDCSCEGAKDGFQDSKSSSTLTGCHDSPLLLSTGGPGDPESLLGTVSHAQELG
IHPYGHQPTAAFSKNKVPSREPVIGNCMDRSSPGQAVELPDHNLGYPARPSVHEHHRPR
ALQRHHTIQNSDDAYVQLDNLPGMSLVAGKALSSARMSDAVLSQSSLMGSQQFQDGENEE
CGASLGGHEHPDLSGDSQHLNSSCYPSTCITDILLSYKHPEVSFSMEQAGV

SEQ ID NO: 153_2R22-5-11_H
MTAVYMNGGGLVNPHYARWDRRDSVESGCQTESSKEGEGQPRQLTPFEKLTQDMSQDEK
VVREITLGRIGFYRIRGEIGSGNFSQVKLGIHSLTKEKVAIKILDKTCLDQKTQRLLSR
EISSMEKLHHPNIIRLYEVVETLSKLHLVMEYAGGELFGKISTEGKLSEPESEKLIQSQI
VSAVKHMHENQIHRDLKAENVFYTSNTCVKVGDFGFSTVSKKGEMLNTFCGSPPYAAPE

FIGURE 1H

LFRDEHYIGIYVDIWALGVLLYFMVTGTMPFRAETVAKLKKSILEGTYSVPPHVSEPCHR
 LIRGVLLQQIPTERYGIDCIMNDEWMQGVYPTPLEPFQLDPKHLSETSTLKEEENEVKST
 LEHLGITEEHIRNNQGRDARSSITGVYRIILHRVQRKKALESVPVMMLPDPKERDLKKGS
 RVYRGIRHTSKFCSIL

SEQ ID NO: 154_R31237_1_H, AAC33487

MSTRTPLPVTNERDTENHTSHGDGRQEVTSRTSRSGARCRNSIASCADEQPHIGNYRLK
 TIGKGNFAKVKLARHILTGREVAIKIIDKTQLNPTSLQKLFREVRIMKILNHPNIVKLFE
 VIETEKTLYLIMEYASGGEVFDYLVAHGRMKEKEARSKFRQIVSAVQYCHQKRIVHRDLK
 AENLLLDADMNIKIADFGFSNEFTVGGKLDTFCGSPPYAAPELFGKKYDGPEDVWSLG
 VILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFLVLNPIKRGTLQ
 IMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMVGMGYSQEEIQESLSKMKYDEITAT
 YLLLGRKSSSELDASDSSSSSNLSLAKVRPSSDLNNSTGQSPHHKVQRSVSSSQKQRRYSD
 HAGPAIPSVVAYPKRSQTSTADGDLKEDGISSRKSSGSAVGKGKIAPASPMLGNASPNK
 ADIPERKKSSTVPSSNTASGGMTRRNTYVCERTTADRHSVIQNGKENSTIPDQRTPVAS
 THSISSAATPDRI RFPRTASRSTFHGQPRERRTATYNGPPASPSLSHEATPLSQTRSRG
 STNLF SKLTSKLT SRNVSAEQDENKEAKPRSLRFTWSMKTTSMDPGDMMREIRKVL D
 ANNC DYEQRERFLFCVHGDGHAENLVQWEMEVC KLPRLSLNGVRFKRISGTSIAFNIA
 SKIANELKL

SEQ ID NO: 155_W90839_M

KGPSWSSRSLGARCRNSIASCPPEQPHVGNRYLLRTIGKGNFAKVKLARHILTGREVAIK
 IIDKTQLNPSSLQKLFREVRIMKILNHPNIVKLFEVIETEKTLYLIMEYASAGEVFDYLV
 SHGRMKEKEARAKFRQIVSAVHYCHQKNIVHRDLKAENLLD AEANI KIADFGFSNEFTL
 GSKLDTFCGSPPYAAPELFGKKYDGPEDVWSLG VILYTLVSGSLPFDGHNKELRERV
 LRGKYRVPFYMSTDCESILRRFLVLNPAKRCTLEQIMKDKWINIGYEGEELKPDTELKEE
 RMPGRKASCSAVGSGSRGLPSSPMVSSAHNPNAEIPERRKDSTSTPNNLPPSMMTRRN
 TYVCTERPGSERPSLLPNGKENS SGT SRVPPASPSHSLAPPSGERSRLARGSTIRSTFH
 GGQVRDRRAGSGSGGVQNGPPASPTLAHEAAPLPSGRPRPTTNLFTKLT SKLTTRVTDE
 PERIGGPEVTSCHLPWDKTETAPRLLRFPWSVKLTSSRPS

SEQ ID NO: 156_406786.5_H

MEVGGLTVFEEDQRCLSLPLVSAEGPAAQTAEPSRSFSSAHRHLSRRNGLSRLCQS
 RTALSEDRWSSYCLSSLAQNICTSKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSSGWSS
 PLLPAPVCNPNKAIFTVDAKTTEILVANDKACGLLGYSQDLIGQKLTQFFLRSDSDVVE
 ALSEEHMEADGHAAVVF GTVVDI ITRSGEKI PVSVMKMRMRQERRLCCVVVLEPVERVST
 WVAFAQSDGTITSCDSLFAHLHGYSGEDVAGQHITDLIPSVQLPPSGQHIPKNLKIQRSV
 GRARDGTTTFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLPDGTIHGI
 NHSFALTFLGYGKTELLGKNITFLIPGFYSYMDLAYNSSQLPDLASCLDVGNESGCGER
 TLDPWQGDPAEGGQDPRINVVLAGGHVVRDEIRKLME SQDI FTGTQTELIAGGQLLSC
 LSPQPAPGVDNVPESGLPVHGEQALPKDQQTALGREEPVAIESPGQDLLGESRSEPVDV
 KPFASCEDSEAPVPAEDGGS DAGMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQ
 LAGGSLLMHCPCYGSEWGLWWSQDLAPSPSGMAGLSFGTPTLDEPWLGVENDREELQTC
 LIKEQLSQLSLAGALDVPHAELVPTCEQAVTAPVSSCDLGGRDLCGGCTGSSSACYALAT
 DLPGGLEAVEAQEVDVNSFSWNKELFFSDQTDQTSNCS CATSELRETPSSSLAVGSDPD
 VGS LQE QGSCVLDRELLLLTGTCVDLGQGRFRFRES CVGHDPTEPLEVCLVSSEHYAASD
 RESPGHVPSTLDAGPEDTCPSAEPRNLNVQVTSTPVI VMRGAAGLQREIQEGAYSGSCYH
 RDGLRLSIQFEVRRVELQGPTPLFCCWLVKDLLHSQRDSAARTRFLASLPGSTHSTAAE
 LTGPSLVEVLRARPWFEPPKAVELEGLAACGEYSQKYSTMSP LGS GAFGFVWTAVDKG
 KNKEVVVKFIKKEKVLEDCWIEDPKLGKVTLEIAILSRVEHANI KVLDIFENQGFQQLV

FIGURE 11

MEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAGQSRLVSAVGYLRLKDIHRDIKDEN
 IVIAEDFTIKLIDFGSAAYLERGKLFYTFCGTIEYCAPEVLMGNPYRGPELEMWSLGVTL
 YTLVFEENPFCELEETVEAAIHPPYLVSKEMLSVSGLLQPVPERRTTLEKLVTDPWVTO
 PVNLADYTWEVFRVKNPESGVLASAASLEMGNRSLSDVAQAQELCGGPVPGEPNGQGCL
 HPGDPRLLTS

SEQ ID NO: 157_AA544838_M 406786_M
 TRPHPCLEPLASFIHQRLVSAVGYLHSGQIIHRDIKDENIVIAEDFTIKLIDFGSAAYL
 ERGKLFYTFCGTIEYCAPEVLIGNPYRGPELEMWSLGVTLTYTLIFEENPFCEVEETMEAV
 IHPPFLVSQELMSLLSGLLQPCPEQRTTLEKLIRDPWVTQPVNLASYTWEVCRTNQPS
 GLLSAASLEIGSRSPSEMAQREGLCGPPAPRETRGDQHCLHLKDPPLPVS

SEQ ID NO: 158_AA785735_H
 MVMADGPRHLQRGVVRVGFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQLDVN
 LEKIYREVQIMKMLDHPHIIKLYQVMETKSMYLVTEYAKNGEIFDYLANHGRLNESEAR
 RKFQWILSAVDYCHGRKIVHRDLKAENLLDNNMNIKIADFGFGNFFKSGELLATWCGSP
 PYAAPEVFEGQQYEGPQLDIWSMGVVLVYLVCGALPFDGPTLPILRQRVLEGRFRIPYFM
 SEDCEHLIRMLVLDPKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQV
 LRLMHSGLIDQKXIESLQNKSYNHFAAIYFLLVERLKSHRSSFPVEQRLDGRQRRPSTI
 AEQTVAKAQTVGLPVTMHSNMRLLRSALLPQASNVEAFSFPASGCQAEAAFMEEECVDT
 PKVNGCLLDVPPVLRKGCQSLPSNMETSIDEGLETEGEAEEDPAHAFAEFQSTRSGQ
 RRHTLSEVTNQLVVMGAGKIFSMNDSPSLSDVDSEYDMGSVQRDNLNFDENPSLKDIML
 ANQPSPRMTSPFISLRPTNPAMQALSSQKREVNHRSPVSFREGRRASDTSLTQGI VAFRQ
 HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVST
 LPASVHPQLSPRQSLETQYLQHRLOKPSLLSKAQNTCQLYCKEPPRSLEQQLOEHRLOOK
 RLFLQKSQLQAYFNQMQUIAESSYPQPSQQPLPRQETPPPSQQAPPFSLTQPLSPVLEP
 SSEQMYSPPFLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQQPPPPPPPPRQPGAAPA
 PLQFSYQTCELPSAASPADYPTPCQYPVDGAQQSDLTGPD CPRSPGLQEAPSSYDPLAL
 SELPGLFDCEMLDVDPQHNGYVLVN

SEQ ID NO: 159_AA207220_H
 MESLVFARRSGPTPSAAELARPLAELIKSPKPLMKKQAVKRHHKHNLRHRYEFLETGL
 KGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHIIAIEHVEFE
 NSSKIVIMMEYASRGDLYDIISERQQLSREARHFFRQIVSAVHYCHQNRVVRDLKLEN
 ILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVDSWSLGVLL
 YILVHGTMPFDGHDHKLIVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRRATLEDVAS
 HWWVNWGYATRVGEQEAPHEGGHPGSDSARASMAWDLRRSSRPLENGAKVCSFFKQHAP
 GGGSTTPGLERQHSLSKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPKGILKKKVSASA
 EGVQEDPPELSPIPASPGQAAPLLPKKGILKKPRQRESGYYSPEPSESSELLEDAGDVVF
 SGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRPLARASRP
 SGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDP
 LGDSCFSLTDCQEVATATYRQALRVCSKLT

SEQ ID NO: 160_AA426580_H, MAK_V_H
 MPAAAGDGLLEGAAPGGGGGAEDAAPAAACEGSFLPAWVSGVPRERLRDFQHHKRVGN
 YLIGSRKLGEESFAKVREGLHVLTKGEKVAIKVIDKKRAKDTYVTKNLRREGQIQQMIRH
 PNITQLLDILETENSYYLMELCPGGNLMHKIYEKKRLEESEARRYIRQLISAVEHLHRA
 GVVHRDLKIENLLDEDNNIKLIDFGLSNCAGILGYSDPFSTQCGSPAYAAPELLARKKY
 GPKIDVWSIGVNMAMLTGTLPTVEPFSLRALYQKMVDKEMNPLPTQLSTGAISFLRSL
 LEPDPVKRPNIQQALANRWLNENYTGKVP CNVTYPNRISLEDLSPSVVLHMTKLGKNS

FIGURE 1J

DVINTVLSNRACHILAIYFLLNKKLERYLSGKSDIQDSLCKYKTRLYQIEKYRAPKESYEA
SLDTWTRDLEFHAVQDKPKKEQEKRGDFLHRPFSKKLDKNLPSHKQPSGSLMTQIQNTKA
LLKDRKASKSSFPDKDSFGCRNIFRKTSDSNCVASSSMEFIPVPPRTPRIVKKEPEHPQ
GPGSTGIPHKEDPLMLDMVRSFESVDRDDHVEVLSPSHHYRILNSPVSLARRNSSERTLS
PGLPSGMSPLHTPLHPTLVSAFHEDKNSPKKEGLCCPPPVPSNGPMQPLGSPNCVKSR
GRFPMMGIGQMLRKRHQSLOPSADRPLEASLPPLQPLAPVNLAFDMADGVKTQC

SEQ ID NO: 161_Z36720_H

MDTKLNMLNEKVDQLLHFQEDVTEKLQSMCRDMGHLEGLHRLEASRAPGPGGADGVPHI
DTQAGWPEVLELVRAMQQDAAQHGARLEALFRMVAAVDRAIALVGATFQKSKVADFLMQG
RVPWRRGSPGDSPEEWVKEEEVCFMPPVPPAPGAAGQSLQKDKGELSAEQGIWATLMTLV
IMVTAANKERVEEEGGKPKHVLSTSGVQSDAREPGEESQKADVLEGTAERLPPIRASGLG
ADPAQAVVSPGQGDGVPQPAQAFPGHLPLPTKVEAKAPETPSENLRGTGLELAPAPGRVNV
VSPSLEVAPGAGQGASSSRPDPEPLEEGTRLTGPGPGPQCPGPPGLPAQARATHSGGETPP
RAALLKGAVAPGFSRRDLVFPISIFCACLGISIHQEMDTPGEMLMTGRGSLGPTLTTEAP
AAAQPGKQGPPTGRCLQAPGTEPGEQTPEGARELSPLQESSSPGGVKAEEEEQRAGAEPG
TRPSLARSDDNDHEVGALGLQQKSPGAGNPEPEQDCAARAPVRAEAVRRMPPGAEAGSV
VLDDSPAPPAPFEHRVSVKETSISAGYEVQCQHEVLGGGRFGQVHRCTEKSTGLPLAAKI
IKVKSADKREDVKNEINIMNQLSHVNLILQLYDAFESKHSCITLMEYVDGGELFDRITDEK
YHLELTVLVFTRQICEGVHYLHQHYILHLDLKPENILCVNQTGHQIKIIDFGLARRYKP
REKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGIVITYMLLSGLSPFLGETDAETMNFIV
NCSWDFDADTFEGLSEEAKDFVSRLLVKEKSCRMSATQCLKHEWLNNLPKASRSKTRLK
SQQLLQKYIAQRKWKKHFYVVTAAANRLRKFTSP

SEQ ID NO: 162_SGK088_H

GEMALFECLVAGPTDVEVDWLCRGRLLQPALLKCKMHFDGRKCKLLLTSVHEDDSGVYTC
KLSTAKDELTC SARLTVRPSLAPLFTRLLEDVEVLEGRAARFDCKISGTPPPVVTWTHFG
CPMEESENLRLRQDGGHLHIAHVGSEDEGLYAVSAVNTHGQAHCSAQLYVEEPRTAAS
GPSSKLEKMPISIPPEPEQGELERLSIPDFLRPLQDLEVLAKELAMLECQVTGLPYPTISW
FHNGHRIQSSDDRRMTQYRDVHRLVFPVAVGPQHAGVYKSVIANKLGAACYAHLYVTDVV
PGPPDGAPQVAVTGRMVTLTWNPPRSLDMAIDPDSLTYTVQHQLVGLSDQWTALVTGLRE
PGWAATGLRKGVQHIIFRVLSTTVKSSSKPSPSEPVLLEHGPTLEEAPAMLDPDIDVYV
VEGQPASVTVTFNHVEAQVWRSCRGALLEARAGVYELSOPDDQYCLRICRVSRDMDGA
LTCTARNRHGTQTCSVTLELAEAPRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKD
EVLLTESSHVSFVYEENECSLVVLSTGAQDGGVYTCTAQNLAGEVSCKAELAVHSAQTAM
EVEGVGEDEDHRGRRLSDFYDIHQEIGRGAFSYLRRIVERSSGLEFAAKFIPSAKPKAS
ARREARLLARLQHDCLVLYFHEAFERRRGLVITELCTEELLERIAKPTVCESEIRAYMR
QVLEGIHYLHQSHVLHLDVKPENLLVWDGAAGEQQVRICDFGNAQELTPGEPQYCQYGT
EFVAPEIVNQSPVSGVTDIWPVGVAFLCLTGISPFVGENDRITLMNIRNYNVAFEETTF
LSLSREARGFLIKVLVQDRLRPTAEETLEHPWFKTQAKGAEVSTDHLKFLSRRRWQRSQ
ISYKCHLVLRPIPELLRAPPERVWVTMPRRPPPSGGLSSSSDSEEELEELPSVPRPLQP
EFGSGRVSLTDIPTEDALGTPETGAATPMDWQEQGRAPSQDQEAPSPEALPSPGQEPAA
GASPRRGELRRGSSAESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEG
EYAQRLLQALRQRLLRGGPEDGKVSGLRGPLLES LGGRARDPRMARAASSEAPHHQPPE
NRGLQKSSSFSGEAEPRGRHRRAGAPLEIPVARLGARRLQESPSLSALSEAQPSSPARP
SAPKPSTPKSAEPSATTSPDAPQPPAPQPAQDKAPEPRPEPVRAKPPAPPPQALQTLALP
LTPYAQIIQSLQLSGHAQGPSQGAAPPSEPKPHA AVFARVASPPPGAPEKRVPSAGGPP
VLA EKARVPTVPPRPGSSLSSSIENLESEAVFEAKFKRSRESPLSLGLRLLSRSRSEERG
PFRGAEEDGIYRPSAGTPLELVRRPERSRSVQDLRAVGEPGLVRRLSLSLSQRLRRT
PAQRHPAWEARGGDGESSEGGSSARGSPVLAMRRRLSFTLERLSSRLQRSSESSEDSSGAS

FIGURE 1K

GRSTPLFGRLRRATSEGESLRRRLGLPHNQLAAQAGATTPSAESLGSEASATSGSSAPGES
 RSRLRWGFSRPRKDKGLSPPNLSASVQEELGHQYVRSESDFPFVFHIKLDQVLLGEAA
 TLLCLPAACPAPHISWMKDKKSLRSEPSVIIVSCKDGRQLLSIPRAGKRHAGLYECSATN
 VLGSITSSCTVAVARVPGKLAPPEVTQTYQDTALVLWKPGDSRAPCTYTLERRVDGESVW
 HPVSSGIPDCYINVTHLPVGVTVRFRVACANRAGQGPFSSNSSEKVFVRGTQDSSAVPSAA
 HQEAPVTSRPARARPPDSPTSLAPPLAPAAPTPPSVTVSPSSPPTPPSQALSSSLKAVGPP
 PQTTPRRHRGLQAARPAEPTLPSTHVTTPSEPKPFVLDTGTPIPASTPQGVKPVSSSTPVY
 VVTSFVSAPPAPPEPPAPEPPPEPTKVTVQSLSPAKEVSSPGSSPRSSPRPEGTTLRQGP
 PQKPYTFLEEKARGRFGVVRACRENATGRTFVAKIVPYAAEGKPRVLQEYEVLRTHHER
 IMSLHEAYITPRYLVLIAESCGNRELLCGLSDRFRYSEDDVATYMVQLLOGLDYLHGHV
 LHLDIKPDNLLLAPDNALKIVDFGSAQYPNPQALRPLGHRTGTLEFMAPEMVKGEPISGA
 TDIWGAGVLTYYIMLSGRSPFYEPDPQETEARIVGGRFADFQLYPNTSQSATLFLRKVLSV
 HPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAAATRHKVLLR
 SYPGGP

SEQ ID NO: 163_AA542015_M SGK088_M
 ATDIWGAGVLTYYIMLSGYSPFYEPDPQETEARIVGGRFADFQLYPNTSQSATLFLRKVLS
 VHPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAAATRHKVLL
 RSYPGSP

SEQ ID NO: 164_R19772_H
 MKGGDRAYTRGPSLGWLFACCCCCFPCRDAYSHSSSENGGKSESVANLQAQPSLNFIHSS
 PGPKRSTNTLKKWLTSPVRRNLNSGKADGNIKKQKKVRDGRKSFDLGSPKPGDETTPQGDS
 ADESKKGWGEDEPDEESHTPLPPPMKIFDNDPTQDEMSSSLAARQASTEVPTAADLVNA
 IEKLVKNKLSLEGSSYRGLKDPAGCLNEGMAPPTPPKNPEEEQKAKALRGRMFVLNELV
 QTEKDYVKDLGIVVEGFMKRIEEKGVPEDMRGKDKIVFGNIHQIYDWHKDFFLAELEKCI
 QEQDRLAQLFIKHERKLHIYVWYCQNKPRSEYIVAEYDAYFEEVKQEINQRLTSLDFLIK
 PIQRITKYQLLLKDFLRYSEKAGLECSIDIEKAVELMCLVPKRCNDMMNLGRLOGFEGTTLT
 AQGKLLQQDTFYVIELDAGMQSRTKERRVFLFEQIVIFSELLRKGSLTPGYMFKRSIKMN
 YLVLEENVNDNDPCKFALMNRETSESVVLQANADIQQAWVQDINQVLETQRDFLNALQSP
 IEYQKERSTAVMRSQPARLPQASPRPYSSVPAGSEKPPKGSSYNPPLPLKISTSNQSP
 GFEYHQPGDKFEASKNDLGGCNGTSSMAVIDYALKENEICVSQGEVVQVLAVNQQNM
 LQYQASDHSPAAEGWVPGSILAPLTKATAAESDGSIKKSCSWHTLRMRKRAEVENTGK
 NEATGPRKPKDILGNKVSVKETNSSESECDLDPNTSMEILNPNFIQEVAPFLVPLVD
 VTCLLGDTVILQCKVCGRPKPTITWKGPQDNIQDNTSSATYTVSSCDSGEITLKI CNLM
 PQDSGIYTCIATNDHGTSTSATVKVQGVPAAPNRPPIAQRSCTSVILRWLPPSSTGNCT
 ISGYTVEYREEGSQIWQOSVASTLDTYLVIEDLSPGCPYQFRVSASNPWGISLPSESEF
 VRLPEYDAAADGATISWKENFDSAYTELNEIGRGRFSIVKKCIHKATRKDVAVKFNKKM
 KKKEQAAHEAALLQHLQHPQYITLHDTYESPTSYYILILELMDDGRLLDYLNMHDELMEEK
 VAFYIRDIMEALQYLHNCRVAHLDIKPENLLIDLRIPVPRVKLIDLEDAVQISGHFHIHH
 LLGNPEFAAPEVIQGIQVSLGTDIWSIGVLTYYVMLSGVSPFLDESKEETCINVCRVDFSF
 PHEYFCGVSNAAARDFINVILQEDFRRRPTAATCLQHPWLQPHNGSYSKIPLDTSRLACFI
 ERRKHQNDVRPIPNVKSIVNVRVNGT

SEQ ID NO: 165_5R72_8_2_H
 MADSGLDKKSTKCPDCSSASQKDVLCVCSSKTRVPPVLVVEMSQTSSIGSAESLISLERK
 KEKNINRDITSRKDLPSRTSNVERKASQQQWGRGNFTEGKVPHIRIENGAAIEEITYFGR
 ILGKGSFGIVIEATDKETETKWAIIKKVNEKAGSSAVKLLEREVNILKSVKHEHIHLEQ
 VFETPKMYLVMELCEDGELKEILDRKGHFSENETRWIQSLASAIAYLHNNDIVHRDLK
 LENIMVKSSLIDNNEINLNIKVTDGLAVKKQSRSEAMLQATCGTPIYMAPEVISAHDY

FIGURE 1L

SQQCDIWSIGVVMYMLLRGEPFPLASSEAKLFELIRKGE LHFENAVWNSISDCAKSVLKQ
 LMKVDPAHRITAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVEENTTEEK NKPS
 TEEKLSYQPWGNVPETNYTSDEEEEEKQSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAE
 IKGEMEKTPVTPSQGTATKYPAKSGALSRTKKKL

SEQ ID NO: 166_SGK309_H

MQCLAAALKDET NMSGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTREN
 VALKVESAAQPKQVLKMEVAVLKKLQSGSLGQGDGKEEMMKPGAKRGKDHVCRFIGCGRNE
 KFNYYVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSGVFLHRDIKPSNF
 AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRRPVRNVAGFRGTVRYASVNAHKNREMGRHD
 DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMKEKYEHRMLLKHPSEFHLFLDHIASLDY
 FTKPDYQLIMSVFENSMKERGIAENEAADFWEKAGTDALLSTSTSTPPPAEHPADGSHVWG
 GQCDASAWGPAPGEHRGCATGRAPEXPGECTPNAREALXGAGPQSPPCPPRGSXGXSL
 GGDRCQPEQTPDQHRQSNCRQGEGRGWPFLLSPPIPSLVPLPCSSXAPCPPPISLLARPLF
 VVPSPALASLCLPSSSSSVSFTLRRPSA

SEQ ID NO: 167_AA234451_H

MSSGGGEQLDILSVGILVKERWKVLRKIGGGGFGEIYDALDMLTRENVALKVESAAQPKQV
 LKMEVAVLKKLQGDHVCRFICGRNDRFNYVVMQLQGRNLADLRRSQSRGTFTISTTLR
 LGRQILESIESIHSVGSXHRDIKPSNFAMGRFPSTCRKCYMLDFGLARQFTNSCGDVRPP
 RAVAGFRGTVRYASINAHNRNREMGRHDDLWSLFYMLVEFVVGQLPWRKIKDKEQVGSIKE
 RYDHRMLKHLPPFEFSIFLDHISSLDYFTKPDYQLLTSVFDNSIKTFGVIESDPFDWEKT
 GNDGSLTTTTTSTTPQLHTRLTPAAIGIANATPIPGDLLRENTDEVFPDEQLSDGENGIP
 VGVSPDKLPGSLGHPRPQEKDVWEEMDANKNKIKLGICKAATEEENSHGQANGLLNAPSL
 GSPIRVRSEITQPDRIPLVRKLRSIHSFELEKRLTLEPKPDTDKFLETWYKIVYFSF

SEQ ID NO: 168_AA435956_H

TFTIFFEMTVFDLEAKSARGGSNLLMDSVSSSFQLFMFQLLRGLAYIHHQHVLHRDLKPQN
 LLISHLGELKLADFLARAKSIPSQTYSSSEVTLWYRPPDALLGATEYSSSELDIWAGCI
 FIEMFQGQPLFPVSNILEQLEKIWEVLGVPTEDTWPVGVSKLPNYPWFPLPTPRSLHV
 VWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQLPDEESLFTVSGV
 RLKPEMCDLLASYQKGHPAQFSKCW

SEQ ID NO: 169_AA626859_H

NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIKICDFGFAQILIPGD
 AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR
 TLGKLI PRHQSI FKSNGFFHGISIPEPEDMETLEEKFSVDVHPVALNFMKGCLKMNPPDDR
 TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQNQLLPLIPGSHISPTPDGRKQVLQLK
 FDHLPNI

SEQ ID NO: 170_AA061797_M

KIALREIRMLKLKHPNLVNLIEVFRKRKMHLVFEYCDHTLLNELERNPNGVSDGVIKSV
 LWQTLQALNFCHKHNCIHRDVKPENILITKQGMKICDFGFARILIPGDAYTDYVATRWY
 RAPELLVGDTKYGSSVDVWAVGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLI PRHQSI
 IFRSNQFFRGISIPEDMETLEEKFSNVQPVALSFMKGCLKMNPPDERLTCAQLLDSAYF
 ESFQEDQMKRKARSEGRSRRRQQNQLLPLIPGSHISPTPDGRKQVVQLKFDHLPNI

SEQ ID NO: 171_AA397553_H

MPNSERHGGKDGSGGASGTLQPSGGGSSNSRERHRLVSKHKRHSKHSKMDGLVTPEA
 ASLGTVIKPLVEYDDISSDSTFSDDMAFKLDRRENDERRGSDRSDDLHKHRHHQHRRSR

FIGURE 1M

DLLKAKQTEKEKSQEVSSKSGSMKDRISGSSKRSNEETDDYGKAQVAKSSSKESRSSKLH
KEKTRKERELKSGHKDRSKSHRKRETPKSYKTVDSPKRRSRSPHRKWSOSSKQDDSPSGA
SYGQDYDLSPSRSHSTSSNYDSYKKS PGSTSRRSQSVSPPYKEPSAYQSSTRSPSPYSRRQR
SVSPYSRRRSSSYERSGSGSYGRSPSPYGRRRSSSPFLSKRSLRSPLPSRKSMKSRSRSP
AYSRHSSSHSKKKRSSSRHSSISPVRPLPNSSLGAELSRKKKRAAAAAAAKMDGKES
KGSPVFLPRKENSSVEAKDSGLESKKLPRSVKLEKSAPDTELNVNTHLNTTEVKNSSDTGK
VKLDENSEKHLVKDLKAQGTDRSKPIALKEEIVTPKETETSEKETPPPLPTIASPPPPPLP
TTTTPPQTPPLPPLPPIPALPQQPPLPPSQPAFSQVPASSTSTLPPSTHSKTS AVSSQAN
SQPPVQVSVKTQVSVTAAI PHLKTSTLPPPLPPLPGGDDMDSPKETLPSKPVKKEKEQ
RTRHLLTDLPLPPELPGGDLSPDSEPKAITPPQQPYKKRPKICCPRYGERRQTESDWG
KRCVDKFDIIGIIGEGTYGVYKARDKDTGELVALKKVRLDNEKEGFPITAI REIKILRQ
LIHRSVNMKEIVTDKQDALDFKKDKGAFYLVFEYMDHDL MGLLESGLVHFS EDHIKSF
KQLMEGLEYCHKNFLHRDIKCSNILLNNSGQIKLADFGLARLYNSEESRPYTNKVITLW
YRPELLELGEERYTPAIDVWSCGILGELFTKKPIFOANLELAQLELISRLCGSPCPAVW
PDVIKLPYFNTMKPKKQYRRRLREEFSPISAALDLDHMLTLDPSKRCTAEQTLQSDFL
KDVELSKMAPDLPHWQDCHELWSKKRRRQQRQSGVVVEEPPPSKTSRKETTSGTSTEPVK
NSSPAPPQPAPGVESGAGDAIGLADITQQNLQSELAVLLNLLQSQTDLSPQMAQLLNI
HSNPEMQQLEALNQSISALTEATSQQQDSETMAPEESLKEAPSAPVILPSAEQMTLEAS
STPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGQGPRTPTMPQEEAAACPPHIL
PPEKRPPEPPGPPPPPPPLVEGDLSSAPQELNPAVTAALLQLLSQPEAEPPGHLPEH
QALRPMEYSTRPRPNRTYGN TDGPETGFS AIDTDERN SGPALTESLVQTLVKNRTFSGSL
SHLGESSYQGTGSGVQFPGDQDLRFARVPLALHPVVGQFPLKAEGSSNSVVAETKLQNY
GELGP GTTGASSSGAGLHWGGPTQSSAYGKLYRGPTRVPPRGGRGRGVPI

SEQ ID NO: 172_AA789239_H

MEMYETLGKVGESYGTVMKCKHKNTGQIVAIKIFYERPEQSVNKIAMREIKFLKQFHHE
NLVNLIEVFRQKKKIHLVFEFIDHTVLDELQHYCHGLESKRLRKYLFQILRAIDYLHSSN
VIIHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYTDYVATRWYRAPELVLKDTSYG
KYVPVDI WALGCM IEMATGNPYLPSSSDLDLLHKIVLKVXFMPELKAKLLQEAKVNSLI
KPKESKENELRKDERKTVYTNTLLSSSVLGKEIEKEKKPKEIKVRVIVKVGGRGDI SEP
KKKEYEGGLQQDANENVHPMSPDTKLV TIEPPNPINPSTNCNGLKENPHCGGSVTMPPI
NLTNSNLMAANLSSNLFHPSVRLTERAKKRTSSQSIGQVMPNSRQEDPGPIQSQMEKGI
FNERTGHSQMANENKRKLNFSRSDRKEFHFPPELPVTIQSKDTKGMEVKQIKMLKRESKK
TESSKIPTLLNVDQNEKQEFIPLSLLSACCPIFTNICSQLTIRVEMAIARGRI

SEQ ID NO: 173_AA124976_M

LADIVHACLQIDPAERTSSTDLLRHDYFTRDGFIEKFIPELRAKLLQEAKVNSFIKPKEN
FKENEPVRDEKKS VFTNTLLYGNPSLYGKEVDRDKRAKELKVRVIKAKGGKGDVPDQKKP
EYEGDHRQQGTADDTQPSSLDKKPSVLELTNPLNPSSENSDGVKEDPHAGGCMIMPPINLT
SSNLLAANLSSNLSHPNSRLTERTKKRTSSQTIGQTLSNSRQEDTGPTQVQTEKGAFNE
RTGQNDQISSGNKRKLNFPKCDRKEFHFPPELPFTVQAKEMKGMEVKQIKVLKRESKKTDS
SKIPTLLSMDPNQEKQEGGDGDCEGKNLKRNRFFFSR

SEQ ID NO: 174_AA575635_M CCRK_M

SASGQLKIADFGLARVFS PDGGRLYTHQVATRWYRAPELLYGARQYDQGVDLWAVGCIMG
ELLNGSPLFPGENDIEQLCCVLRILGTPSPRVWPEITELPDYNKISFEEQAPVPLEEVL P
DASPGALDLLGQFLLYPPRQRI AASQALLHQYFFTA PLPAHPSELPI PQRPGGPAPKAHP
GPPHVHDFHVD RPIEESLLNPELIRPFIPEG

FIGURE 1N

SEQ ID NO: 175_AA631990_H

MIT SISTEKS GH THYPFMITTLQYYRGRGGKTAVVRHFS AEGPF AFAEMRHSKRTHCPDW
DSRESWGHE SYRGSHKRKRSSHSTQENRHCKPHHQFKE SDCHYLEARSLNERDYRDRRY
VDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRSEIV
DTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAA RSEIQVLEHLNSTDPNSVFR C
VQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLFPQIDHIRQMAYQICQSINFLHHNKL
THTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVD FGSATYDDEHHSTLVSTRH
YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGP I PQHMIQ
KTRKRKYFHNNQLDWEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLF DLVRRMLEYDPTQ
RITLDEALQHPFFDLLKKK

SEQ ID NO: 176_AA557536_H

MCTVVDPRIVRRYLLRRQLGQGRTFREITLLQVSGLGPPVQSPCPGTDLSRQERNWPSWA
PEHSPSWPSSRLRLSPQEFGDHPNII SLLDVIRAENDRDIYLVFEFMDTDLNAVIRKGG L
LQDVHVR SIFYQLLRATRFLHSGHVVRHDQKPSNVLLDANCTVKLCDFGLARSLGDLPEG
PEDQAVTEYVATRWYRAPEVLLSSHRYTASCPRYTLGVDMWSLGCILGEMLRGRPLFPGT
STLHQLELILETIPPPSEEXRPRQTL DALLPPDTSPEALDLLRLLVFAPDKRLSATQAL
QHPYVQRFHCPSDEWAREADVRPRAHEGVQLSVPEYRSRVYQMI LECGSSSGTSREKGPE
GVSPSQAHLHKPRADPQLPSRTPVQGP RPQPSSPGHDPAEHES PRAAKNVPRQNSAPLL
QTALLNGERPPGAKEAPPLTSLVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV
RVASVQQVPPRLPPEARPGRRMFST SALQGAQGGARALLGGYSQAYGTVCHSALGHLPLL
EGHHV

SEQ ID NO: 177_N28606_H, MOK_H

MKNYKAIGKIGEGTFSEVMKMQLSRDGNYYACKQMKQRFESIEQVNNLREIQALRRLNPH
PNILMLHEVVFDKSGSLALICELMDMNIYELIRGRRYPLSEKKIMHYMYQLCKSLDHIH
RNGIFHRDVKPENILIKQDVLKLGDFGSCRSVYSKQPYTEYISTRWYRAPECLLTDGFYT
YKMDLWSAGCVFYEIASLQPLFPGVNELDQISKIHDVIGTPAQKILT KFKQSRAMNFD FFP
FKKGSGIPLLTNLSPOCLSLHAMVAYDPDERIAAHQALQHPYFQEQRKTEKRALGSHR
KAGFPPEHPVAPEPLSNSCQISKEGRKQKQSLKQEEDRPKRRGPAYVMELPKLKLSGVVRL
SSYSSPTLQSVLGS GTNGRVPVLRPLKCI PASKKTD PQDKLPAPQQCRLPTIVRKGR

SEQ ID NO: 178_AB023153_H, ICK_H

MNRYTTIRQLGDGT YGSVLLGRSIESGELIAIKMKRKFYSWEECMNQREVKSLKLNHA
NVVKLKEVIRENDHLYFIFEYMKENLYQLIKERNKLPESAIRNIMYQILQGLAFI HKLG
FFHRDLKPENLLCMGPELVKIADFG LAREIRSKPPYTDYVSTRWYRAPEVLLRSTNYSSP
IDVWAVGCIMAEVYTLRPLFPGASEIDTIFKICQVLGTPKKT DWPEGYQLSSAMNFRWPQ
CVPNNLKTLPNASSEAVQLLRDMLQWDPKKRPTASQALRYPYFQVGHPLGSTTQNLQDS
EKPQKGILERAGPPPYIKPVPPAQPPAKPHTRISSRQHQASQPPLHLTPYKAEVSRTDH
PSHLQEDKPSPLLFP SLHNKHPQSKITAGLEHKNGEIKPKSRRRWGLISRSTKDSDDWAD
LDDLDFSPSLSRIDLKNKKRQSDDTLCRFESVLDLKPSEPVG TGN SAPTQTSYQRRDTPT
LRSAAKQHYLKH SRYLPGISIRNGILSNPGKEFIPNPWSSSGLSGKSSGTMSVISK VNS
VGSSSTSSSGLTGNYVPSFLKKEIGSAMQRVHLAPIPDPSPGYSSLKAMRPHPGRPFLDT
QPRSTPGLIPRPPAAQPVHGR TDWASKYPSRR

SEQ ID NO: 179_AA839940_M

SSNNGMSAEEEEIGPGA EPMRGPSLATRDWRDET VGT TDLQQGIDPGAVSPEPGKD HAAQ
GPGRTEAGRVSSAAEAAIVVLDDSAAPPAPFEHRVVS IKDTLISAGYTVSQHEVLGGGRF
GQVHRCTERSTGLALA AKIIKVKNVKDREDVKNEVNIMNQLSHVNLIQLYDAFESKNSFT
LIMEYVDGGELFDRITDEKYHLTEL DVVLFTRQICEGVHYLHQHYILHLDLKPENILCVS

FIGURE 10

QTGHQIKIIDFGLARRYKPREKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLL
SGLSPFLGETDAETMNFIVNCSDWDFDADTFKGLSEEAKDFVSRLLVKEKSCRMSTQCLK
HEWLNHLPAKASGSNVLRSQQLLQKYMAQSKWKHFHVVAVNRLRKFPCTP

SEQ ID NO: 180_AA460132_H
MAAARATTPADGEEPAPAEALAAARERSSRFLSGLLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRTVQEARALLRCRRAGISAPVVFVDYASNCLYMEEIEGVS
TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVLDLYVLEKAFSLTHPNTETVF EAFLSYSTSSKKARPVLKKLD
EVRLRGRKRSVMG

SEQ ID NO: 181_SGK034_H
QREKVNQGNMPLQSTFLAMDTEEGVEVVWNLHFGDRKAFAAHEEKIQTVEQLVLVDH
PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKTKKNHKAMNARAWKRWCTQILS
ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSINALPDDLRSPIRAEREELR
NLHFFPPEYGEVADGTAVDIFSGMCALEMAVLEIQTNGDTRVTEEAIRARHSLSDPNM
REFILCCLARDPARRPSAHSLLFHRVLFVHSLKLLAAHCFIQHQYLMPENNVVEEKTAM
DLHAVLAELPRRRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAP
PPEEVQAKAPTPEPFDSETRKVIQMOCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLL
PTDSAQDLASELVHYGFLHEDDRMKLA AFLESTFLKYRGTA

SEQ ID NO: 182_AA103218_M SGK034_M
HASAPEYGEVNDGTGFVDIFSGMCALEMAVLEIQANGDTRVTEEAIRARHSLSDPNMR
EFILSCLARDPARRPSAHLNLLFHRVLFVHSLKLLAAHCFIQHQYLMPENNVVEEKTAM
LHAVLAEMPQPHGPPMQWRYSEVSFLELDKFLEDVRNGIYPLMNFAAARPLGLPRVLAP
PEEAQAKAPTPEPFDSETRKVVQMOCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLP
TDSAQDLAAELVHYGFLHEDDRMKLA AFLETTFLKYRGTA

SEQ ID NO: 183_NEK7_H, N34132_H
MSGGAAEKQSSTPGSLFSLSPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHT
MDKDSRGAAATTTTEHRFFRRSVICDSNATALELPGLPLSLPQPSIPAAVPQSAPPEPH
REETVTATATSQVAQPPAAAAPGEQAVAGPAPSTVPSSTSKDRPVSQPSLVGSKEEPP
ARSGSGGSAKEPQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVYKGLD
TETTVEVAVCELQDRKLTKEQRFKEEAEMLKGLQHPNIVRFYDSWESTVKGKKCIVLV
TELMTSGTLKTYLKRFKVMKIKVLRSWCRQILKGLQFLHTRTPLIHRDLKCDNIFITGP
TGSVKIGDLGLATLKRAFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLMATSEY
PYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEIEGCIRQNKDERYSIKDLLNHAFQ
EETGVRVELAEEDDGEKIAIKLWLRIEDIKKLKGKYKDNEAIEFCFDLERDVPEDVAQEM
VESGYVCEGDHKTMAKAIKDRVSLIKRKREQRQLVREEQENKKQEESLQKQVEQSSASQ
TGIKQLPSASTGIPTASTTSASVSTQVEPEEPEADQHQQLOYYQPSISVLSDGTVD SGQG
SSVFTESRVSSQQTVSYGFPXHEQAHSTGTVPGHIPSTVQAQSQPHGVYPPSSVQQGIQQ
TAPPQQTQVQYLSQTSSTSEATTAQPVSQPQAPQVLPQVSAGKQSTQGVSVQVAPAEVAV
AQPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSVRSRHE
KTSRPKLRILNVSNKGDRVVECQLETHNRKMTVFKFDLDGDNPEEIIATIMVNNDFILAE
RESFVDQVREIEKADEMLSEDVSVPEEGDQGLQKDDYGFSGSQKLEGEFKQPIPA
SSMPQQIGIPTSSLTQVVHSAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPGMN
LSHSASSLSLQQA FSELRRQMTEGPNTAPPNFSHTGPTFPVPPFLSSIAGVPTTAAAT
APVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATSTGVVTSGLPPIPPVSESPVLSSV
SSITIPAVVSISTTSPSLQVPTSTSEIVVSSTALYPSVTVSATSASAGGSTATPGPKPPA
VVSQQAAGSTTVGATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTS

FIGURE 1P

HSSTTGLAFSLSAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPL
 LPQVPSIPPLVQPVANVPAVQQTLIHSQOPALLPNQPHTHCPEVDSDTQPKAPGIDDIK
 TLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVAPSKLLTSTTSTCLPP
 TNLPLGTVALPVTPVVTGQVSTPVSTTTSGVKPGTAPSKPPLTKAPVLPVGTLPAGTL
 PSEQLPFPFGPSLTQSQQPLEDLDAQLRRTLSPEMITVTSVAVGPVSMAAPTAITEAGTQP
 QKGVSVQKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTSESS
 VLSSSSPESTLVKPEPNGITIPGISSDVPESAHTTASEAKSDTGQPTKVGRFQVTTTAN
 KVGRFSVSKTEDKITDTKKEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSD
 PEAAFLSRDVGSGSPHSPHQLSSKSLPSQNLSQLSNSFNSSYMSSDNESDIEDLDL
 LELRRLRDKHLKEIQDLQSRQKHEIESLYTKLGKVP PAVIIPPAAPLSGRRRRPTKSKGS
 KSSRSSSLGNKSPQLSGNLGQSAASVLHPQQTLPHPGNIPEGQNLQLLOPLKPSPSDN
 LYSFTSDGAISVPSLSAPGQGNKATIIVQKQ

SEQ ID NO: 184_BCON3_H

MSEGESQTVLSSSGDPKVESSSSAPGLTSVSPVPTSTTSAASPEEEEESEDESEILEESP
 CGRWQKRREEVNRNVPIDISAYLAMDEEGVEVWNEVQFSEKKNYKLQEEKVRAVFDN
 LIQLEHLNIVKFHYWADIKENKARVIFITEYMSSGSLKQFLKKTCKKNHKTMEKAWKRW
 CTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINNHVKTCTREEQKNL
 HFFAPEYGEVTNVTTAVDIYSFGMCALEMAVLEIQNGESSYVPQEAISSAIQLLEDPLQ
 REFIQKCLQSEPARRPTARELLFHPALFEVPSLKLAAHCIVGHQHMIPENALEEITKNM
 DTSVLAIEIPAGPGREPQVTLYSQSPALEDKFLDVRNGIYPLTAFGLPRPQQPQQEEV
 TSPVPPSVKTPPTPEPAEVETRKVVLMQCNIESVEEGVKHHLTLLLKLEDKLNRLHSCDL
 MPNENIPELAAELVQLGFISEADQSRLTSLLEETLNKFNFARNSTLNSAAVTVSS

SEQ ID NO: 185_AA711829_M

LKQFLKKTCKKNHKTMEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIK
 IGSVAPDTINNHVKTCTREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEMAVLEIQNG
 GESSYVPQEAISSAIQLLEDLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLKLAA
 AHCIVGHQHMIPENALEEITKNMDTSVLAIEIPAGPGREPQVTLYSQSPALEDKFLDVR
 RINGIYPLTAFGLPRPQQPQQEEVTSPVPPSVKTPPTPEPAEVETRKVVLMQCNIESVEEG
 VKHHLTLLLKLEDKLNRLHSCDLMPNESIPDLAAELVQLGFISEADQSRLTSLLEETLNK
 FNFTRNSTLNTATVTVSS

SEQ ID NO: 186_AA099102_H

MSSCVSSQPSSNRAAPQDELGGRGSSSSSESQKPCEALRGLSSLSIHLGMESFIVVTECEP
 GCAVDLGLARDRPLEADGQEVPLDTSGSQARPHLSGRKLSLQERSQGGLAAGGSLDMNGR
 CICPSLPYSPVSSPQSSPRLPRRPTVESHHVSI TGMQDCVQLNQYTLKDEIGKGSYG VVK
 LAYNENDNTYYAMKVLSSKKLIRQAAFPRRPPRGRTRPAPGGCIQPRGPIEQVYQEIAIL
 KKL DHPNVVKLVEVLDDPNEDHLYMVFEVLVQGPVMEVPTLKLPLEDQARFYFDLIKGI
 EYLHYQKIHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNYVGTPAFMAPESLS
 ETRKIFSGKAKDVWAMGVTL YCFVFGQCPFMDERIMCLHSKIKSQALEFPDQPDIAEDLK
 DLITRMLDKNPESRIVVPEIKLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPS
 LATVILVKTMIKRSGNPFEGSRREERSLSAPGNLLTKKPTRECESLSELKEARQRRQP
 PGHRPAPRGGGG SALVRGSPCVESCWAPAPGSPARMHPLRP EAMEPE

SEQ ID NO: 187_5R69_17_2_H

MQEIPQEIQIKEIKKEQLSGSPWILLRENEVSTLYKGEYHRAVPAIKVFKKLQAGSIAIVR
 QTFNKEIKTMKKFESPNILRIFGICIDETVTPPQFSIVMEYCELGTRELLDREKDLTLG

FIGURE 1Q

KRMVLVLGAARGLYRLHHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQTSMSLGTT
REKTRVKSTAYLSPQELEDVIFYQYDVKSEIYSFGIVLWEIATGDIPFQGECECDWLSQW
L

SEQ ID NO: 188_H85811_H

MAPVYEGMASHVQVFSPTLQSSAFCSVKKLKIEPSSNWDMTGYGSHSKVYSQSKNIPLS
QPATTTVSTSLPVPNPSPLEQTIIVPGSTGHIIVVTSASSTSVTGQVLGGPHNLMRRSTV
SLLDTYQKCGLRKSEEIENTSSVQIIIEHPPMIQNNASGATVATATTSTATSKNSGSNS
EGDYQLVQHEVLCSMTNTYEVLEFLGRGTFGQVVKCWKRGTNEIVAIKILKNHPSYARQG
QIEVSILARLSTESADDYNFVRAYECFQHKNTCLVFEMLEQNLDFLKQNKFSPLPLKY
IRPVLQQVATAMKLSLGLIHADLKPENIMLVDPSRQPYRVKVIDFGSASHVSKAVCST
YLQSRYYRAPEIILGLPFCEAIDMWSLGCVIAELFLGWPLYPGDSEYDQIRYISQTQGLP
AEYLLSAGTKTTRFFNRDTSPPYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVN
MTTDLGSDMLVEKADRREFIDLLKMLTIDADKRITPIETLNHPFVTMTHLLDFPHSTH
VKSCFQNMIEICKRRVNMVYDTVNQSKTPFITHVAPSTSTNLMTFNQLTTVHNQPSAASM
AAVAQRSMPLQGTGTAQICARPDPFQQAIVCPPGFQGLQASPSKHAGYSVRMENAVPIVT
QAPGAQPLQIQPGLLAQQAWSGTQQIILLPPAWQQLTGVATHTSVQHATVIPETMAGTQQ
LADWRNTHAHGSHYNPIMQQPALLTGHVTLPAAQPLNVGVAVHVMRQQPTSTTSSRKSQKH
QSSVRNVSTCEVSSSQAISSPQRSKRKENTPPRCAMVHSSPACSTSVTCGWGDVASSTT
RERQRQTIVIPDTPSPTVSVITISSDTDEEEEQKHAPTSTVSKQRKNVISCVTVHDSFYS
DSSSNTSPYSVQQRAGHNNANAFDTKGSLENHCTGNPRTIIVPPLKTQASEVLVECDLSV
PVNTSHHSSSYKSKSSSNVTSTSGHSSGSSSGAITYRQQRPGPHFQQQQPLNLSQAQQHI
TTDRGTGSHRRQAYITPTMAQAPYSFPHNSPSHGTVHPLAAAAAAHLPTQPHLYTYTA
PAALGSTGTVAHLVASQGSARHTVQHTAYPASIVHQPVPVSMGPRVLPSPTIHPSQYPAQF
AHQTYISASPASTVYTYGYPPLSPAKVNQYPYI

SEQ ID NO: 189_DYRK3_H

MMIDETKCPPCSNVLCNPSEPPPPRRRLNMATQFTGDHTQHFLDGGEMKVEQLFQEFGNR
KSNTIQSDGISDSEKCSPTVSQKSSDCLNTVKSNSSSKAPKVPLTPEQALKQYKHHLT
AYEKLIEINYPEIYFVGPNAKKRHGVIGGPNNGGYDDADGAYIHVPRDHLAYRYEVLKII
GKGSFGQVARVYDHKLRYVALKMVRNEKRFHRQAEEIRILEHLKKQDKTGSMNVIHML
ESFTFRNHVCMFELLSIDLYELIKKNKFQGFVQLVRKFAQSILQSLDALHKNKIIHCD
LKPENILLKHHGRSSTKVIDFGSSCFEYQKLYTYIQSRFYRAPEIILGSRYSTPIDIWSF
RCILAEELLTGQPLFPGEDEGDQLACMMELLGMPPPKLLEQSKRAKYFINSKGI PRYCSVT
TQADGRVVLVGGRSRRGKKRGPPGSKDWGTALKGCDLYLFIIEFLKRCLHWDPSARLTQAQ
ALRHPWISKSVPRPLTTIDKVSGRVVPNPASAFQGLGSKLPPVVGIANKLKANLMSETNG
SIPLCVLPKLIS

SEQ ID NO: 190_AA589241_M DYRK3_M

TRPELLGMPPQKLLQSKRAKYFINSKGLPRYCSVSTQTDGRVVLGGRSRRGKKRGPPG
SKDWATALKGCGDYLFIEFLKRCLQWDPSARLTQAQALRHPWISKSTPKPLTMDKVPGKR
VVNPTNAFQGLGSKLPPVVGIAASKLKANLMSETSGSIPLCVLPKLIS

SEQ ID NO: 191_5R72_16_2_H

MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACPVKPEPPEINLVLY
PQGLTGEEVYVKVDLRVKCPPTYPDVVPEIELKNAKGLSNESVNLLKSRLEELAKKHCGE
VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQORLLEAKRKEEQEQREILHEIQ
RRKEEIKKEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAILHGGSPDFVGNKGR
ANSSGRSRRERQYSVCNSEDSPGSCIEILYFMGSPDQLMVHKGKICIGSDEQLGKLVYNAL
ETATGGFVLLYEWVLQWQKKMGPFLLTSQEKEKIDKCKKQIQGTETEFNSLVKLSPNVVR

FIGURE 1R

YLAMNLKEQDDSI VVDILVEHISGVSLAAHL SHSGPI PVHQLRRYTAQLLSGLDYLSHSNS
 VVHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKG
 VWRLGLLLLLSL SQQECGEYPVTIPSDL PADFQDFLKKCVCLDDKERWSPQQLLKHSFIN
 PQPKMPLVEQSPEDSGGQDYVETVIPS NRLPSAAFFSETQORQFSRYFIEFEELQLLGKA
 FGAVIKVQNKLDGCCYAVKRIPINPASRQFRRIKGEVTLLSRLHHENIVRYNNAWIERHE
 RPAGPGTPPPDSGPLAKDDRAARGQPASDTDGLDSVEAAAPPPILSSSVIEWSTSGERSAS
 ARFPATGPGSSDDEDDDEHGGVFSQSFLPASDSESDIIFDNEDENSKSQNQDEDCNEK
 NGCHESESPVTTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH
 EKGMIHRDLKPVNI FLDSDDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGHLTG
 MVGTALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMTASERIFVLNQLRDPTSP
 KFPEDFDDGEHAKQKSVISWLLNHDPKRPTATELLKSELLPPPQMESELHEVLHHTLT
 NVDGKAYRTMMAQIFSQRISPAIDYTYDSILKGNFSIRTAKMQQHVCETIIRIFKRHGA
 VQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNINLKRKRYCIE
 RVFRPRKLDRFHPKELLECAFDIVTSTNSFLPTAEIITYIYEIIQEFPALQERNYSIYL
 NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSLSSNSLCRLYKF
 IEQKQDLQDLMPTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYK
 VQQHNGIIFQFVAFIKRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSIADK
 ISAAVLNMEESVTISSCDLLVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQ
 EYCRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETETELVDHVLQKLRTKVTDERN
 REASDNLAVQNLKGSFSNASGLFEIHGATVVPISVLAPEKLSASTRRRYETQVQTRLQT
 SLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC
 DEIYNIKVEKKVSVLFLYSYRDDYRILF

SEQ ID NO: 192_R43524_H, HRI_H

MLGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQQPTFP
 FAVANQLLLVSLLEHLSHVHEPNPLRSRQVFLLCQTFIKMGLSSFTCSDEFSSRLRHH
 NRAITHLMRSAKERVRQDPCEDISRIQKIRSREVALEAQT SRYLNEFEELVILGKGGYGR
 VYKVRNKLDGQYYAIKKILIKGATKTVCMKVLREV KVLAGLQHPNIVGYHTAWIEHVHVI
 QPRADRAAIELPSLEVLSDQEEDREQCGVKND ESSSSSIIFAEPTPEKEKRFGESDTENQ
 NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQPLRRNSHLEESFTSTEE
 SSEENVNVLFGQTEAQYHMLMLHIQMQLCELSLWDWIVERNKRGREYVDESACPYVMANVAT
 KIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWTNRN
 GKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSLGVVLELFPQFPGTEMERAEVLTGL
 RTGQLPESLRKRCVPVQAKYIQHLTRRNSSQRP SAIQLLQSELFQNSGNVNLTLQMKIIEQ
 EKEIAELKKQLNLLSQDKGVRDDGKDGGVG

SEQ ID NO: 193_17000057519457_H

MAAARATTPADGEEPAPAEALAAARERSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
 HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFVDYASNCLYMEIEGVS
 TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
 LIDFGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
 EVRLRGRKRSMVG

SEQ ID NO: 194_AA013524_M

LVQQGAEARVFRGRFQGRAAVVKHRFPKSYRHPELEARLGRRRTVQEARALLRCRRAGIA
 APVVFVDYASNCLYMEIEEDSVTVRDYIQSTMETEKDPQCLDLARRMGQVLAMHDQD
 LIHGDLTTSNMLLRPLAQLHIVLIDFGLSFVSGLPEDKGVDLYVLEKAFLSTHPHTETA
 FEAFKSYGASSKKSSPVLKKLDEVRLRGRKRSMVG

FIGURE 1S

SEQ ID NO: 195_17000139801197_H, IRAKM_H
MAGNCGARGALSAHTLLFDLPPALLGELCAVLDS CDGALGWRGLAERLSSSWLDVRHIEK
YVDQKSGSTRELLWSWAQKNKTIGDLLQVLQEMGHRAIHLITNYGAVLSPSEKSYQEGG
FPNILFKETANVTVDNVLIPHEHNEKGVLLKSSISFQNIIEGTRNFHKDFLIGEGEIFEVY
RVEIQNLTYAVKLFKQEKMMQCKKHWKRFLESEVLLL FHHPNILELAAYFTETEFKFLI
YPYMRNGTLFDRLQCVGDTAPLPWHIRIGILIGISKAIHYLHNVPQCSVICGSISSANIL
LDDQFQPKLTD FAMAHRSHLEHQSTINMTSSSSKHLWYMPEEYIRQGKLSIKTDVYSF
GIVIMEVLTGCRVVLDDPKHIQLRDLRELMEKRGDLSCLSF LDKKVP PCPRNFS AKLFC
LAGRCAATRAKLRPSMDEV LNTLESTQASLYFAEDPPTSLKSFRCPSPLFLENVPSIPVE
DDESQNNLLPSDEGLRIDRMTQKTPFECSQSEVMFLSLDKKPESKRNEEACNMPSSSCE
ESWFPKYIVPSQDLRPYKVNIDPSSEAPGHSCSRPVESSCSSKFSWDEYEQYKKE

SEQ ID NO: 196_AA840598_M IRAKM_M
MWKRFLESEVLLLFRHPHILELAAYFTETEFKCLVYPYMSNGTLFDRLQCTNGTTPLSW
HVRISVLIGIAKAIQYLHNTQPCAVICGNVSSANILLDDQLQPKLTDFAAAHFRPNLEQQ
SSTINMTGGGRKHLWYMPEEYIRQGRLSVKTDVYSFGIVIMEVLTGCKVVLDDPKHVQLR
DLLMEKRGDLSCLSF LDRKIPPCPRNFS AKLFSLAGRCVATKAKLRPTMDEV LSSLE
STQPSLYFAEDPPTSLKSFRCPSPLFLDNVPSIPVEDDENQNNHSPVPKEVLGTDRTVQK
TPFECSQSEVTLGLDRNRGNRGSEADCNVPSSSHEECWSPELVAPSQDLSPTVISLGSS
WEVPGHSYSGKPMKRCSSGLFCSEHEQSKKQ

SEQ ID NO: 197_AA088547_H
MASAVRGSRPWPRLGLQLQFAALLGLTSPQVHTLRPENLLL VSTLDGSLHALSKQTGDL
KWTLRDDPVIEGPMYVTEMAFLSDPADGSLYILGTQKQGLMKLPFTIPELVHASPCRSS
DGVFYTGKQDAWVVDPESETQMTLTTEGPSTPRLYIGRTQYVTMHDPRAPALRWNT
TYRRYSAPPMDGSPGKYM SHLASCGMGLLLTVDPGSGTVLWTQDLGVPVMGVYTWHDGL
RQLPHLTLARDTLHFLALRWGHIRLPASGPRDTATLFTLDTQLLMTLYVGKDETFYVS
KALVHTGVALVPRGLTLAPADGPTTDEVTLQVSGEREGSPSTAVRYPGSGVALPSQWLLI
GHHELPPVLHTTMLRVHPTLGSGTAETRPENTQAPAFFLELLSLSREKLWDSELHPEEK
TPDSYLGLGPQDLLAASLTAVLLGGWILFVMRQVVEKQOETPLAPADFAHISQDAQSLHS
GASRRSQKRLQSPSKQAQPLDDPEAEQLTVVGKISFNPKDVLGRGAGGTFVFRGQFEGRA
VAVKRLRECFGLVRREVQLQESDRHPNVLR YFCTERGPQFHYIALELCRASLQEYVEN
PDLDRGGLEPEVVLQQLMSGLAHLHSLHIVHRDLKPGNILITGPD SQGLGRVVLSDFGLC
KKLPAGRCFSFLHSGIPGTEGWMAPELLQLLPDPSPTSAVDIFSAGCVFYVLSGGSHPF
GDSLYRQANILTGAPCLAHLEEEVHDKVVARDLVGAMLSPLPQPRPSAPQVLAPFFWSR
AKQLQFFQDVS DWLEKESEQEPLVRALEAGGCAVVRDNWHEHIS MPLQTDLRKFRSYKGT
SVRDLLRAVRNKKHHYRELPEVVRQALGQVPDGFVQYFTNRFPRLLLHTHRMRSCASES
LFLPYYPDSEARRPCPGATGR

SEQ ID NO: 198_HGP_6644466
MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTGVNVYLMKRSRGLSHSP
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGE
KSLNDLIEERYKASQDPFPAAILKVALNMARGLYLHQEKLLHGD IKSSNVVIKGD FE
TIKICDVGVSPLDENMTVTDPEACYIGTEPWKPKEAVEENGVI TDKADIFAFGLTLWEM
MTLSIPHINLSNDDDDDKTFDESDFDEAYYAALGTRPPINMEELDESYQKVIELFSVC
TNEDPKDRPSAAHIVEALETDV

SEQ ID NO: 199_AA449542_M
SPRGLSHSPWAVKKISLLCDDHYRTVYQKRLTDEAKILKLNHPNIGYRAFTEASDGSL
CLAMEYGGEKSLNDLIEERNKDSGSPFPAAVILRVALHMARGLYLHQEKLLHGD IKSS

FIGURE 1T

NVVIKGFETIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEALEENGIITDKADV
AFGLTLWEMMTLCIPHVNLPDDDDVEDATFDESDFDDEAYYAALGTRPSINMELDDSYQK
AIELFCVCTNEDPKDRPSAAHIVEALELDGQCCGLSESKH

SEQ ID NO: 200_5R57_10_2_M TESK2_M
LLSDSLYLPWTVRVKLAYGIAGVLSYLFHFKGIFHRDLTSKV

SEQ ID NO: 201_AA232253_H
MSSLGASFVQIKFDDLQFFENC GGGSFGSVYRAKWISQDKEVAVKLLKIEKEAEILSVL
SHRNIQFYGVILEPPNYGIVTEYASLGSLYDIINSNRSEEMDMHIMTWATDVAKGMHY
LHMEAPVKVIHRDLKSRNVVIAADGVVKICDFGASRFHNHTTHMSLVGTFFPWMAPEVIQS
LPVSETCDTYSYGVVLWEMLTREVPFKGLEGLQVAWLVEKNERLTIPSSCPRSFAELLH
QCWEADAKKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAERCEIEATLERLKKLERD
LSFKEQELKERERRLKMWEQKLTQSNTPLLPSEIGAWTEDDVYCWWQQLVRKGDSSAE
MSVYASLKFENNI TGKRLLLLEEDLDKDMGIVSKGHI IHFKSAIEKLTHDYINLFHFPP
IKDSGGEPEENEKEIVNLELVFGFHLKPGTGPQDCKWKMYMEMDGDEIAITYIKDVTFTNT
NLPDAEILKMTKPPFVMEKWIIVGIAKSQTVECTVTYESDVRTPKSTKHVHLIQWSRTKPQ
DEVKAVQLAIQTLFTNSDGNPGSRSDSSADCQWLDTLRMRQIASNTSLQRSQSNPILGSP
FFSHFDGQDSYAAAVRRPQVPIKYQQITPVNQSRSSSPTQYGLTKNFSSLHLNSRDSGFS
SGNTDTSSERGRYSDRSRKYGRGSI SLNSSPRGRYSGKSQHSTPSRGRYPGKFYRVSQS
ALNPHQSPDFKRSRDLHQPNITPGMPLHPETDSRASEEDSKVSEGGWTKVEYRKKPHRP
SPAKTNKERARGDHRGWRNF

SEQ ID NO: 202_AI375137_H
MGNYKSRTQTCTDEWKKKVSESYVITIERLEDDLQIKEKELTELNRNIFGSDEAFSKVNL
NYRTENGLSLLHLCCICGGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL
LHSGADIQQVGYGGLTALHIATIAHLEAADVLLQHGANVNIQDAVFFTPLHIAAYYGHE
QVTRLLLKFGADVNVSGEVGDRPLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVP
FCSRFGHHDIVKYLQSDLEVQPHVNIYGDTPHLACYNKGFEVAKETIQISGTESLTK
ENIFSETAFHSACTYKSIDLVKFLLDQNVININHQRDGTGLHSACYHGHIRLVQFLL
DNGADMNLVACDPSRSSGEKDEQTCMLWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG
GDGSYVSVSPPLGKIKSMTKEKADILLRAGLP SHFHLQLSEIEFHEIIGSGSFGKVYKG
RCRNKIVAIKRYRANTYCSKSDVDMFCREVSILCQLNHPCVIQFVGACLN DPSQFAIVTQ
YISGGSLSFLLHEQKRILDQSKLIIAVDVAKGMEYLHNLTPQIHRDLNSHNILLYEDG
HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT
GEIPFAHLKPAAAAADMAHYHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE
ECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA
LSQSAGQYSSQGLSLEEMKRSLQYTPIDKYGYVSDPMSSMHFHS CRNSSSFEDSS

SEQ ID NO: 203_H97685_H
MESERSPLYRQLIDLGYLSSSHWNCGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRL
VDAAKALNLVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMNIANRKQEE
MKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEVGTREIKCCIRQIQELIISRLNQA
VANKLISSVDYLRESFVGTLERCLQSLEKSQDVSVHITSNYLKQILNAAHYHEVTFHSGS
SVTRMLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAKSICSQFRTRLNS
SHEAFAASLRQLEAGHSGRLEKTEDLWLRVRKDHAPRLARLSLESRLQDVLLHRKPKLG
QELGRGQYGVVYLC DNWGGHFP CALKSVVPPDEKHWNDLALFHYMRSLPKHERLVDLHG
SVIDYNYGGGSSIAVLLIMERLHRDLTYTGLKAGLTLETRLQIALDVVEGIRFLHSQGLVH
RDIKLNVLDDKQNRAKITDLGFCKPEAMMSGSI VGTPIHMAPELFTGKYDNSVDVYAFG

20/119

FIGURE 1U

ILFWYICSGSVKLPEAFERCASKDHLWNNVRRGARPERLPVFDDEECWQLMEACWDGDPLK
RPLLGIQVQMLQGIMNRLCKSNSEQPNRGLDDST

SEQ ID NO: 204_W20810_M

DVNLKASKASDVYSFGILVWAVLAGREAELVDKTSLIRETVCDRQSRPPLTELPPGSPET
PGLEKLEKELMIHCWGSQSENRPSTFQDCEPKTNEVYNLVKDKVDAAVSEVKHYLSQHRSSG
RNLSAREPSQRGTEMDCPRETVMVKMLDRHLLEEPSGPVPGKCPERQAQDTSVGPATPAR
TSSDPVAGTPQIPHTLPFRGTTGPGVFTETPGPHQORNQGDGRHGTPWYPWTPPNPMTGP
PALVFNNCSEVQIGNYNLSLVAPPRTTASSSAKYDQAQFGRGRGWQPFHK

SEQ ID NO: 205_AA744236_H

MGENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYKRENEDKVNKAAKHLKTL
RHPCLLRFLSCTVEADGIHLVTERVQPLEVALETLSAEVCAGIYDILLALIFLHDRGHL
THNNVCLSSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPPEEMSPEFTT
LPECHGHARDAFSFGLVESLLTILNEQVSADVLSSFQQLHSTLLNPIPKCRPALCTLL
SHDFFRNDLFLEVNVFLKSLTLKSEEEKTEFFKFLDRVSCLEELIASRLVPLLLNQLVF
AEPVAVKSFLPYLLGPKKDHQGETPCLLSPALFQSRVIPVLLQLFEVHEEHVRMVLSSH
IEAYVEHFTQEQLKKVILPQVLLGLRDTSDSIVAITLHSLAVLVSLLGPEVVVGGERTKI
FKRTAPSFTKNTDLSLEGDPFSQPIKFPINGLSDVKNSTEDSENFPSSSKKSEEPDWSE
PEEPENQTVNIQIWPPEPCDDVKSQCTTLDVEESSWDDCEPSSLDTKVNPGGGITATKPV
TSGEQKPIPALLSLTEESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSELG
LGEEFTIQVKKKPVKDPMDWFADMIPEIKPSAAFLILPELRTEMVPKKDDVSPVMQFSS
KFAAAEITEGEAEGWEEEGELNWNEDNNW

SEQ ID NO: 206_AI052250_H

MESMLNKLKSTVTKVTADVTSAVMGIPVTREFDVGRHIASGCNGLAWKIFNGTKKSTKQE
VAVFVFDKKLIDKYQKFEKQIIDSCLKRGVQQLTRLRHPRLLTVQHPLEESRDCLAFCTE
PVFASLANVLGNWENLPSPISPDIKDYKLYDVETKYGLLQVSEGLSFLHSSVKMVHGNIT
PENIILNKSGAWKIMGFDFCVSSTNPSEQEPKFPCKEWDPNLPSLCLPNPEYLAPEYILS
VSCETASDMYSLGTVMYAVFNKGKPIFEVKNQDIYKSFSRQLDQLSRLGSSSLTNIPEEV
REHVKLLLNVTPTVRPDADQMTKIPFFDDVGAVTLQYFDTLFQRDNLQKSQFFKGLPKVL
PKLPKRIVIVQRILPCLTSEFVNPDMPFVLPNVLLIAEECTKEEYVKLILPELGPVFKQQ
EPIQILLIFLQKMDLLLTKTPPDEIKNSVLPVYRALEAPSIQIQELCLNIPTFANLID
YPSMKNALIPRIKNACYKHLPLRFV

SEQ ID NO: 207_AA278842_H

MWFFARDPVRDFPFELIPEPPEGGLPGPWALHRGRKKATGSPVSI FVYDVKPGAEETQV
AKAAFKRFTLRHPNIIAYIDGLETEKCLHVVTEAVTPLGIYLKARVEAGGLKELEISWG
LHQIVKALSFLVNDCSLIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQNGGGPPRKGIPE
LEQYDPPELADSSGRVVREKWSADMWRLGCLIWEVFNGLPRAAALRNPGKIPKTLVPHY
CELVGANPKVRPNPARFLQNCRAPGGFMSNRFVETNLFLEEIQIKEPAEKQKFFQELSKS
LDAFPEDFCRHKVLPLQLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVKMFSS
TDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVHGFLLDTNPAIREQTVKSMLLLAPKLN
EANLNVELMKHFARLQAKDEQGPIRCNTTVCLGKIGSYLSASTRHRVLTSAFSTRATRDPF
APSRVAGVLGFAATHNLYSMNDCAQKILPVLCLGLTVDPKSVRDQAFKAIRSFLSKLESV
SEDPTQLEEVKEDVHAASSPGMGGAASWAGWAVTGVSSTLSKLIRSHPTTAPTETNIPQ
RPTPEGVPAPAPTVPATPTTSGHWETQEEDKDTAEDSSSTADRWDDWGSLEQEAESVL
AQQDDWSTGGQVSRASQVNSDHKSSKSPESDWSWEAEGSWEQGWQEPSSQEPDPGTR
LASEYNWGGPSSDKGDPFATLSARPSTQPRPDSWGEDNWEGLTDSRQVKAELARKKRE
ERRREMEAKRAERKVAKGPMKLGARKLD

FIGURE 1V

SEQ ID NO: 208_AA599286_H

MAFMEKPPAGKVLDDTVPLTAAIEASQSLQSHTEYIIRVQGGISVENSWQIVRRYSDFD
LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD
PNNYSANYTEIALQQVSMFFRSEPKEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLWS
ADLGPDKYLSKDFQCLIKLLPSCLHPYIYRVTFATANESSALLIRMFNEKGTLDLIYK
AKPKDPFLKKYCNPKKIQGLELQIKTYGRQILEVLKFLHDKGFPYGLHASNVMLDGD
CRLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP
PAPSMVAVLESTLSCEACKNGMPTISRLLQMPFLSDVLLTTSEKPQFKIPTKLKEALR
IAKECIEKRLIEEQKQIHQHRRLTRAQSHHGSEERKKRILARKKSKRSALENSEEHS
KYSNSNNSAGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPAAPLPPASTEAPAQLS
SQAVNGMSRGALLSSIQNFQKGTLRKAKPVITVLRSAEASCLHLEGKVLFYSSPLPPN
YPLPGKVIAEPVQPQTVLFCRCCKQLFERNNSLSRIKLGWHAKKKKKK

SEQ ID NO: 209_AA425725_H

MSASTGGGGDGGSGGSSSSSQASCGPESSGSELALATPVPQMLQGLLGSDDDEEQEDPKD
YCKGGYHPVKIGDVFNGRYHVVRKLGWGHFSTVWLCWDIQRKRFVALKVVKSAHYTETA
VDEIKLLKCVRSDSPDPKRETIVQLIDDFRISGVNGVHVMVLEVLGHQLLKWIIKSNY
QGLPVPCKSIVRQVLHGLDYLHTKCKIHTDIKPENILLCVGDAYIRRLAAEATEWQQA
GAPPPSRISIVSTAPQEVLTGKLSKNKRKKMRKRKQKRLLEERLRDLQRLAMEAATQA
EDSGRLDGGSGSTSSSGFSGSLFSPASCSILSGSSNQRETGGLSPSTPFGASNLLVNP
LEPQNADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEYGPADIWSTACMAF
ELATGDYLFEPHSGEDYSRDEDHIAHIVELLGDI PPAPALSGRYSREFFNRRGELRHIHN
LKHWGLEYEVLMEKYEWPLEQATQFSAFLPMMEYIPEKRASAADCLOHPWLNP

SEQ ID NO: 210_SGK022_H

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGGPSEFIQRFLPRELQ
IVRTL DHKNI IQVYEMLESADGKICLVMELAEGGDVDFCVLNGGPLPESRAKALFROMVE
AIRYCHGCGVAHRDLKCENALLQG FNKL TDFGFAKVL PKSHRELSQTFCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSPFTHLSISADCQD
LLKRLLPEPDMILRPSIEEVSHPWLAST

SEQ ID NO: 211_AA060026_M SGK022_M

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKIIDKMGGPEEFIQRFLPRELQ
IVRTL DHKNI IQVYEMLESADGKIYLVMELEAGGDVDFCVLNGGPLPESRAKALFROMVE
AIRYCHGCGVAHRDLKCENALLQG FNKL TDFGFAKVL PKSRRELSQTFCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSPFTHLGISTECQD
LLKRLLPEPDMILRPSIEEVSHPWLAST

SEQ ID NO: 212_AA399669_H

MGKGDVLEAAPT TTTAYHSLMDEYGYEVGKAIGHGSYGSVYEA FYTKQKVMVAVKII SKKK
ASDDYLNKFLPREIQQVMKVL RHKYLINFYRAIESTSRVYIILELAQGGDVLEWIQRYGA
CSEPLAGKWFSQLTLGIAYLHKSIVHRDLKLENLLLDKWENVKISDFGFAKMVPSNQPV
GCSPXYRQVNCFSHLSQTYCGSFAYACPEILRGLPYNPFLSDTWSMGVILYTLVVAHLPF
DDTNLKKLLRETQKEVTFPANHTISQECKVQLLIACVAQWRKTQARPLSPLL

SEQ ID NO: 213_AA758539_H

MDDATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRRKTPTDFVERFLPRE
MDILATVNHGSI IKTYEIFETSDGRIYIIMELGVQGDLLFIKQCQALHEDVARKMFRL
SSAVKYCHDLDIVHRDLKCENLLLDKDFNIKLSDFGFSKRCLRDSNGRIILSKTFCGSAA

FIGURE 1W

YAAPEVLQSIPIYQPKVYDIWSLGVILYIMVCGSMPYDDSDIRKMLRIQKEHRVDFPRSKN
LTCECKDLIYRMLQPDVSQLHIDEILSHSWLQPPKPKATSSASFKEGEGKYRAECKLD
TKTGLRPDHRPDHKLGAKTQHRLLVVPENENRMEDRLAETSRAKDHHISGAEVGKAST

SEQ ID NO: 214_AA883975_H

MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKYKGTVAIKVVDRRRAPPDFVNKFLPRE
LSILRGVRPHPHIVHVFIEVCNGKLYIVMEAAATDLLQAVQRNGRIPGVQARDLFAQIA
GAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGRAHGYPDLSTTYCGSAAYASP
EVLGIPYDPKKYDVWSMGVVLYVMVTGCMFPDDSDIAGLPRRQKRGVLYPEGLELSERC
KALIAELLQFSPSARPSAGQVARNCWLRAGDSG

SEQ ID NO: 215_AA905446_H

VGRQETGVRRAFLICQPISPPLTSSEFIQRFLPRELQIVRTL DHKNI IQVYEMLESADG
KICLVMELAEAGDVFDCVLNGGPLPESRAKALFROMVEAIRYCHGCGVAHRDLKCENALL
QGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEVLQGI PKXMLWQQQKGVSPFTHL
SISADCQDLLKRLLPEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 216_H29974_H

YSLLAIEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVELALAEFWALTSLKRRHQNV
VQFEECVLQRNGLAQRM SHGNKSSQLYLRLVETSLKGERILGYAEPCYLWFVMEFCEGG
DLNQYVLSRRPDPATNKSFMLQLTSAIAFLHKNHIVHRDLKPDNILITERSGTPILKVAD
FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYMAPEVWEGHYTAKADIFALG
IIIWAMIERITFIDSETKKEL LGTYIKQGT EIVPVGEALLENPKMELHIPQKRRTSMSEG
IKQLLKDMLAANPQDRPDAFELETRMDQVTCAA

SEQ ID NO: 217_AA498104_M H29974_M

PLLLPPPPAAMETGKENGARRGKSPERKRRSPVQORVLCEKLRPAAQAMPAGAEVPGEA
FLARRRPDGGGDV PARPRYSLLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVE
LALAEFWALTSLKRRHQNVVQFEECVLQRNGLAQRM SHGNKNSQLYLRLVETSLKGERIL
GYAEPCYLWFVMEYCEGGDLNQYVLSRRPDPATNKSFMLQLTSAIAFLHKNHIVHRDLK
PDNILITERSGTPILKVADFGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYM
APEVWEGHYTAKADIFALGIIIWAMIERITFIDSETKKEL LGTYIKQGT EIVPVGEALLE
NPKMELHIPQKRRTSMSEGVKQLLKDMLAANPQDRPDAFELETRMDQVTCAA

SEQ ID NO: 218_AA215311_H

MVSSQPKYDLIREVGRGSYGVVYEAVIRKTSARVAVKKIRCHAPENVELALREFWALSSI
KSQHPNVIHLEECILQKDMVQKMSHGSNSSLYLQLVETSLKGEIAFDPRSAYYLWFVMD
FCDGGDMNEYLLSRKPNRKTNTSFMLQLSSALAFHKNQI IHRDLKPDNILISQTRLDT
DLEPTLKVADFGLSKVCASGQNPEEPVSVNKCFLSTACGTD FYMAPEVWEGHYTAKADI
FALGIIIWAMLERITFIDTETKKEL LGSYVKQGT EIVPVGEALLENPKMELLI PVKKKSM
NGRMKQLIKEMLAANPQDRPDAFELELRVLVQIAFKDSSWET

SEQ ID NO: 219_AA018361_H

MRAAFPAGGAGGSVEPPSARPAPQAGTAARSEEAPARAQAAGMAGPGWGPRLDGFILT
ERLGS GTYATVYKAYAKD TREVVAIKCVAKKSLNKASVENLLTEIEILKGIRHPHIVQL
KDFQWSDNIYLIMEFCAGGDL SRFIHTRRILPEKVARVFMQQLASALQFLHERNISHLD
LKPQNILLSSLEKPHLKLADFGFAQHMSPWDEKHLVLRGSPLYMAPEMVCQRQYDARVDLW
SMGVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLSRDCRDLLQRLLERDPSR
RISFQDFFAHPWVDLEHMPSGESLGRATALVVQAVKKDQEGDSAAALSLYCKALDFFVPA

FIGURE 1X

LHYEVDQRKEAIKAKVGQYVSRAEELKAIVSSSNQALLRQGTSARDLLREMARKPRLL
AALEVASAAMAKEEAAGGEQDALDLYQHSLGELLLLLRSRPRAGGSCFTLRFRRTSWPELN
T

SEQ ID NO: 220_AA311714_H
MENFILYEEIGRSKTVVYKGRRKGTINFVAILCTDKCRRPEITNWVRLTREIKHKNIIVT
FHEWYETSNHLWLXENLPEDVVREFGIDLISGLHHLHKLGLFCDISPRKILLEGPGTL
KFSNFCLAKVEGENLEEFFALVAAEEGGDNGENVLKKSMKSRVKGSPVYTAPENVRGAD
FSISSDLWSLGCCLLYEMFSGKPPFFSESSELTEKILCEDPLPPIPKDSSRPKASSDFIN
LLDGLLQDRDPQKRLTWTRLLQHSFWKAFAGADQESSVEDLSLSRNTMECSGPDQSKELL
QNSQSRQAKGHKSGQPLGHSFRLENPTFRPKSTLEGQLNESMFLSSRPTPTSTAVEV
SPGEDMTHCSPQKTSPLTKITSGHLSQODLESQMRELIYTDSDLVVTPIIDNPKIMKQPP
VKFDAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMGASRAKLNLLCYLCVV
AGHQEVATRLLHSPLFQLLIQHLRIAPNWDIRAKVAHVIGLLASHTTELQENTPVVETTS
SIGIGILNCLVQHSTPVPRQCLVYV

SEQ ID NO: 221_SGK384_H
SLAHVLRARQILTEPEVRDYLRLGLVSGRLRYLHQRCILHR

SEQ ID NO: 222_AA210451_M SGK384_M
MGQQHGTRNGLTHRELPRGVGLLLAMALMNVALYLCLDQLFISPRSTADSRRCPPGYFR
MGRMRNCSRWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALSRLTRLEMKEDFLH
GLQMLKSLQSEHVTVLVGYCEEDGTILTEYHPLGSLSNLEETLNLISKYQDVNTWQHRLQL
AMEYVSIINYLHHSPLGTRVMCDSDNLPKTLISQYLLTSNFSIVANDLDALPLVDHDSGVL
IKCGHRELHGDFVAPEQLWPYGEDTPFQDDLMPSYNEKVDIWKIPDVSSFLLGHVEGSDM
VRFHLFDIHKACKSQIPAERPTAQNVLDAYQRVFHSRLRDTVMSQTKEML

SEQ ID NO: 223_SGK071_2_H
EVVAVQMMVECMDDHYASQALEELMPLLLKLRHAHISVYQELFITWNGEISSLYLCLVMEF
NELSFQEVIEDKRKAKKIIDSEWMQNVLGQVLDALAYLHHLDIHRNLKPSNIIILISSDH
CKLQDLSSNVLMTDKAKWNIRAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIIIDMTSC
SFMDGTEAMHLRKSRLQSPGSLKAVLKTMEEKQIPDVETFRNLLPLMLQIDPSDRITIKD
VVHITFLRGSFKSSCVSLTLHRQMVPASITDMLLEGNVASILGDAGDTKGERALKLLSMA
LASYCLVPEGSLFMPLALLHMDQWLSCDQDRVPGKRDFAKGLKGLGPIPKGLPWPP
ELVEVVVTTMELHDRVLDVQLCACSLLLHLLGQALVHHPEAKAPCNQAITSTLLSALQSH
PEEEPLLVMVYSLLAITTTQESESLSSEELQNAGLLEHILEHLNSSLERSDVCASGLGLLW
ALLLDDPILALQRPRKKRAPNHGKPGKPNPASTQSIIVNKAPLEKVPDLISQVLATYPA
DGEMAEASCQVFWLLSLLGCIKEQQFEQVVALLLQSIRLCQDRALLVNNAYRGLASLVKV
SELAAFKVVVQEEGGSGLSLIKETYQLHRDDPEVVENVGMLLVHLASYEEILPELVSSSM
KALLQEIKERFTSSSLVSDSSAFSKPGLPPGSGPQLGCTTSGGLE

SEQ ID NO: 224_AA118352_M SGK071_M
EEDPCQKSWMAPEALKFSFSTKSDIWSLGCIIIDMATCSFLNDTEAMQLRKAIRHHPGSL
KPILKTMEEKQIPGTDVYYLLLPFMLHINPSDRLAIKDVMQVTFMSNSFKSSSVLNMQR
QKVPIFITDVLLEGNMANILGSWLCASFVNDNRHCDSGIGSQRLGFDQSVSWTEHPLKD
VMQNFSSRPEVQLRAINKLLTMPEDQLGLPWPTELLEEVISIIKQHGRILDILLSTCSLL
LRVLGQALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISSQGQISEEL
EEGLFQLAQENLEHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHP
EDVEIAEAGCAVLWLLSLLGCIKESQFEQVVLLLRSIQLCPGRVLLVNNAFRGLASLAK

FIGURE 1Y

VSELVAFRIVVLEEGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGG
IKDLVQVIRGRFTSSLELISYADEILQVLEANAQPGLOEDQLEPPAGQEAPLQGEPLFRP

SEQ ID NO: 225_018653.9_H

GRGRGAGHARGLGRGPAGRRAPPRSLSRPGPGPSRAGPAGRGEGSDAAPAGGSGRGFL
RLLPAGLRPQRALRSGSEPPRPGQSPEPSPAPGAGRRGGRGELARQIRARYEEVQRYSRG
GPGPGAGRPERRRRLMDLAPGGPGLPRPRPPWARPLSDGAPGWPPAPGPGSPGPGPRLGCA
ALRNVSGAQYMGSGYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGVRRGCYRLAA
HKLLKEMVLLERLRHPNVLQLYGYCYQDSEDIPTLTITITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKVTDLDDARVEETPCAGSTDCI
LEFPARNFTLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDISVNATGE
LAWGVDETLAQLEKVLHLYRSGQYLQNSTASSSTEYQCI PDSTI PQEDYRCWPSYHHGSC
LLSVFNLAEAVDVCESHAQCRAFFVTNQTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

SEQ ID NO: 226_AA396601_M

TRPGCAALRNVSGAQYVGSYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGARRG
CYRLAAHKLLKEMVLLERLRHPNVLQLYGYCYQDSEGIPTLTITITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVNGELKVTDLDDARVEETPCT
SSADCTLEFPARNFSLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDISI
VNATGELAWGVDETLAQLETAHLFRSGQYLQNSTSSRAEYQRI PDSAITQEDYRCWPSY
HHGGCLLSVFNLAEAIDVCESHAQCRAFFVTNQTWTGRKL VFFKTGWNQVVPDAGKTTY
VKAPG

SEQ ID NO: 227_VRK3_H

MISFCPDCGKSIQAAFKFCPYCGNSLPVEEHVGSQTFVNPHVSSFQGSKRGLNSSFETSP
KKVKWSSTVTSRRLSLFSDGDSSESEDTLSSSERSKSGSGSRPPTPKSSPQKTRKSPQVTR
GSPQKTSCSPQKTRQSPQTLKRSRVTTSLALPTGTVLTDKSGRQWKLKSFQTRDNQGIL
YEAAPTSTLTCDSGPQKQKFSKLDAKDGRLFNEQNFFQRAAKPLQVNWKKLYSTPLLA
IPTCMGFGVHQDKYRFLVLP SLGRSLQSALDVSPKHVLSERSVLQVACRLDDALEFLHEN
EYVHGNVTAENIFVDPEDQSQVTLAGYGFAFRYCPSGKHVAYVEGSRSPHEGDLEFISMD
LHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGP CGH
WIRPSETLQKYLKVMALTYEEKPPYAMLRRNNLEALLQDLRVSPYDPIGLPMVP

SEQ ID NO: 228_S71575_M VRK3_M

IPTCIGFGIHQDKYRFLVFP SLGRSLQSALDDNPKHVVSERCVLQVACRLDDALEYLHEN
EYVHGNLTAENVFVNPEDLSQVTLVGYGFTYRYCPGGKHVAYKEGSRSPHDGDLEFISMD
LHKGCGPSRRSDLQTLGYCMLKWLYGSLPWTNCLPNTTEKITRQKQKYLDSPERLVGLCGR
WNKASETLREYLKVMALNYEEKPPYATLRNSLEALLQDMRVSPYDPLDLQMPV

SEQ ID NO: 229_AA45427_H

MGHALCVCSRGTVIIDNKRYLFIQKLGEFFSYVDLVEGLHDGHFYALKRILCHEQQDRE
EAQREADMHRFLFNHPNIRLVAYCLRERGAKHEAWLLLPFFKRGTLWNEIERLKDKNFL
TEDQILWLLLGICRGLEAIHAKGYAHRDLKPTNILLGDEGQPVLMDLGSMNQACIHVEGS
RQALTLDQWAAQRCTISYRAPELFSVQSHCVIDERTDVWSLGCVLAMMFEGEPYDMVFQ
KGDSVALAVQNQLSIPQSPRHSSALRQLLNSMMTVDPHQPHIPLLLSQLEALQPPAPGQ
HTTQI

SEQ ID NO: 230_H05721_H

MAVRQALGRGLQLGRALLLRFTGKPGRAYGLGRPGPAAGCVRGERPGWAAGPGAEP RRVG
LGLPNRLRFFRQSVAGLAARLQRQFVVRWAGCAGPCGRAVFLAFGLGLGLIEEKQAESRR

FIGURE 12

AVSACQEIQAIFTQKSKPGPDPLDTRRLQGFRLEEYLIQSIGKGCSAAVYEATMPTLPQ
 NLEVTKSTGLLPGRGPGTSAPGEGQERAPGAPAFPLAIKMMWNI SAGSSSEAILNTMSQE
 LVPASRVALAGEYGAVTYRKS KRGPQLAPHPNI IRVLRAFTSSVPLLP GALVDYPDVLP
 SRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNTSPRLAAMMLLQ LLEGVDHLVQQGIAH
 RDLKSDNILVELDPDGPWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVST
 ARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFGYQGKAHLESRSYQEAQLPALPESVPP
 DVRQLVRALLQREASKRPSARVAANVLHLSLWGEHILALKNLKLDKMVGWLLQOSAATLL
 ANRLTEKCCVETKMMLFLANLECETLCQAALLLCSWRAAL

SEQ ID NO: 231_AI086865_H

MEKYERIRVVGRAFGIVHLCRLKADQKLVIIKQIPVEQMTKEERQAAQNECQVLKLLNH
 PNVEIYYENFLEDKALMIAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALHHVH
 THLILHRDLKTONILLDKHRMVVKIGDFGISKILSSKSTPCYISPCEGKPYNQKSDIW
 ALGCVLYELASLKRAFEAANLPALVLKIMSGTFAPISDRYSPELRQLVLSLLSLEPAQRP
 PLSHIMAQPLCIRALLNLHTDGREVRGPQQHREQDHQCPLQGI IMTFGSGSNGCLGHGS
 LTDISQPTIVEALLGYEMVQQVEEALSFTLLGSAPLDQEPLLSIDLGTASAAVTGEEDL
 GSGDVNRLPSWERGHLLAGVASSTDVSTFSEGDCKEPDKCCWRHKQCTGHI IYPFASDCV
 RHSLHLHSVNHCNCSNRLKDSSSEDSSSRGAGPTCSHVIESPCFELTPEEEHVERFRYGW
 CKSYRPVSVAVIHPLYHECGADDLNKXKRKRKRKRKRKPP IPTQVGPATASPD LGTSMAT
 GTPDSTAPITIWRSSEPTGKGQGSKVIKKVKKKKEKEKDKEEMDEKAKLKKKAKKGQLTK
 KKSPVKLEPSPDPVSRSL SARQLARMSSESPESREELESEDSYNGRGQGELSSSEDI VESS
 SPRKRENTVQAKKTGAKPSQARKVNKRKSPPGSPNPNS

SEQ ID NO: 232_AA836348_H

MSVLGEYERHCDSINSDFGSESGCGDSSPGPSASQGPRAAGGAAEQEELHYIPIRVLGR
 GAFGEATLYRRTEDDSL VVWKEVDLTRLSEKERRDALNEIVILALLQHDNI IAYYNHMD
 NTTLLIELEYCNGGNLYDKILRQKDKLFEEEMVVWYLFQIVSAVSCIHKAGILHRDIKTL
 NIFLTKANLIKLG DYGLAKKLNSEYSMAETLVGTPYYMSPELCQGVKYNFKSDIWAVGCV
 IFELLTLKRTFDATNPLNLCVKIVQGIRAMEVDSSQYSLELIQMVHSCLDQDPEQRPTAD
 ELLDRPLLKRKRSSSTVTEAPIAVVTSRTSEVYVWGGGKSTPQKLDVIKSGCSARQVCAG
 NTHFAVVTVKELYTWNMQGGTKLHGQLGHGDKASYRQPKHVEKLQGKAIRQVSCGDDF
 TVCVTDEGQLYAFGSDYYGCMGVDKVAGPEVLEPMQLNFFLSNPVEQVSCGDNHVVVLT
 NKEVYSWGCGEYGRGLDSEEDYYTPQKVDVPKALI I VAVQCGCDGTFLLTQSGKVLACG
 LNEFNKLGLNQCMGSI INHEAYHEVPYTTSTFLAKQLSFYKIRTIAPGKTHTA AIDERGR
 LLTFGCNKGQLGVGNKYKRLGINLLGGPLGGKQVIRVSCGDEFTIAATDEKVLNSKTIR
 SNSSGLSIGTVFQSSSPGGGGGGGGGEEEDSQQESETPDPSGGFRGTMEADRGMEGLISP
 TEAMGNSNGASSCPGWLKELNAEFI PMPDPSPLSAAFSESEKDTLPYEELQGLKVA
 SEAPLEHKPQVEASVTELFAPESQLVTSAESCSNLCWEGNTTDS SCVCVQLSAGGG

SEQ ID NO: 233_R86668_H, MKK6_H

MNLLLSYRDVQDYSAI IELVETLQALPTCDVAEQHNVC FHYTFALNRRNRPGDRAKALSV
 LLPLVQLEGSVAPDLYCMCGRIYKDMFFSSGFQDAGHREQAYHWYRKAFDVEPSLHSGIN
 AAVLLIAAGQHFEDSKELRLIGMKLGCLLARKGCVEKMQYYWDVGFYLGAI LANDPTQV
 VLAAEQLYKLNAPIWYLVSMETFLLYQHFRPTPEPPGGPPRAHFWLHFLQSCQPFKT
 ACAQGDQCLVLVLEMNKVL LPAKLEVRGTDVPSTVTL SLEPETQDIPSSWTFPVASICG
 VSASKRDERCCFLYALPPAQDVQLCFPSVGHCQWFCGLIQAVVTNPDSTAPAEAEAGAGE
 MLEFDYEYETETGERLVLGKGTYG VYAGRDRHTRVRIA I KEI PERDSRFSQPLHEEIALH
 RRLRHKNIVRYLGSASQGGYLKIFMEEVPGGSLSSLLRSVWGPKDNESTISFYTRQILQ
 GLGYLHDNHI VHRDIKGDNLINTFSGLLKI SDFGTSKRLAGITPCTETFTGTLOQYMAPE
 IIDQGRGYGKAADIWSLGCTVIEMATGRPPFHELGSPPQAAMFQVGMKVHPPMPSSLSA

FIGURE 1AA

EAQAFLLRTFEPDPRLRASAQTLLGDPFLQPGKRSRSPSSPRHAPRPSDAPSASPTPSAN
STTQSQTFPCPQAPSQHPSPPKRCLSYGGTSQRLRVPEEPAAEEPASPEESSGLSLLHQE
SKRRAMLAHVLEQELPALAENLHQEQKQEQGARLGRNHVEELLRCLGAHIHTPNRRQLAQ
ELRALQGRLRAOGLGPALLHRPLFAFPDAVKQILRKRQIRPHWMFVLDSSLRAVRAALG
VLGPEVEKEAVSPRSEELSNEGDSQQSPGQQSPLPVEPEQGPAPLMVQLSLLRAETDRLR
EILAGKEREYQALVQORALQRLNEEARTYVLAPEPPTALSTDQGLVQWLQELNVDSGTIQM
LLNHSFTLHTLLTYATRDDLITRIRGGMVCRIWRAILAQRAGSTPVTSGP

SEQ ID NO: 234_PAK6_H

MFGKKKKKIEISGPSNFEHRVHTGFDPOEQKFTGLPQQWHSLLADTANRPKPMVDPSCIT
PIQLAPMKTIVRGNKPKETSINGLLEDFDNISVTRSNLSLRKESPTPDQGASSHGPCHA
EENGFITFSQYSSSDTTADYTTKEYREKSLYGGDLDPYYRGSHAQKQNGHVMKMKHGEA
YYSEVKPLKSDFAFSAFYHSHLDSLSPSEYSDLKWEYQRASSSSPLDYSFQFTPSRTA
GTSGCSKESLAYSESEWGPSLDDYDRRPKSSYLNTSPQPTMRQSRSGSGLQEPMPFPG
ASAFKTHPQGHSYNSYTPRLSEPTMCIPKVDYDRAQMVLSPLSGSDTYPRGPAKLQPS
QSKSGYSSSSHQYPSGYHKATLYHHPSLQSSSQYISTASYLSSLSLSSSTYPSPWSSSS
DQQPSRVSEHQFRAALQLVVSPGDPREYLANFIKIGEGSTGIVCIATEKHTGKQVAVKKM
DLRKQQRRELLFNEVVIMRDYHHDNVVDMYSSYLVGDELWVMEFLEGGALTDIVTHTRM
NEEQIATVCLSVLRALSYLHNQGVHRDIKSDSILLTSDGRIKLSDFGFCQVSKVPRK
KSLVGTPTYWMAPEVISRLPYGTEVDIWSLGIMVIEMIDGEPPYFNEPPLQAMRIRDSLP
PRVKDLHKVSSVLRGFLDLMLVREPSQRATAQELLGHPFLKLAGPPSCIVPLMRQYRHH

SEQ ID NO: 235_SURTK106_H

MNDRNEIQMEAKLQSLTIIAQEILCRFFITLRRHARFLLTKLGRQGMARSGITHSCAVCI
LCGPSREGDSPVAMGMTRMLLECSLSDKLCVIEKQYEVIIVPTLLVTIFLILLGVILWL
FIREQRTQQQRSGPQGIAPVPPPRDLSWEAGHGGNVALPLKETSVENFLGATTPALAKLQ
VPREQLSEVLEQICSGSCGPIFRANMNTGDPSKPKSVILKALKEPAGLHEVQDFLGRIQF
HQYLKGKHKNLVQLEGCCTEKLPLYMVLEDVAQGDLLGFLWTCRRDVMTMDGLLYDLTEKQ
VYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT
IPLKWLAPERLLLRPASIRADVWSFGILLYEMVTLGAPPYEVPPPTSILEHLQRRKIMKR
PSSCTHTMYSIMKSCWRWREADRPSRELRLRLEAAIKTADDEAVLQVPELVVPELYAAV
AGIRVESLFYNYSML

SEQ ID NO: 236_AA098024_M

LQEKHLFHGDVAARNILIQSDLTPKLCHLGLAYEVHAHGAISSARSSTIPLKWLAPERLL
LRPASIRGDIWSFGILLYEMVTLGAPPYEVPPPTSILQYLQKKIMKRPSSCSHAMYNIM
KCCWRWSEDSRPLLQVLLQRLLEAASRSADDKAVLQVPELVVPELYADVAGIRAESISYSF
SVL

SEQ ID NO: 237_SGK2ALPHA_H

MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNYGKVLLAKRKSDGAF
YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE
LFFHLQRRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDVGL
CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDQVS
QMYENILHQPLQIPGGRTVAACDLLQSLLLHKDQQRQLGSKADFLEIKNHVFFSPINWDDL
YHKRLTPFPNPNTGPADLKHFDPFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE
DDDILDC

FIGURE 1BB

SEQ ID NO: 238_CCRK_H

MDQYCILGRIGEGAHVFKAKHVETGEI IALKKVALRRLEDGFPNQALREIKALQEMED
NQYVVQLKAVFPHGGGFVLAFAEFMLSDLAEVVRHAQRPLAQAQVKSQMLLKGVAFCHA
NNIVHRDLKPANLLISASGQLKIADFGGLARVFS PDGSRLYTHQVATRSVGCIMGELLNGS
PLFPGKNDIEQLCYVLRILGTPNPQVWPELTEL PDYNKISFKEQVPMPLEEVLPDVSPQA
LDLLGQFLLYPPHQRIAASKALLHQYFF TAPLPAHPSELPI PQLGGPAPKAHPGPPHIH
DFHVDRLPLEGVAVEPRADSALHPGGVRSWPWSRLPAPQDHSVHLFLCHLPGF TLQGLPMA
TVGPHHTLPLSPCEGWSRGRGHVPSQEYENIQSSRGDSWPVLGEPYLLCATDVPIRTVSS
AASQGLHMQNDDACLGAASPECCLLVKEKCRE

SEQ ID NO: 239_TESK2_H

MDRSKRNSIAGFPFPRVERLEEFEGGGGGEGNVSQVGRVWPSSYRALISAFSRLTRLDDFT
CEKIGSGFFSEVFKVRHRASGQVMALKMNTLSSNRANMLKEVQLMNRLSHPNILRYINSG
NLEQLLDSNLHLPWTVRVKLAYDIAVGLSYLHFKGI FHRDLTSKNCLIKRDENGYS AVVA
DFGLAEKIPDVSMGSEKLAVVGSPFWMAPEVLRDEPYNEKADVFSYGIILCEIIARIQAD
PDYLPRTENFGLDYDAFQHMVGDCPPDFLQLT FNCCNMDPKLRPSFVEIGKTLEEILSRL
QEEEQERDRKLQPTARGLLEKAPGVKRLSSLDDKIPHKSPCPRRTIWLRSQS DIFSRKP
PRTVSVLDPYRPRDGAARTPKVNPFSARQDL MGKIKFFDLPSKSVISLVFDLDAPGPG
TMPLADWQEPLAPPIRRWRS LPGSPEFLHQEACPFVGREESLSDGPPRLSSLKYRVKEI
PPFRASALPAAQAHEAMDCSILQEENGFGSRPQGTSPCPAGASEEMEVEER PAGSTPATF
STSGIGLQTQKQDG

FIGURE 2A

SEQ ID NO: 1_X69117_H BARK2_H

ATGGCGGACCTGGAGGCCGTGCTGGCCGATGTCAGTTACCTGATGGCCATGGAGAAGAGC
AAGCGACCCCGGCCCGCCGCGCCAGCAAGAGGATCGTCCTGCCGGAGCCAGTATCCGG
AGTGTGATGCAGAAGTACCTTGCGAGAGAGAAATGAAATAACCTTTGACAAGATTTTCAAT
CAGAAAATTGGTTTCTTGCTATTTAAAGATTTTGTGTTGAATGAAATTAATGAAGCTGTA
CCTCAGGTGAAGTTTATGAAGAGATAAAGGAATATGAAAACTTGATAATGAGGAAGAC
CGCTTTTGCGAGAAGTCGACAAATTTATGATGCCTACATCATGAAGGAACCTCTTTCCTGT
TCACATCCTTTCTCAAAGCAAGCTGTAGAACACGTACAAAGTCATTTATCCAAGAAACAA
GTGACATCAACTCTTTTTCAGCCATACATAGAAGAAATTTGTGAAAGCCTTCGAGGTGAC
ATTTTTCAAAAATTTATGGAAGTGACAAGTTCCTAGATTTTGTGAGTGGAAAAACGTT
GAATTAATATCCATTTGACCATGAATGAGTTCAGTGTGCATAGGATTATTGGACGAGGA
GGATTCGGGGAAGTTTATGGTTGCAGGAAAGCAGACACTGGAAAAATGTATGCAATGAAA
TGCTTAGATAAGAAGAGGATCAAAATGAAACAAGGAGAAACATTAGCTTTAAATGAAAGA
ATCATGTTGTCTCTTGTCAGCACAGGAGACTGTCCTTTTCAATTGTATGTATGACCTATGCC
TTCCATACCCCGAGATAAACTCTGCTTCATCCTGGATCTGATGAACGGGGGCGATTTGCAC
TACCACCTTTCACAACACGGTGTGTTCTCTGAGAAGGAGATGCGGTTTTATGCCACTGAA
ATCATTTCTGGGTCTGGAACACGTGCACAATCGGTTTTGTTGTCTACAGAGATTGAAGCCA
GCAAATATTCTCTTGGATGAACATGGACACGCAAGAATATCAGATCTTGGTCTTGCCTGC
GATTTTTCAAAAAGAGCCTCATGCGAGTGTGGCACCCATGGGTACATGGCTCCCGAG
GTGCTGCAGAAGGGGACGGCCTATGACAGCAGTGGCGACTGGTTCTCCCTGGGCTGCATG
CTTTTCAAACCTTCTGAGAGGTACAGCCCTTTCAGACAACATAAAACCAAAGACAAGCAT
GAAATTGACCGAATGACACTCACCGTGAATGTGGAACCTTCAGACACCTTCTCTCCTGAA
CTGAAGTCCCTTTTGGAGGGCTTGCTTCAGCGAGACGTTAGCAAGCGGCTGGGCTGTCAC
GGAGGCGGCTCACAGGAAGTAAAGAGCACAGCTTTTTCAAAGGTGTTGACTGGCAGCAT
GTCTACTTACAAAAGTACCCACCACCCTTGATTCCTCCCCGGGGAGAAGTCAATGCTGCT
GATGCCCTTGATATTGGCTCATTTGATGAAGAGGATACCAAAGGGATTAAGCTACTTGAT
TGCGACCAAGAACTCTACAAGAACTTCCCTTTGGTCATCTCTGAACGCTGGCAGCAAGAA
GTAACGGAAACAGTTTATGAAGCAGTAAATGCAGACACAGATAAAATCGAGGCCAGGAAG
AGAGCTAAAAATAAGCAACTTGGCCACGAAGAAGATTACGCTCTGGGGAAGGACTGTATT
ATGCACGGGTACATGCTGAACTGGGAAACCCATTTCTGACTCAGTGGCAGCGTCGCTAT
TTTTACCTCTTTCAAATAGACTTGAATGGAGAGGAGAGGGAGAGTCCCGGCAAAATTTA
CTGACAATGGAACAGATTCTCTCTGTGGAAGAACTCAAATTAAGACAAAAATGCATT
TTGTTTCAATAAAAGGAGGGAAACAATTTGTCTTGCAATGTGAGAGTGATCCAGAGTTT
GTGCAAGTGAAGAAAGAGTTGAACGAAACCTTCAAGGAGGCCAGCGGCTATTGCGTCGT
GCCCCGAAGTTCTCAACAAACCTCGGTCAAGTACTGTGGAGCTCCCAAAGCCATCCCTC
TGTCACAGGAACAGCAACGGCCTCTGA

SEQ ID NO: 2_AA144574_M BARK2_M

CTGCTTCGTAGTCTACAGAGACCTGAAGCCTGCGAACATCCTCCTAGATGAATATGGGCA
CGTGAGGATATCGGATCTCGGCCTTGCTGTGATTTCTCCAAAAAGAGCCTCATGCCAG
CGTGGGCACCCATGGGTACATGGCTCCCGAGGTGTTGCAGAAGGGAACGTGCTATGACAG
CAGCGCCGACTGGTTCTCCCTGGGCTGTATGCTCTTCAAACCTTCTGCGGGGCCACAGCCC
CTTCAGGCAGCATAAAACCAAAGACAAGCATGAGATAGACCGAATGACCCTGACCGTGAA
CGTGCAGCTTCCAGATGCCCTTCTCCCCTGAGCTGAGGTCCCTCTTAGAGGGTTTGCTCCA
GCGGGACGTGAGCCAGCGGCTGGGCTGCGGAGGAGGAGGGGCACGAGAGTTGAAGGAGCA
CATCTTCTTCAAGGGCATTGACTGGCAGCATGTGTACTTACGGAAGTACCCGCCACCCCT
AATCCCTCCTCGGGGAGAGGTCAACGCTGCAGATGCCCTTCGATATCGGCTCCTTCGATGA
GGAAGACACCAAAGGCATTAAGCTGTTGGACTGTGACCAGGACCTCTATAAGAACTTCCC
ACTGGTGATCTCCGAGCGCTGGCAGCAAGAAGTGGTGGAGACCATCTATGACCGCGTCAA
TGCTGATACTGATAAAATCGAGGCCAGGAAGAAGGCTAAAAATAAGCAACTTGGTCAAGA

FIGURE 2B

GGAAGATTACGCTATGGGGAAGGACTGCATCATGCACGGGTACATGCTGAAGCTGGGGAA
CCCCTTTCTCACACAGTGGCAAAGACGCTATTTTTACCTGTTCCCCAACAGACTGGAGTG
GAGAGGAGAGGGCGAGTCTCGGCAAAGTCTACTGACCATGGAACAGATCATGTCTGTGGA
GGAGACCCAGATTAAAGACAGAAAAGTGCATCTTACTCAGGATAAAGGGAGGGGAAGCAATT
TGTCTTGCAATGTGAGAGTGACCCCGAGTTTGACACAGTGGCTGAAGGAGCTGACCTGCAC
CTTCAATGAGGCCAGAGACTGCTGCGCCGTGCCCCAAATTCCTCAACAAACCACGGGC
CGCCATCCTGGAGTTCTCCAAGCCACCCTGTGTACAGAAATAGCAGCGGCCTCTGAAC
CACAGAGCAGCGGGGCCTGAAGGAGGGGCCCCAGCTCTTCAGCCCAGGAGTGGAACGAAG
CCACGGGGAAACCGTGTGGGGCTAAGACACAGTGTCTCTGAGCACTGACGGGGCTGCTCCA
AGCCGAGGAGGCTCAGGACACCAGGGCGGCCTTCTGGGAGCTGGGACATCCTCGGGGCTG
TCCTATCCACACTCGAAATTACTGAAGAAGCAGAGGCATTCTGCTGTG

SEQ ID NO: 3_AA826850_H

GAAGAGGATGGGCTCGTCCATGTGCGCGGCCACCGCGCGGAGGCCGGTGTGTTGACGACAA
GGAGGACGTGAACCTTCGACCACTTCAGATCCTTCGGGCCATTGGGAAGGGCAGCTTTGG
CAAGGTGTGCATTGTGCAGAAGCGGGACACGGAGAAGATGTACGCCATGAAGTACATGAA
CAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCGGGAGCTGGAGATCCT
GCAGGAGATCGAGCACGTCTTCCTGGTGAACCTCTGGTACTCCTTCAGGACGAGGAGGA
CATGTTTCATGGTTCGTGGACCTGCTACTGGGCGGGGACCTGCGCTACCACCTGCAGCAGAA
CGTGCAGTTCTCCGAGGACACGGTGAGGCTGTACATCTGCGAGATGGCACTGGCTCTGGA
CTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAACATTCTCCTGGA
TGAGAGAGGACATGCACACCTGACCGACTTCAACATTGCCACCATCATCAAGGACGGGGA
GCGGGCGACGGCATTAGCAGGCACCAAGCCGTACATGGCTCCGGAGATCTTCCAXTCTTT
TGTC AACGGCGGGACCGGCTACTCCTTCGAGGTGGACTGGTGGTGGTGGGGGTGATGGC
CTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCGTGGAGTC
CCTGGTGCAGCTGTTTCAGCACCGTGAGCGTCCAGTATGTCCCCACGTGGTCCAAGGAGAT
GGTGGCCTTGCTGCGGAAGCTCCTCACTGTGAACCCCGAGCACCGGCTCTCCAGCCTCCA
GGACGTGCAGGCAGCCCCGGCGCTGGCCGGCGTGCTGTGGGACCACCTGAGCGAGAAGAG
GGTGGAGCCGGGCTTCGTGCCAACAAGGCCGTCTGCACTGCGACCCACCTTTGAGCT
GGAGGAGATGATCCTGGAGTCCAGGCCCTGCACAAGAAGAAGAAGCGCCTGGCCAAGAA
CAAGTCCCGGGACAACAGCAGGGACAGCTCCAGTCCGAGAATGACTATCTTCAAGACTG
CCTCGATGCCATCCAGCAAGACTTCGTGATTTTTTAACAGAGAAAAGCTGAAGAGGAGCCA
GGACCTCCCGAGGGAGCCTCTCCCCGCCCTGAGTCCAGGGATGCTGCGGAGCCTGTGGA
GGACGAGGCGGAACGCTCCGCCCTGCCCATGTGCGGCCCCATTGCCCCCTCGGCCGGGAG
CGGCTAGGCCGGGATGCCCCGTGGTCTCACCCCTTGAGCTGCTTTGGAGACTCGGCTGCC
AGAGGGAGGGCCATGGGCCGAGGCCTGGCATTCACGTTCCCACCCAGCCTGGCTGGCGGT
GCCCACAGTGCCCCGGACACATTTACACCTCAGGCTCGTGGTGGTGCAGGGGACAAGAG
GCTGTGGGTGCAGGGGACACCTGTGGAGGGCATTTCCTGTTGGGCCCCGAGACCCGCCTA
GATGGAGGAAGCGCTGCTGGGCGCCCTCTTACCGCTCACGGGGAGCTGGGGCCATGGATG
GGACAGGAGTCTTTGTCCCTGCTCAGCCCGGAGGCTGTGCACGGCCCTCGTCACAAGGTG
ACCCCTGCAGCACAGGCCGCGGGTGCCCCAGGCTCGGCTCAGTTCTTGGAGGTCAAGGGC
ATGGGTGGGGTAGTGGGTGGGGAGGTGAATGTTTTCTAGAGATTCAAAGTCTCCAGCA
ATTTCTGTATAGTTTTACCTCTGAGAATTACAATGTGAGAACCGCTC

SEQ ID NO: 4_AA960957_H

GTCCCACATCCCGCATCCGGCATCCAGCGGCCGGGCATGTAGCAGCGGCAGCAACGGCG
GAATATGGGCGGGAACCACTCCACAAGCCCCCGTGTGTTGACGAGAATGAGGAAGTCAA
CTTTGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCAT
CGTGCAGAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTG
CATCGAGAGGGATGAGGTTCCGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGA

FIGURE 2C

GCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTTCATGGT
GGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTTAC
AGAGGGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAG
GTACCACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACA
TGTTTCACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTC
CATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCAGGTGTACATGGACAGAGG
CCCCGATACTCGTACCCTGTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCT
GCGGGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCATCGATGAAATCCTCAACAT
GTTCAAGGTGGAGCGTGTCCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCT
GAGGAAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCTTCATGACATACAGAG
CGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGCACTGATGCCCGG
CTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCACATTTGAGCTTGAAGAGATGAT
TCTAGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGA
TGGCACAAGGACAGCTGCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCG
GGAGGAATTCATCATATTCAACAGAGAGAAGCTCAGGAGGCAGCAGGGACAGGGCAGCCA
GCTCCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCTCCAGGACGGGTG
CAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCACACTTG
TTGCTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCCCTCTTTGTGC
CCTGATGGTCCCTGTCTCACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGA
GCTGGGAAGCCTGGGTTCTGGTCCCATCTCCATGACTGATTACGTGTGACCTCAGACAA
GTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTTAAACACTTCTGCC
CCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAAACCTT
TGATATTTATAAAATCATTTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCC
ATTCGCCAAAGCAATCAAACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTTAGA
GGGCACCTTCGAAAAACACAGCCCTGACAGCAAAATAAAGGTCTGATATGTTGGCCCCCTT
CTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTTCATGTGCATTCT
CTGGCAGGCCACAGTCTGAGCTTGTAAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCCTCATTTAAGAAGACTATCCTTACCTTTT
AGTTTCAGCAGTCCTCACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCA
TTCAGATGAGAGTTGGGTGCTGAGCATTGGTTACTCCTGCAGAGTGTAATCAGCACCCC
ATCCAAGTGGCCCCGAAAGCCAGACCTGCAGCAGAACTCTCCAAGTCTCTATCAGCTTTC
AGGGTTTTCTCTCCTGGGAAGGGTGTAAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAG
AAAGTTTTATTTTCAAGAGGAAATGGGTTACACAAAAAGCAAACCTACATTCTGATCTGCT
CAGGGAGAAGCTTGCCTTTGAACTGGAAGATGTTGGGATGAGCAGGGAAAGCTTAGACTT
TGGAGTCAGGTTTGTGTTTCAAGATCCAGCCCTGCTGGCTACTAAGTAACTGGGAGACCTT
AGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCTCATTTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTG
GATGACTCATAGAATGGCCTTTTTTGTGAGCATAATCGTCATCATTATTTAGATACTTTC
TTCCTTCACTCACCCAGCAGGTGAGTTTCTGTGCAAAACAAACCTGTTTAGGATTCTTCC
AAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGCTGAAGTTCGACTGTG
TTTTTATTTTTTTCATCCAAGTTCATTTTCACTTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTCTCTTAGATTTCTTAAAGACATTTTAAATGTATGGTTAGGTTTTAT
ATTTTTATTTTTTAAAAAGAAATAGTCAGTGTTTTCTCCTTTCAACCGAGACTATTTTC
TGGATTGTGTGCTCCTCGTCAGTTGACTTGTGTTTGCACACTTTTCTTACTTCATGTCCC
CATCAACAACCGTCTGCTCCCCACCTCCCCCAGGAAATAAGGGGCCTGCTCCTCTCCCT
ACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCACGA
ATTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCCTGGTTCTGTTCAAGT
TGGCATTTCTTGTGTTGGAATAAACTATTTCTTGGACATTCTTTC

FIGURE 2D

SEQ ID NO: 5_TBK1_H

TCCTGAGTCTCGAGGAGGCCGCGGGAGCCCCGCGGCGGTGGCGCGCGGAGACCCGGCTG
GTATAACAAGAGGATTGCCTGATCCAGCCAAGATGCAGAGCACTTCTAATCATCTGTGGC
TTTTATCTGATATTTTAGGCCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGA
AAACTGGTGATTTATTTGCTATCAAAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGG
ATGTTCAAATGAGAGAATTTGAAGTGTTGAAAAAACTCAATCACAAAAATATTGTCAAAT
TATTTGCTATTGAAGAGGAGACAACAACAAGACATAAAGTACTTATTATGGAATTTTGTC
CATGTGGGAGTTTATACACTGTTTTAGAAGAACCCTTCTAATGCCTATGGACTACCAGAAT
CTGAATTCTTAATTGTTTTGCGAGATGTGGTGGGTGGAATGAATCATCTACGAGAGAATG
GTATAGTGCACCGTGATATCAAGCCAGGAAATATCATGCGTGTTATAGGGGAAGATGGAC
AGTCTGTGTACAACTCACAGATTTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGT
TTGTTTTCTCTGTATGGCACAGAAGAATATTTGCACCCTGATATGTATGAGAGAGCAGTGC
TAAGAAAAGATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAA
CATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGA
ATAAAGAAGTGATGTATAAAATAATTACAGGAAAGCCTTCTGGTGCAATATCTGGAGTAC
AGAAAGCAGAAAATGGACCAATTGACTGGAGTGGAGACATGCCTGTTTTCTTGCACTCTTT
CTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCTTGCAAACATCCTTGAAGCAGATCAGG
AAAAGTGTTGGGGTTTTGACCAGTTTTTTGCAGAACTAGTGATATACTTCACCGAATGG
TAATTCATGTTTTTTTCGCTACAACAAATGACAGCTCATAAGATTTATATTCATAGCTATA
ATACTGCTACTATATTTTATGAAGTGGTATATAAAACAAACCAAAATTTATTTCTTCAAATC
AAGAAGTTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACATT
TCCCTAAAAGTACTGAGGAAAACCTATATTTGTAGTAAGCCGGGAACCTCTGAATACCA
TAGGATTAATATATGAAAAAATTTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG
GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTGTGTTATGCCTGCAGAATTGCCA
GTACCTTACTGCTTTATCAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGAATTAA
TTAAAGATGATTACAATGAAAGTGTTCACAAAAAGACAGAAGTTGTGATCACATTGGATT
TCTGTATCAGAAACATTGAAAAAACTGTGAAAGTATATGAAAAGTTGATGAAGATCAACC
TGGAAGCGGCAGAGTTAGGTGAAATTTTACAGACATACACACCAAAATTGTTGAGACTTTCCA
GTTCTCAGGGAACAATAGAAACAGTCTTCAGGATATCGACAGCAGATTATCTCCAGGTG
GATCACTGGCAGACGCATGGGCACATCAAGAAGGCACTCATCCGAAAGACAGAAATGTAG
AAAAACTACAAGTCTGTAAATTCATGACAGAGATTTACTATCAGTTCAAAAAAGACA
AAGCAGAACGTAGATTAGCTTATAATGAAGAACAAATCCACAAATTTGATAAGCAAAAAAC
TGTATTACCATGCCACAAAAGCTATGACGCACTTTACAGATGAATGTGTTAAAAAGTATG
AGGCATTTTTTGAATAAGTCAGAAGAATGGATAAGAAAGATGCTTCATCTTAGGAAACAGT
TATTATCGCTGACTAATCAGTGTTTTGATATTGAAGAAGAAGTATCAAAATATCAAGAAT
ATACTAATGAGTTACAAGAACTCTGCCTCAGAAAATGTTTACAGCTTCCAGTGGAATCA
AACATAACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACTCTTGGA
TGAAGAAATTAAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGCTGAAAATAACCACA
TTTTAGAAAGGTTTGGCTCTTTAACCATGGATGGTGGCCTTCGCAACGTTGACTGTCTTT
AGCTTTCTAATAGAAGTTTAAGAAAAGTTTCCGTTTGCACAAGAAAATAACGCTTGGGCA
TTAAATGAATGCCTTTATAGATAGTCACCTGTTTCTACAATCCAGTATTTGATGTGGTCTG
TGTAATATGTACAATATTGTAAATACATAAAAAATATACAAATTTTTGGCTGCTGTGAA
GATGTAATTTTATCTTTTAAACATTTATAATTATATGAGGAAATTTGACCTCAGTGATCAC
GAGAAGAAAGCCATGACCGACCAATATGTTGACATACTGATCCTCTACTCTGAGTGGGGC
TAAATAAGTTATTTTCTCTGACCGCCTACTGGAAATATTTTTAAGTGAACCAAAATAGG
CATCCTTACAAATCAGGAAGACTGACTTGACACGTTTGTAATGGTAGAACGGTGGCTAC
TGTGAGTGGGGAGCAGAACCGCACCACTGTTATACTGGGATAACAATTTTTTTGAGAAGG
ATAAAGTGGCATTATTTTATTTTACAAGGTGCCCAGATCCCAGTTATCCTTGTATCCATG
TAATTTTCAGATGAATTATTAAGCAAACATTTTAAAGTGAATTCATTATTAAGAACTATTC
ATTTTTTTCTTTGGCCATAAATGTGTAATTGTCAATTAATTTCTAAGGTCATTTCAACT

FIGURE 2E

GTTTTAAGCTGTATATTTCTTTAATTCTGCTTACTATTTTCATGGAAAAAATAAATTTCT
CAATTTTAAAAAA

SEQ ID NO: 6_AA305176_H

TGGCTGCTCGCGGAGGGGCGAGTGTACGCGGGGCCGCTGTAGGCTGTCCAGCGATGGATCC
CACC CGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGAGGGCGTGAATAG
GATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATT CAGCATAGTGAAGCCCATTAGCCG
GGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTGTATGCAGTAAAGGT
TGTTAAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCAAGCTGAGAGAGA
TGCACTGGCACTAAGCAAAAGCCCATTTCATTGTCCATTTGTATTATTCACTGCAGTCTGC
AAACAATGTCTACTTGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCTCTCCTACA
TATATATGGTTATTTTGATGAAGAGATGGCTGTGAAATATATTTCTGAAGTAGCACTGGC
TCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGACAATATGCT
TATTTCTAATGAGGGTCATATTAACTGACGGATTTTGGCCTTTCAAAGTTACTTTGAA
TAGAGATATTAATATGATGGATATCCTTACAACACCATCAATGGCAAAACCTAGACAAGA
TTATTCAGAACCCCAAGGACAAGTGTTATCGCTTATCAGCTCGTTGGGATTTAACACACC
AATTGCAGAAAAAATCAAGACCCTGCAACATCCTTT CAGCCTGTCTGTCTGAAACATC
ACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGACACTACGCCTTA
TTCTAGCAAATTACTAAAATCATGTCTTGAAACAGTTGCCTCCAACCCAGGAATGCCTGT
GAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCCAGTGCCAG
TAGTCAATCCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAGCAGTCCCAAATG
GGAAAAAGATTGCCAGGTTTGAGGGACATTTATCTTAATGAAAATCAATTATGTATGTCA
AATGAATGTGAGAAATATTATACCTTTTCATATAAATTCCATAAAGAAATGAAATTGTTA
CATGAATGGCAGTCATAGTATTAATCAGAAATTCATTTTCTGCACATTCTGTCAAATTC
TTTTGAAATATTTCAATTTCTCATTCAATTGTGACATTGTTCTTACTTGATTATATAATGA
GATTCTTGCAAGTAAATTGATAATAAATGCTTGGCTTCTGTGTATCTAGGTGGACCTCACT
TGTTTTTAGAAGTCCTTCCCATGATACAGACATTGGCTTGTTGGTTTTGTTTTATTTTGT
TTTTAACATATGTCATTTAAAAACTCATATTACCTCCTTTT

SEQ ID NO: 7_AA116841_M

CCACGCGTCCGATCCCATGGCCAGAAGGCGAAGAAAAGCTATCTGATAATGCTCAAAGTG
CAATGGACATGCTTTTAAACCATTTGATGATTCAAAGAGAGCTGGAATGAGAGAACTAAAAC
AGCATCCTCTCTTCAGTGAAGTGGACTGGGAAAATCTGCAGCATCAGACTATGCCTTTTCG
TACCCCAACCAGACGACGAAACAGATACATCCTATTTTGAAGCCAGAAATAATGCTCAAC
ATCTGACCGTATCTGGGTTTAGTCTGTAGCACATGCGTGTCAATTTTATCTAACTTGTGA
TATAGAATTAAGTTTTACAGTAATATGCTACTTAATACTAGATTGGTCTAAATGGGATAA
AAGTCATTATTTTACCCAGACTGAACAGCTTTTAAATTACTAAGTACAACAGTTTTTACAG
AATTAATAATACTATAAGCAATATAATCAGTAATTAATCTTTACCTTAGAAGTGTATATAA
GCCATAATAGCTTTTTTTCATCTTATTTATTCACTGCACTTTATGAAGAGCAAAGTATCAA
TAAACTAAAACACTACCACTCTAAATAGAGGGAGTGAGCCGT

SEQ ID NO: 8_AA256100_H

AGGGAGCTGACGGGCGCCCGGCTGCGGTCCGTGCGGAGGCTGAGCCGGCCGCGGGC
GCGACCGGAGGCAGTTTCCGTTACTATGGCAATGACGGCAGGGACTACAACAACCTTTCC
TATGAGCAACCATACCCGGGAAAGAGTGAAGTGTAGCCAAGCTCACATTGGAGAATTTTA
TAGCAACCTAATTTTACAGCATGAAGAGAGAGAAAACAGGCAGAAGAAATTAGAAGTGGC
CATGGAAGAAGAAGGATTAGCAGATGAAGAGAAAAAGTTACGTCGATCACAACACGCTCG
CAAAGAAACAGAGTTCTTACGGCTCAAAGGACCAGACTTGGCTTGGATGACTTTGAGTC
TCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTGCGGTTGGTCCAGAAGAAAGATAC
AGGCCATATCTATGCAATGAAGATATTGAGAAAGTCTGATATGCTTGAAAAAGAGCAGGT

FIGURE 2F

GGCCCATATCCGAGCAGAAAGAGATATTTTGGTAGAAGCAGATGGTGCCTGGGTGGTGAA
GATGTTTTACAGTTTTTCAGGATAAGAGGAATCTTTATCTAATCATGGAATTTCTCCCTGG
AGGTGACATGATGACATTGCTAATGAAGAAAGACACCTTGACAGAAGAGGAAACACAGTT
CTACATTTTCAGAGACTGTTCTGGCAATAGATGCGATCCACCAGTTGGGTTTCATCCATCG
GGATATTAAGCCAGACAACCTTTTATTGGATGCCAAGGGTCATGTAAAATTATCTGATTT
TGGTTTTATGTACGGGATTAAAGAAAGCTCACAGGACTGAATTTTATAGAAATCTCACACA
CAACCCACCAAGTGACTTCTCATTTTCAGAACATGAACTCAAAGAGGAAAGCAGAACTTG
GAAGAAGAACAGGAGACAACCTGGCATATTCCACAGTTGGGACACCAGATTACATTGCTCC
AGAAGTATTCATGCAGACTGGTTACAACAAATTTGTGTGACTGGTGGTCTTTGGGAGTGAT
TATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATA
CAGAAAAGTGATGAACTGGAAAGAACTCTGGTATTTCTCCAGAGGTACCTATATCTGA
GAAAGCCAAGGACTTAATTTCTCAGATTTTGTATTGATTCTGAAAACAGAATTGGAAATAG
TGGAGTAGAAGAAATAAAAGGTCATCCCTTTTTTGAAGGTGTCGACTGGGAGCACATAAG
GGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAGCATTGATGATACTTCAAATTTTGA
TGACTTCCCTGAATCTGATATTTTACAACCAAGTGCCAAATACCACAGAACCGGACTACAA
ATCCAAAGACTGGGTTTTTCTCAATTATACCTATAAAAGGTTTGAAGGGTTGACTCAACG
TGGCTCTATCCCCACCTACATGAAAGCTGGGAAGTTATGAATGAAGATAACATTCACCCA
TAACCAAGAGAACTCAGGTAGCTGCATCACCAGGCTTGCTTGGCGTAGATAACAATACAC
TGAAATACTCCTGAAGATGGTGGTGCTTATTGACTACAAGAGGAAATTCTACAGGATTAG
GATTTCTAAGACTACTATAGGAATTGGTTGGCAGTGCCAGCTGGCTCTTTTTTTTAATAT
TTTATTATTTTTTGTAACTTTATTATATGAAGGTACTGGAATAAAAGGAACAGACATCCC
TTTCTAACTGCACTGCCTACATGCGTATTAAGGTCCATTCTGCCTGTGTGTGCTGTGGCT
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CTAACCTGTAGGTAACACTGCAGTATTGATGTTTTACTGCAAATCTTATGGGTCTAGATA
ATCAGTAAAAGCCATCTTCCATAGTTGGTGTTAGAACATTGCCCTATTGGTTTGGACATC
TGTAGAATATATATGAAGACAATTTCTGTAATGGTTTTAAGAGATTTAAAAAGAAATTCA
CTGGTTCTTTACAAAATAGAATTTATCATCAAGTTATTACACAAACTTCACAGTAAGGAG
TGACAAGTTTATAATAAGGAAGACAAAGTTTAAACACCTTCACTCAAGCACTCCACTAATA
TATTTACGTTGCATTTCAGAAATACTGATGACCTTCATATACGTAGTCTGTATACTCATAG
GGAGATGTACTGTATTATATAACATGTAAAGTTGATTTTTCTTGTGACAAGAGAACTTCTT
TTTTTAAACAAGAGGACATGGCATTATTTTAAATTTGATTATGGTGAGTTGAATTTAAGACA
TGACCATGAAGGCTGCTTGTAGAATTAGTGATTTTTTATTAAACTATTTTTTTTAAATGTC
AAACTTCTATCATGTAAATGGACTTATAGAGAACAAAAAGCTATTTACTTTGGTTTTCTA
GAAAGTTGTTACATATCATGGCTGGTTAACTTTTATTTCTTTTGATGAAAATTTTTCTTT
TGATAGTACTTGTATTATTGTGCCATTATTTTCTTATGCTCCAAATGTACCAAAGATCTT
GAACAGAGTGGATGTTTCACACTGAGTAGAATTTTCTTTTCTGTGGGCATGCTGTATTTC
AGACCTGACAGATCTTTGATAGAGGTCAGCTTATTAAAGGGCAATATTGTTCTTGTTTAG
CTACATCACTGTGGTGAATATAGATGGAATTAAGGAAGTAAATGCAGGCCAGGGGGTTGT
GATGAGAGGATAGGGGAGATAATATCAGCATCAAATTTCTTTGGGTATCTCTCTAAGAATT
AAATAATCTTTTCTAGCTTAATATTTTAAATTTCTAATTCAAACAACCTCTGAGGTTTTGGTT
TCATTAGTAATAGTTGAGGAATAATATACTAGCAAAGAATGGCCTAATGTTTGTCTAATC
TGTTAATGGATGAAATTTTTTAAAGATACAACCATGATAACCATTATAAATGATCTATGA
TCAAATCTAAAGTGATGAATTATTTGTAGGAATGTCTTCCTAATGGGGAAGAATTGCAT
AGGAGCATTATGCAAATCTACACAAGCTTTTATAAATGTTGCTGCTGGGTAGCTCCACAG
TGTTTCATAAGGCCATCCTGTTTCCCCCACTCCCCCATTTTTGGTTTGTCTTTTAA
ATATTTGTTGAGTACTTACGTGTTTATCTAACAGTTCATTCCATTTTCTAGTCTGGAT
TTTTTGAGTATTTAGGAAAGAGAGCTATTAAAACTCTGGGGATTTCTCAATGTGACTAA
CTCTAATTTTTCTAATTATAACTGCCTTTAATTAACATAATATTAATTTTGCTGAGGTT
TATGAGATTTTCTACCCACATCGCTCCCTTTTTTTTAAAGGACTGTTTTGCTAGTG
TGATAATGAATAGGTAAGATATGAGATAATTGCAACATTGTCTAGTCTAGTATGGTAA

FIGURE 2G

CTATTCTTGAAATGGTATTGAAAAATACCGTTAATTCAAATTGACAGAGATTGATAAAAA
GAAACTGATTTACCTAAGTTTACTTTTAAATTGCATAATAGAGCATTTTTTTGTTTTGAGT
TCCCTCATTCTTATTACCAGAAAGAGCTTGCAAATAGTTTTACTTTCTTGGCACTGGAAG
GGTAGTTCTGGAAAGCTACTTTGTTGAGAGTCTCATTCTTCCCTGGAGTTAATAGAGTGA
TTCACAATCTTTGGGGTTTTCTCCTCATCAAAGCATTCTTAAGTGCCTATCTAAAAGC
AATTAAAGACTGTGTCTGCCCTTTAGAAGCTAAGAATTTGATTTCATGATGCAAATTAAC
AGATAATTTGCAAAGTACCCTTGAGATTGAATTTTCTCTATTATATATTTCCCATATTTT
AGGTGAATAATTTAATTTAAATGACAAAACCTATCTAGTCAACTGGGCATAATGACATT
TTCTTTAAATTAGACTCTATTTTGAATTA AAAAGAGTTTTATTATAAACCGTGTGTTTTTG
GTTTTTCTAAGTATATAGAAAGCTTGATAATTCAGATTTATCAATTTCTGATTTAATG
TAGACTTTGACTTTTTTTATTAAAAACCTTTGTATTAAAGCAAGTTATGTTATTTTTCTTT
TATGCATTTATTACTAACATAGCTTTAAATCTTTAAATGTATTGAAGCATTGTGCTGTCT
GAAAATAAGGAATTGCTTATAAACCCAGCCACTTCTGAATACAATATGTAGCTGATTTAAT
AAGCTAGTTAGTGAATGGAAAATAAGTGTGGAGTATTA AAAATGTTCTTTGGTTGGTAAG
GCCTAAGATAGGGTTTCATTTATTTCTATACTTTTTCTGTTTTTTAAACACCTGCATATT
TTTATGTAAATCTCTAAATTTAAATATTTTAAAGTACATTTATTTTTGGTGTGTTTATTGT
ATAAAACCTTAGACAATCAATCAGTCAGTCTTTACTGACAGGAGCAGCAGCTATCTGTCT
TTTGCTGATCTACAAATAAATGAATTGAGAATTTAGTCCATAGAGGTCCCTGGCTACCAA
ACACATTTCTCCTTTGAATTGTTAAATTCAGAACATTCAAATAACTGTTTTGCTACAAC
CCATGATTATTTTCTGTGTGTGTTATTTAAATTTACTTTCTCTTTAGAAGTGCATTTAT
TTCTGAAAAATCTTAATGAAACAAACGCTTAGAACAAATATAAATATGAGACACTTGGGA
CTACTAGAGATATTTTAGATTTTTATGAAAAAAATGTGAGGGGATATTGCTGCTTTAAAA
AGGAATAAAGTAATAAAAAATATATCTCAGCTATTTTTTTAAAGCAATATAATTAGCAAT
TGTCTAGAAAAGTAATCATGAGGCTACTGAGTTTGGTGTTTCAAGTACTGAGTTTCAAAAA
TGTTTTGGTGGCATGAGGACAAAATTTTATTGAAGGTAAGATAAGAATAAAAACTATGTT
TAC

SEQ ID NO: 9_AA210825_H

CACGAGGGCTACTGGCGCCTGGCGACCCTCCCTGCCCCCACCCAACCCCGCTCCGGCAA
CGCCCCCTTCCTCACGGCTCCCGACCGAACTTTCTCCAACCTCTGCGACTCGTGAGATT
CCCTTCTACCCACTCCGGCCCTCGGGACCCCTCTGCCCATCCCTGGCCGGTCCGGTCCC
TGCGAACCCCTTTATCTCTGGAATCCACTCGGTCCCCGACTCAGAGACTCCTGCCCTCCA
CCCCAAGGACCCCGCCATCCTCAGGTCCCTCCGCCTGCCAGATCTTTTCTCGGATCCC
CGCTCTCCACACCTGCTCACGAGATCCCGCGGATCTAGAACCAGGGTCCCCGGGGC
CCCCCGGCGGGTCCCGGGTGGGCTCCAGGCGGGCGGTCCCGGCCCTCCCCCATGGCCAC
CGCCCCCTCATTATCCCGCCGGGCTCCCTGGCTCTCCCGGGCCGGGTCTCCTCCGCCCC
CCGGCGGCCTAGAGCTGCAGTCGCCGCCACCGCTACTGCCCCAGATCCCGGCCCGGGTT
CCGGGGTCTCCTTTACATCCAGATCGGGCTGACCCGCGAGTTCTGTGCTGTTGCCCGCCG
CCTCCGAGCTGGCTCATGTGAAGCAGCTGGCCTGTTCCATCGTGGACCAGAAGTTCCCTG
AGTGTGGCTTCTACGGCCTTTACGACAAGATCCTGCTTTTCAAACATGACCCACGTCCG
CCAACCTCCTGCAGCTGGTGCCTCGTCCGGAGACATCCAGGAGGGCGACCTGGTGGAGG
TGGTGTGTCGGCCTCGGCCACCTTCGAGGACTTCCAGATCCGCCCGCACGCCCTCACGG
TGCACTCCTATCGGGCGCCTGCCTTCTGTGATCACTGCGGGGAGATGCTCTTCGGCCTAG
TGCGCCAGGGCCTCAAGTGCAGTGGCTGCGGGCTGAAC'TACCACAAGCGCTGTGCCTTCA
GCATCCCCAACAACTGTAGTGGGGCCCCGAAACGGCGCCTGTCATCCACGTCTCTGGCCA
GTGGCCACTCGGTGCGCCTCGGCACCTCCGAGTCCCTGCCCTGCACGGCTGAAGAGCTGA
GCCGTAGCACCACCGAACTCCTGCCTCGCCGTCCCCCGTCATCCTCTTCTCCTCTTCTG
CCTCATCGTATACGGGCCGCCCCATTGAGCTGGACAAGATGCTGCTCTCCAAGGTCAAGG
TGCCGCACACCTTCTCATCCACAGCTATACACGGCCCACCGTTTGCCAGGCTTGCAAGA
AACTCCTCAAGGGCCTCTTCCGGCAGGGCCTGCAATGCAAAGACTGCAAGTTTAACTGTC

FIGURE 2H

ACAAACGCTGCGCCACCCGCGTCCCTAATGACTGCCTGGGGGAGGCCCTTATCAATGGAG
ATGTGCCGATGGAGGAGGCCACCGATTTTCAGCGAGGCTGACAAGAGCGCCCTCATGGATG
AGTCAGAGGACTCCGGTGTTCATCCCTGGCTCCCACTCAGAGAATGCGCTCCACGCCAGTG
AGGAGGAGGAAGGCGAGGGAGGCAAGGCCAGAGCTCCCTGGGGTACATCCCCCTAATGA
GGGTGGTGCAATCGGTGCGACACACGACGCGGAAATCCAGCACCACGCTGCGGGAGGGTT
GGGTGGTTTATTACAGCAACAAGGACACGCTGAGAAAGCGGCACTATTGGCGCCTGGACT
GCAAGTGTATCAGCTCTTCCAGAACAACACGACCAACAGATACTATAAGGAAATTCGCG
TGTCAGAAATCCTCAGGTGGAGTCCGCCAGAACTTCAGCCTTGTGCCGCCGGGCACCA
ACCCACACTGCTTTGAGATCGTCACTGCCAATGCCACCTACTTCGTGGGCGAGATGCCTG
GCGGGACTCCGGGTGGGCCAAGTGGGCAGGGGGCTGAGGCCGCCCGGGGGCTGGNNGAGA
CAGCCATCCGCCAGGCCCTGATGCCCGTCATCCTTCAGGACGCACCCAGCGCCCCAGGCC
ACGCGCCCCACAGACAAGCTTCTCTGAGCATCTCTGTGTCCAACAGTCAGATCCAAGAGA
ATGTGGACATTGCCACTGTCTACCAGATCTTCCCTGACGAAGTGCTGGGCTCAGGGCAGT
TTGGAGTGGTCTATGGAGGAAAACACCGGAAGACAGGCCGGGACGTGGCAGTTAAGGTCA
TTGACAAACTGCGCTTCCCTACCAAGCAGGAGAGCCAGCTCCGGAATGAAGTGGCCATTC
TGCAGAGCCTGCGGCATCCCGGGATCGTGAACCTGGAGTGCATGTTTCAGACGCCTGAGA
AAGTGTGTTGTGGTGATGGAGAAGCTGCATGGGGACATGTTGGAGATGATCCTGTCCAGTG
AGAAGGGCCGGCTGCCTGAGCGCCTCACCAAGTTCCTCATACCCAGATCCTGGTGGCTT
TGAGACACCTTCACTTCAAGAACATTGTCCACTGTGACTTGAAACCAGAAAACGTGTTGC
TGGCATCAGCAGACCCATTTCCTCAGGTGAAGCTGTGTGACTTTGGCTTTGCTCGCATCA
TCGGCGAGAAGTCGTTCCGCCGCTCAGTGGTGGGCACGCCGGCCTACCTGGCACCCGAGG
TGCTGCTCAACCAGGGCTACAACCGCTCGCTGGACATGTGGTCAGTGGGCGTGATCATGT
ACGTCAGCCTCAGCGGCACCTTCCCTTTCAACGAGGATGAGGACATCAATGACCAGATCC
AGAACGCCGCCCTTCATGTACCCGGCCAGCCCCCTGGAGCCACATCTCAGCTGGAGCCATTG
ACCTCATCAACAACCTGCTGCAGGTGAAGATGCGCAAACGCTACAGCGTGGACAAATCTC
TCAGCCACCCCTGGTTACAGGAGTACCAGACGTGGCTGGACCTCCGAGAGCTGGAGGGGA
AGATGGGAGAGCGATACATCAGCATGAGAGTGACGACGCGCGCTGGGAGCAGTTTGCAG
CAGAGCATCCGCTGCCTGGGTCTGGGCTGCCCACGGACAGGGATCTCGGTGGGGCCTGTC
CACCACAGGACCACGACATGCAGGGGCTGGCGGAGCGCATCAGTGTCTCTGAGGTCTTG
TGCCCTCGTCCAGCTGCTGCCCTCCACAGCGGTTCTTTCAGAGATCCCAGCAATGAACTG
TTCTAGGGAAAGTGGCTTCTGCCCCAACTGGATGGGACACGTGGGAGTGGGGTGGGGG
GAGCTATTTCAGGCCCTCCCTGTTTCCCAGCAATTAAACGGACTCATCTCTGGCC
CCATGGCCTTGATCTCAGCAAAA

SEQ ID NO: 10_AA127299_H

ATTCAATTCAATAATTGTTGGTGCAAAAGATTTGCTTGCTATGGATTCAAATGGTCTTTCT
GATCCTTACATCAAAATCACAAATCTTTCTCAAAAACGAAAGTGATTAAGAAAACCTTG
ACTCCAACCTTGGAAATGAACTTTTTTTGTGCATTTTCCAGAAAAACAACCCTTGAATTA
GAATGTTGGGACCACGATACTTTTTCAGATGATTTTATTGGCAAGGCTCCATTTCTTTG
GCAGAGATTCCAGCTTTGGCAGAAGTTGATATGTGGATAGATATGAAAACGAAAAAAGGA
GAATTTGCAGGAAAA

SEQ ID NO: 11_AA316804_H

ATGTCTGCAAATAATTCCCCTCCATCAGCCCAGAAGTCTGTATTACCCACAGCTATTCCCT
GCTGTGCTTCCAGCTGCTTCTCCGTGTTCAAGTCTTAAGACGGGACTCTCTGCCCGACTC
TCTAATGGAAGCTTCAGTGACCATCACTACCAACTCCAGAGGCTCAGTGCATACAGTT
TCATTTCTACTGCAAATTGGCCTCACACGGGAGAGTGTTACCATTGAAGCCCAGGAACTG
TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT
GGATTCTTTGGCATGTATGACAAAATCTTCTCTTTTCGCCATGACATGAACTCAGAAAAAC
ATTTTGAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGGTT

FIGURE 21

CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTTCGTCCACATACTCTCTATGTACAT
TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT
CAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAAACGATGTGCCTTCAAGATT
CCAAATAACTGTAGTGAGTAAGAAAGAGACGTCTGTCAAATGTATCTTTACCAGGACCC
GGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTTCCCAGTGAAGAGTCA
CATGTCCACCAGGAACCAAGTAAGAGAATTCTTCTTGGAGTGGTCGCCCCAATCTGGATG
GAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCTGTTCACTCTTACACC
CGTCCCACGATATGTCACTACTGCAAGCGGTTACTGAAAGGCCTCTTTCGCCAAGGAATG
CAGTGTAAGATTGCAAATTCACCTGCCATAAACGCTGTGCATCAAAAGTACCAAGAGAC
TGCCTTGGAGAGGTTACTTTCAATGGAGAACCTTCCAGTCTGGGAACAGATACAGATATA
CCAATGGATATTGACAATAATGACATAAATAGTGATAGTAGTCGGGGTTTGGATGACACA
GAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTG
GAAAGAGATGAAGAAGCCGTTAAAACAATCAGTCCATCAACAAGCAATAATATTCCGCTA
ATGAGGGTTGTACAATCCATCAAGCACACAAAGAGGAAGAGCAGCACAAATGGTGAAGGAA
GGGTGGATGGTCCATTACACCAGCAGGGATAACCTGAGAAAGAGGCATTATTGGAGACTT
GACAGCAAATGTCTAACATTATTTTCAAGATGAATCTGGATCAAAGTATTATAAGGAAATT
CCACTTTTCAAGAAATCTCCGCATATCTTACCACGAGATTTTCAAAACATTTTACAAGGC
AGCAATCCACACTGTTTTTGAATCATTACTGATACTATGGTATACTTCGTTGGTGAGAAC
AATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTTGGACTTGATGTAGCA
CAGAGCTGGGAAAAAGCAATTTCGCCAAGCCCTCATGCCTGTTACTCCTCAAGCAAGTGTT
TGCACCTTCTCCAGGGCAAGGGAAAGATCACAAGATTTGTCTACAAGTATCTCTGTATCT
AATTGTCAAGTTTCAAGGAGAATGTGGATATCAGTACTGTTTACCAGATCTTTGCAGATGAG
GTGCTTGGTTTCAAGGCCAGTTTGGCATCGTTTTATGGAGGAAAACATAGAAAAGACTGGGAGG
GATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAACAAGAAAGTCAACTC
CGTAATGAAGTGGCTATTTTACAGAATTTGCACCATCCTGGGATTGTAAACCTGGAATGT
ATGTTTGAACCCCAAGACGAGTCTTTGTAGTAATGGAAAAGCTGCATGGAGATATGTTG
GAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATTACTAAATTCATGGTC
ACACAGATACTTGTGTGCTTTGAGGAATCTGCATTTTAAAGAAATATTGTGCACTGTGATTTA
AAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCCCTCAGGTGAAGCTGTGTGAC
TTTGGATTTGCACGCATCATTGGTGAAAAGTCATTCAAGGAGATCTGTGGTAGGAACCTCCA
GCATACTTAGCCCTGAAGTTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG
TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCTTTTAAATGAGGATGAA
GATATAAATGACCAAATCCAAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAGAA
ATTTCTGGTGAAGCAATTGATCTGATAAAACAATCTGCTTCAAGTGAAGATGAGAAAACGT
TACAGTGTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC
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SEQ ID NO: 12_PKNBETA_H

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AACCGCCGCTGGAGCAGCTGCATGGCGAGCTGCGGGAGCTGCACGCCCCGAATCCTGCTG
CCCCGGCCCTGGGCCTGGCCAGCTGAGCCTGTGGCCTCAGGACCCCGGCCGTGGGCAGAG
CAGCTCAGGGCTCGGCACCTAGAGGCTCTCCGGAGGCAGCTGCATGTGGAGCTGAAGGTG
AAACAGGGGGCTGAGAACATGACCCACACGTGCGCCAGTGGCACCCCCAAGGAGAGGAAG
CTCCTTGCAGCTGCCCAGCAGATGCTGCGGGACAGCCAGCTGAAGGTGGCCCTGCTGCGG
ATGAAGATCAGCAGCCTGGAGGCCAGTGGGTCCCCGGAGCCAGGGCCTGAGCTACTGGCG
GAGGAGCTACAGCATCGACTGCACGTTGAGGCAGCGGTGGCTGAGGGCGCCAAGAACGTG

FIGURE 2J

GTGAAACTGCTTAGTAGCCGGAGAACACAGGACCGCAAGGCACTGGCTGAGGCCAGGC
CAGCTACAGGAGTCCTCTCAGAACTGGACCTCCTGCGCCTGGCCTTGGAGCAGCTGCTG
GAGCAACTGCCTCCTGCCCACCTTTGCGCAGCAGAGTGACCCGAGAGTTGCGGGCTGCG
GTGCCTGGATACCCCCAGCCTTCAGGGACACCTGTGAAGCCCACCGCCCTAACAGGGACA
CTGCAGGTCCGCCTCCTGGGCTGTGAACAGTTGCTGACAGCCGTGCCTGGGCGCTCCCCA
GCGGCCGCACTGGCCAGCAGCCCCCTCCGAGGGCTGGCTTCGGACCAAGGCCAAGCACCAG
CGTGGCCGAGGCGAGCTTGCCAGTGAGGTGCTGGCTGTGCTAAAGGTGGACAACCGTGTT
GTGGGGCAGACGGGCTGGGGCAGGTGGCCGAACAGTCCTGGGACCAGACCTTTGTCATC
CCACTGGAGCGAGCCCGTGAGCTGGAGATTGGGGTACACTGGCGGGACTGGCGGCAGCTA
TGTGGCGTGGCCTTCCTGAGACTTGAAGACTTCCTGGACAATGCCTGTCACCAACTGTCC
CTCAGCCTGGTACCGCAGGGACTGCTTTTTGCCCAGGTGACCTTCTGCGATCCTGTCAAT
GAGAGGCGGCCCCGGCTGCAGAGGCAGGAACGCATCTTCTCTAAACGCAGAGGCCAGGAC
TTCCTGAGGCGTTCGCAGATGAACCTCGGCATGGCGGCCTGGGGGCGCCTCGTCATGAAC
CTGCTGCCCCCTGCAGCTCCCCGAGCACAATCAGCCCCCTAAAGGATGCCCTCGGACC
CCAACAACACTGCGAGAGGCCTCTGACCCTGCCACTCCAGTAATTTCTGCCCAAGAAG
ACCCCTTGGGTGAAGAGATGACACCCCCACCAAGCCCCACGCCTCTACCTCCCCAG
GAGCCAACATCCGAGGAGACTCCGCGCACCAACAGTCCCCATATGGAGCCTAGGACTCGA
CGTGGGCCATCTCCACCAGCCTCCCCACCAGGAAACCCCTCGGCTTCAGGACTTCCGC
TGCTTAGCTGTGCTGGGCCGGGACACTTTGGGAAGGTCTCTGGTCCAGTTCAAGGGG
ACAGGGAAATACTACGCCATCAAAGCACTGAAGAAGCAGGAGGTGCTCAGCCGGGACGAG
ATAGAGAGCCTGTACTGCGAGAAGCGGATCCTGGAGGCTGTGGGCTGCACAGGGCACCCT
TTCCTGCTCTCCCTCCTTGTCTGCTTCCAGACCTCCAGCCATGCCCGCTTTGTGACTGAG
TTTGTGCCTGGTGGTGACCTCATGATGCAGATCCACGAGGATGTCTTCCCCGAGCCCCAG
GCCCCGCTTCTACGTGGCTTGTGTTGTCTGGGGCTGCAGTTCTTACACGAGAAGAAGATC
ATTTACAGGGACCTGAAGTTGGATAACCTTCTGCTGGATGCCCAGGGATTCTGAAGATC
GCAGACTTTGGACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGT
GGCACCCCGAGTTCTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACAGGCCGCTC
GACTGGTGGGCGCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCA
GGGGACACAGAGGAAGAGGTGTTTGAAGTGCATCGTCAACATGGACGCCCCCTACCCCGGC
TTTCTGTGCGGTGCAAGGGCTTGAGTTCAATCAGAAGCTCCTCCAGAAGTGCCCGGAGAAG
CGCCTCGGGGACGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACC
ACCAACTGGCAAGCCCTGCTCGCCCGCACCATCCAGCCCCCTTCGTGCCTACCCTGTGT
GGCCCTGCGGACCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACC
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TTTGTGTGAGAGCGATTCTTGAACCTGA

SEQ ID NO: 13_AI021023_M_PKNBETA_M

GCTGAAGTGGGATAACCTTCTGCTGGATGCCCAGGGATTCTGAAGATCGCAGACTTTGG
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GTTCTTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACAGGGCTGTGGACTGGTGGGG
GCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCAGGGGACACAGA
GGAAGAGGTGTTTGAAGTGCATCGTCAACATGGACGCCCCCTACCCCGGCTTTCTGTGCGT
GCAAGGGCTTGAGTTCAATCAGAAGCTCCTCCAGAAGTGCCCGGAGAAGCGCCTCGGGGC
GGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACCACCAACTGGCA
AGCCCTGCTCGCCCGCACCATCCAGCCCCCTTGTGCTTACCCTGTGTGGCCCTGCGGA
CCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACCCACCTGCACC
CCACAGCCTCCTCACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGACTTTGTGTGAGA
GCGATTCTTGAACCTGAGGGCATCTCCTGGCACCTCTGTCCCTTCCCCACAGACTG
TTAGAGCCTCTGCTCGTTACCCGTGCGCCCTGCCTGGAGGTCCAGGCCTTGCTGGGTAC
TTCTGAGCCCTTGGGATTCAAAGTGGCAGCCATGGGGCCACTGTTGTGGGCTTTGCTCAG

FIGURE 2K

TGTCACTGGGCAAAGTGTGTCCCTTCCCCCTCCAGCTCGCCCTCTTCTACCTCCCAGCGA
GACCTGGCCAGAAAGGGTGCCGAGCAAGGAGTGATATGGTTTGTCTTTTAAAGACTGG
ACTTGCTTTATATTAAATTTGTAAAAGTG

SEQ ID NO: 14_H19102_H

GGTGGCAACATCCGGGGTCCCTGGGCCCCGAGGCTGGAAGAGCCTCTGGACAGGTTTGGGA
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GAATCCCTAAAGCCAGCCCCAGTACTGGTAGAGAAGCCTCTGCCAGAGTGGCCAGTGCCT
CAGTTCATCAACCTCTTTCTACCAGAGTTTCCCATTAGGCCCATTAGGGGGCAGCAGCAG
CTGAAGATTTTAGGCCCTCGTGGCTAAAGGCTCCTTTGGAAGTGTCTCAAGGTGCTAGAT
TGCACCCAGAAAGCTGTATTTGCAGTGAAGGTGGTGCCCAAGGTAAAGGTCTACAGAGG
GATACCGTGAGGCAGTGCAAAGAGGAGGTTAGCATCCAGCGACAGATCAACCATCCCTTT
GTACACAGCTTGGGGGACAGCTGGCAGGGGAAAACGGCACCTTTTCATTATGTGTAGCTAC
TGCAGCACAGATCTGTACTCCCTTTGGTTCGGCTGTTGGCTGCTTTCCTGAGGCTTCCATC
CGTCTCTTTGCTGCCGAGTTGGTGCTGGTACTGTGTTATCTCCATGACTTGGGCATCATG
CATCGAGATGTGAAGATGGAGAATATTCTTCTAGATGAACGAGGCCATCTGAAACTGACA
GACTTTGGTCTGTCCCGCCACGTGCCCCAGGGAGCTCAAGCCTACACTATCTGTGGCACT
CTTCAGTACATGGCCCCAGAGGTCCTAAGTGGAGGACCTTACAACCATGCTGCTGATTGG
TGGTCCCTGGGTGTCTTGCTTTTCTCTCTGGCGACTGGAAAAGTTTCCAGTGGCTGCAGAG
AGAGATCATGTGGCCATGTTGGCAAGTGTGACCCACAGTGACTCTGAGATCCCAGCTTCT
CTTAACCAGGGCCTCTCACTCCTGCTCCATGAGCTCTTATGCCAGAACCCCCCTCCATCGT
CTACGTTATCTGCATCACTTCCAGGTCCACCCTTTCTTTTCGGGGTGTGGCCTTCGACCCA
GAGCTCCTACAGAAAGCAGCCAGTGAACCTTTGTACGGAGACACAAGCTACCCAGCCCAGT
TCAGCGGAGACCATGCCCTTTGACGACTTTGACTGTGATCTGGAGTCCTTCTTGCTCTAC
CCTATCCCTGCTTGA

SEQ ID NO: 15_AA476563_H

ATGGAATTCTTTAGGATAGACAGTAAGGATAGCGCAAGTGAACCTCTGGGACTTGACTTT
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GACACCATTAGCAGGGGCTCAGATGACTCAGTGCCAGTTATTTCTGTTTAAAGATGCTGCT
TTTGATGATGTGAGTGCTGATGAAGGAAGACCTGATCTTCTGTAAATTTACCTGGT
GAATTGGAGTCAACAAGAGAAGCTGCAGCAATGGGACCTACTAAGTTTACACAACTAAT
ATAGGGATAATAGAAAATAAATCTTGGAGCCCTGATGTTTATGCCTCAGGCTTAGT
ACTGAACAATGCCAAGCACATGAGGAGAAAGGCATAGAGGAACTGAGTGATCCCTCTGGG
CCCAAATCCTATAGTATAACAGAGAAACACTATGCACAGGAGGATCCCAGGATGTTATTT
GTAGCAGCTGTTGATCATAGTAGTTCAGGAGATATGTCTTTGTTACCCAGCTCAGATCCT
AAGTTTCAAGGACTTGGAGTGGTTGAGTCAGCAGTAACTGCAAACAACACAGAAGAAAGC
TTATCCGTATTTGTAGTCCACTCTCAGGTGCTAATGAATATATTGCAAGCACAGACACT
TTAAAAACAGAAGAAGTATTGCTGTTTACAGATCAGACTGATGATTGGCTAAAGAGGAA
CCAACCTCTTTATTCCAGAGAGACTCTGAGACTAAGGGTGAAAGTGGTTTAGTGCTAGAA
GGAGACAAGGAAATACATCAGATTTTTGAGGACCTTGATAAAAAATTAGCACTAGCCTCC
AGGTTTTACATCCCAGAGGGCTGCATTCAAAGATGGGCAGCTGAAATGGTGGTAGCCCTT
GATGCTTTACATAGAGAGGGGAATTGTGTGCCGCGATTTGAACCCAAACAACATCTTATTG
AATGATAGAGGACACATTCAGCTAACGTATTTAGCAGGTGGAGTGAGGTTGAAGATTCC
TGTGACAGCGATGCCATAGAGAGAATGTACTGTGCCCCAGAGGTTGGAGCAATCACTGAA
GAACTGAAGCCTGTGATTGGTGGAGTTTGGGTGCTGTCTCTTTGAACTTCTCACTGGC
AAGACTCTGGTTGAATGCCATCCAGCAGGAATAAATACTCACACTACTTTGAACATGCCA
GAATGTGTCTCTGAAGAGGCTCGCTCACTCATTCAACAGCTCTTGCAGTTCAATCCTCTG

FIGURE 2L

GAACGACTTGGTGCTGGAGTTGCTGGTGTTGAAGATATCAAATCTCATCCATTTTTTACC
CCTGTGGATTGGGCAGAACTGATGAGATGA

SEQ ID NO: 16_AA626690_H

ATGCTACCATTCGCTCCTCAGGACGAGCCCTGGGACCGAGAAATGGAAGTGTTTCAGCGGC
GGCGGCGCGAGCAGCGCGAGGTAAATGGTCTTAAATGGTTGATGAGCCAATGGAAGAG
GGAGAAGCAGATTCTTGTCATGATGAAGGAGTTGTTAAAGAAATCCCTATTACTCATCAT
GTTAAGGAAGGCTATGAGAAAGCAGATCCTGCACAGTTTGAGTTGCTCAAGGTTCTTGGT
CAGGGGTCATTTGGAAAGGTTTTTCTTGTTAGAAAGAAGACCGGTCTGATGCTGGGCAG
CTCTATGCAATGAAGGTGTTAAAAAAGCCTCTTTAAAGTTTCGAGACAGAGTTCCGACA
AAGATGGAGAGGGATATACTGGTGGAAGTAAATCATCCATTTATTGTCAAATTGCACTAT
GCCTTTCAGACTGAAGGGAACTGTACTTAATACTGGATTTTCTCAGGGGAGGAGATGTT
TTCACAAGATTATCCAAAGAGGTTCTGTTTACAGAGGAAGATGTGAAATCTACCTCGCA
GAACCTGGCCCTTGCTTTGGATCATCTGCACCAATTAGGAATTGTTTATAGAGACCTGAAG
CCAGAAAACATTTTGCTTGATGAAATAGGACATATCAAATTAACAGATTTTGGACTCAGC
AAGGAGTCAGTAGATCAAGAAAAGAAGGCTTACTCATTTTGTGGTACAGTAGAGTATATG
GCTCCTGAAGTAGTAAATAGGAGAGGCCATTCCCAGAGTGCTGATTGGTGGTCATATGGT
GTTCTTATGTTTGAAATGCTTACTGGTACTCTGCCATTTCAAGGTAAAGACAGAAATGAG
ACCATGAATATGATATTAAAAGCAAACTTGGAATGCCTCAATTTCTTAGTGCTGAAGCA
CAAAGTCTTCTAAGGATGTTATTCAAAAGGAATCCAGCAAATAGATTGGGATCAGAAGGA
GTTGAAGAAATCAAAAGACATCTGTTTTTGC AAATATTGACTGGGATAAAATTATATAAA
AGAGAAGTTCAACCTCCTTTCAAACCTGCTTCTGGA AAAACCAGATGATACTTTTTGTTTT
GATCCTGAATTTACTGCAAAAACACCTAAAGATTCTCCCGGTTTGCCAGCCAGTGCAAAT
GCTCATCAGCTCTTCAAAGGATTGAGCTTTGTTGCAACTTCTATTGCAGAAGAAATATAAA
ATCACTCCTATCACAAGTGCAAATGTATTACCAATTGTTGAGATAAATGGAATGCTGCA
CAATTTGGTGAAGTATATGAATTGAAGGAGGATATTGGTGTGGCTCCTACTCTGTTTGC
AAGCGATGCATACATGCAACTACCAACATGGAATTTGCAGTGAAGATCATTGACAAAAGT
AAGCGAGACCCTTCAGAAGAGATTGAAATATTGATGCGCTATGGACAACATCCCAACATT
ATTACTTTGAAGGATGTCTTTGATGATGGTAGATATGTTTACCTTGTTACGGATTTAATG
AAAGGAGGAGAGTTACTTGACCGTATTCTCAAACAAAATGTTTCTCGGAACGGGAGGCT
AGTGATATACTATATGTAATAAGTAAGACAGTTGACTATCTTCATTGTCAAGGAGTTGTT
CATCGTGATCTTAAACCTAGTAATATTTTATACATGGATGAATCAGCCAGTGAGATTCA
ATCAGGATATGTGATTTTGGGTTTGCAAAACAACTTCGAGGAGAAAATGGACTTCTCTTA
ACTCCATGCTACACTGCAAACTTTGTTGCACCTGAGGTTCTTATGCAACAGGGATATGAT
GCTGCTTGTGATATCTGGAGTTTAGGAGTCCTTTTTTACACAATGTTGGCTGGCTACACT
CCATTTGCTAATGGCCCCAATGATACTCCTGAAGAGATACTGCTGCGTATAGGCAATGGA
AAATTCTCTTTGAGTGGTGGA AACTGGGACAATATTTTCAGACGGAGCAAAGGATTTGCTT
TCCCATATGCTTCATATGGACCCACATCAGCGGTATACTGCTGAACAAATATTAAAGCAC
TCATGGATAACTCACAGAGACCAGTTGCCAAATGATCAGCCAAAGAGAAATGATGTGTCA
CATGTTGTTAAGGGAGCAATGGTTGCAACATACTCTGCCCTGACTCACAAGACCTTTCAA
CCAGTCCTAGAGCCTGTAGCTGCTTCAAGCTTAGCCAGCGACGGAGCATGAAAAAGCGA
ACATCAACTGGCCTGTAA

SEQ ID NO: 17_AA215680_H

ATGAGCCTGGTGGCCTGTGAGTGCTGCCCAGCCCCGGCCTGGAGCCTGAGCCTTGCTCA
CGAGCACGGTCCCAAGCTCACGTGTACCTGGAGCAGATTGCAACAGGGTGGCTCTGGGA
GTGCCTGACATGACAAAACGTGACTATCTGGTGGATGCGGCCACGCAGATCCGGCTGGCC
CTGGAGCGCGATGTTAGTGAGGACTATGAGGCGGCCTTCAACCACTATCAGAATGGCGTG
GACGTGCTGCTCCGTGGCATACAGTTGACCCCAACAAGGAGCGACGTGAGGCTGTGAAG
CTGAAAATTACCAAATACCTGCGGCGGGCAGAGGAGATCTTCAACTGCCACCTGCAGCGG

FIGURE 2M

CCGCTGAGCAGTGGAGCCAGCCCCAGCGGGGTTTCAGCAGCCTGAGGCTCCGGCCCATT
CGCACGCTGAGCTCTGCCGTGGAGCAGCTGAGGGGCTGCAGGGTGGTCGGGGTCATCGAG
AAGGTGCAGCTGGTCCAGGACCCGGCAACCGGAGGGACCTTTGTGGTGAAGAGCCTACCC
AGGTGCCACATGGTGAGCAGGGAGCGGCTGACCATCATCCCACACGGAGTCCCTACATG
ACGAAGCTGCTCAGGTACTTTGTGAGCGAGGACTCCATCTTCCTGCACCTGGAGCATGTG
CAAGGAGGCACTCTCTGGTCCCACCTGCTCTCCCAGGCGCACTCCCGACATTCTGGGCTC
AGCTCTGGCTCTACCCAGGAGAGGATGAAGGCTCAGCTCAACCCCCACCTCAACCTCCTG
ACCCAGCGAGGCTTCCCTCAGGCCATGCCCCTGCCAGGACAGAATCGCCCTGGAGCCT
CCTAGGACTTCTCCGAACCTTCTCCTAGCTGGGGAGGCCCCATCCACCAGACCCAGAGG
GAGGCTGAAGGTGAACCCACAGCCAGGACCAGCACCTCTGGCTCCTCGGACCTTCCAAAG
GCCCCAGGTGGCCACCTGCACCTTCAAGCTAGGAGGGCTGGCCAGAACTCAGACGCTGGG
CCCCCTCGGGGGCTCACTTGGGTTCTTGAGGGGGCCGGCCCGGTGCTAGGGGGCTGTGGC
CGAGGCATGGATCAGAGCTGCCTGTCAGCAGATGGGGCCGGCCGGGGCTGTGGCAGGGCC
ACCTGGAGTGTGAGAGAGGAGCAGGTGAAGCAGTGGGCGGCAGAGATGCTGGTAGCGCTG
GAGGCGCTGCACGAGCAGGGGGTGTGTGCCGGGACCTCCACCCCGGGAACCTGCTCCTG
GACCAGGCAGGTCACATCCGGCTCACATATTTTGGCCAGTGGTCAGAGGTGGAGCCCCAG
TGCTGCCGGGAGGCCGTGGACAATCTCTACAGCGCCCCAGAGGTGGGTGGGATTTCCGAG
CTGACGGAAGCCTGTGACTGGTGGAGCTTTGGGTCTCTACTGTATGAACTGCTGACGGGA
ATGGCACTGTCCCAGAGCCACCCTTCAGGAATCCAGGCCCACACCCAGCTCCAGCTGCCC
GAGTGGCTCAGTCGCCCAGCGGCTCTCTGCTGACTGAGCTGCTGCAGTTCGAGCCTACC
CGGCGCCTGGGCATGGGAGAAGGTGGTGTGAGCAAACTCAAGTCCCATCCCTTTTTTCAGT
ACCATCCAATGGAGCAAGCTGGTGGGGTAA

SEQ ID NO: 18_SGK_H

ATGACGGTGAAAACCTGAGGCTGCTAAGGGCACCCCTCACTTACTCCAGGATGAGGGGCATG
GTGGCAATTCTCATCGCTTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTTATTTCAG
AAGATTGCCAATAACTCCTATGCATGCAAACACCCTGAAGTTCAGTCCATCTTGAAGATC
TCCCAACCTCAGGAGCCTGAGCTTATGAATGCCAACCCTTCTCCTCCACCAAGTCCTTCT
CAGCAAATCAACCTTGGCCCGTCTGTCCTCATGCTAAACCATCTGACTTTTCACTTC
TTGAAAGTGATCGGAAAGGGCAGTTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCAGAA
GAAGTGTCTATGCAGTCAAAGTTTTACAGAAGAAAGCAATCCTGAAAAAGAAAGAGGAG
AAGCATATTATGTCGGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCCCTTTTCTGGTG
GGCCTTCACTTCTTCTTCCAGACTGCTGACAAATTGTACTTTGTCTAGACTACATTAAT
GGTGGAGAGTTGTTCTACCATCTCCAGAGGGAACGCTGCTTCTTGGAACACGGGCTCGT
TTCTATGCTGCTGAAATAGCCAGTGCCCTTGGGCTACCTGCATTCACTGAACATCGTTTAT
AGAGACTTAAACACAGAGAATATTTTGTAGATTACAGGGACACATTGTCCTTACTGAT
TTCGGACTCTGCAAGGAGAACATTGAACACAACAGCACAACATCCACCTTCTGTGGCACG
CCGGAGTATCTCGCACCTGAGGTGCTTCATAAGCAGCCTTATGACAGGACTGTGGACTGG
TGGTGCTGGGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCCGCCTTTTTATAGCCGA
AACACAGCTGAAATGTACGACAACATTCTGAACAAGCCTCTCCAGCTGAAACCAAATATT
ACAAATTCCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAGGACAGGACAAAGCGGCTC
GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGTCTTCTTCTTAAATTAACCTGG
GATGATCTCATTAATAAGAAGATTACTCCCCCTTTTAACCCAAATGTGAGTGGGCCCCAAC
GAGCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTGGCAAG
TCCCCTGACAGCGTCTCGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTCTCTAGGC
TTTTCTATGCGCCTCCCACGGACTCTTCTCTCTGA

SEQ ID NO: 19_AA107515_M

CGGGTCGACCCACGCGTCCGCCGGTTTCACTGCTCCCCTCAGTCTCTTTTGGGCTCTTTC
CGGGCATCGGGACGATGACCGTCAAAGCCGAGGCTGCTCGAAGCACCCCTTACCTACTCCA

FIGURE 2N

GAATGAGGGGAATGGTAGCGATTCTCATCGCTTTTATGAAACAGAGAAGGATGGGCCTGA
ACGATTTTATTTCAGAAGATTGCCAGCAACACCTATGCATGCAAACACGCTGAAGTTCAGT
CCATTTTGAAAATGTCCCATCCTCAGGAGCCGGAGCTTATGAACGCTAACCCCTCTCCTC
CGCCAAGTCCCTCTCAACAAATCAACCTGGGTCCGTCCTCCAACCCCTCACGCCAAACCCCT
CCGACTTTCACCTTCTTGAAAGTGATCGGAAAGGGCAGTTTTTGAAAGGTTCTTCTGGCTA
GGCACAAGGCAGAAGAAGTATTCTATGCAGTCAAAGTTTTACAGAAGAAAGCCATCTGA
AGAAGAAAGAGGAGAAGCATATTATGTGAGAGCGGAATGTTCTGTTGAAGAATGTGAAGC
ACCCTTTCTGGTGGGCCTTCACTTCTCATTCCAGACCGCTGACAAGCTCTACTTTGTCC
TGGACTACATTAATGGTGGAGAGCTGTTCTACCATCTCCAGAGGGAGCGCTGCTTCTGG
AACCACGGGCTCGATTCTACGCAGCTGAAATAGCCAGTGCCCTGGGCTATCTGCACTCCC
TAAACATCGTTTATAGAGACTTAAAACCTGAGAATATTCTCCTAGACTCCCAGGGGCACA
TCGTCTCACTGACNTATTTAGCTGCGTAGAATCGAGCATAACGGGACAACATCTACCT
TCTGTGGCACGCTGAGTATCTGGCTCCTGAGGTCTCCATAAGCAGCCGTATGACCGGA
CGGTGGACTGGTGGTGTCTTGGGGCTGTCTGTATGAGATGCTCTACGGCCTGCCCCCGT
TTTATAGCCGGAACACGGCTGAGATGTACGACAATATTCTGAACAAGCCTCTCCAGTTGA
AACCAAATATTACAAACTCGGCAAGGCACCTCTGGAAGGCCTCTGCAGAAGGACCGGA
CCAAGAGGCTGGGTGCCAAGGATGACTTTTATGGAGATTAAGAGTCATATTTTCTTCTCTT
TAATTAAGTGGGATGATCTCATCAATAAGAAGATTACACCCCATTTAACCCAAATGTGA
GTGGGCCCAGTGACCTTCGGCACTTCGATCCCGAGTTTACCGAGGAGCCGGTCCCCAGCT
CCATCGGCAGGTCCCCTGACAGCATCCTTGTACGGCCAGTGTGAAGGAAGCAGCAGAAG
CCTTCCTCGGCTTCTCCTATGCACCTCCTGTGGATTCTTCCTCTGAGTGCTCCCGGGAT
GGTCTGAAGGACTTCCTCAGCGTTTCTTAAAGTGTTCGTTAGCCTTTGGTGGAGTTG
CCAGCTGACAGAACATTTTAAAAGAATTTGCACACCTGGAAGCTTGGCAGTCTCGCCTGC
CCGGCGTGGCGCGACGCAGCGCGCTGCTTGATGGGAGCTTCCGAAGAGCACACCCTC
CTCTCAATGAGCTTGTGAGGTCTTCTTTCTTCTCTTCTTCCACGTGGTGCTAGCTCC
AGGCGAGCGAGCGTGAGAGTGCCGCTGAGACAGACACCTTGGTCTCAGTTAGAAGGAAG
ATGCAGGTCTAAGAGGAATCCCGCAGGTCTGTCTGAGCTGTGATCAAGAATATTCTGCA
ATGTGCCTTTTCTGAGATCGTGTAGCTCCAAAGCTTTTCTTATCGCAGAGTGTTTCAGT
TTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTTCCTTGGCGGATTTCCCGTGTGTGCA
GTGGCGTGAGTGCTATGCCTGATCACAGACGGTTTTGTGTGAGCATCAATGTGACAC
TTGCAGGACACTACAATGTGGGACATTGTTGTTTCTTCCACATTTGGAAGATAAATTTA
TGTGTAGACTGTTTGTAAAGATATAGTTAATAACTAAAACCTATTGAAACGGTCTTGCAA
TGACGAGCATTGAGATGCTTAAGGAAAGCATTGCTGCTACAAATATTTCTATTTTTAGAA
AGGGTTTTTATGGACCAATGCCCCAGTTGTCAGTCAAAGCCGTTGGTGTGTTTTCATTGTTT
AAAATGTACCTATAAAAACGGGCATTATTTATGTTTTTTTTTCCCTTTGTTTCATATTCTTT
TGCATTCTGATTATTGTATGTATCGTGTAAGGAAGTCTGTACATTGGGTTATAACACT
AGATATTTAAACTTACAGGCTTATTTGTAAACCATCATTTTAATGTACTGTAATTAACAT
GGGTTATAATATGTACAATTCCTCCTCCTTACCACACAACCTTTTTTTGTGTGCGATAAAC
CAATTTTGGTTTGCAATAAAATCTTGAAAACCT

SEQ ID NO: 20_AA109508_M

CCACCTGCAGCGGGAGCGCGGTTCTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGT
GGCCAGCGCCATTGGCTACCTGCACTCCCTCAACATCATTTACAGGGATCTGAAACCAGA
GAACATTCTCTGGACTGCCAGGGACACGTGGTGCTGACGGATTTTGGCCTCTGCAAGGA
AGGTGTAGAGCCTGAAGACACCACATCCACATTCTGTGGTACCCCTGAGTACTTGGCACC
TGAAGTGCTTCGGAAAGAGCCTTATGATCGAGCAGTGGACTGGTGGTGGTGGGGCAGT
CCTCTACGAGATGCTCCATGGCCTGCCGCCCTTCTACAGCCAAGATGTATCCCAGATGTA
TGAGAACATTCTGCACCAGCCGCTACAGATCCCCGGAGGCCGGACAGTGGCCCGCTGTGA
CCTCCTGCAAAGCCTTCTCCACAAGGACCAGAGGCAGCGCTGGGCTCCAAAGCAGACTT
TCTTGAGATTAAGAACCATGTATTCTTCAGCCCCATAAACTGGGATGACCTGTACCACAA

FIGURE 20

GAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTGA
CCCAGAGTTCACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGC
CAGCAGCTCTGGGGCCTCAAGTGCATTCTCTGGGATTTTCTTATGCGCCAGAGGATGATGA
CATCTTGGATTGCTAGAAGAGAAGGACCTGTGAACTACTGAGGCCAGCTGGTATTAGTA
AGGAATTACCTTCAGCTGCTAGGAAGAGCGACTCAAACCTAACAATGGCTTCAACGAGAAG
CAGGTTTATTTTTTCCAGCACATAAAAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAG
GACAGGTCATCAGATACTCAGAGGCTGTATCTCTGCCCTGCCAACCTTGACAAATGGCTT
CCAATGTTAGGTTTGTCTACAAGATGGTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAG
GGAAGGGAAAATGGAGGAAAGGGGAGAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAA
AAGCTCCACCCAATGACTTCTGCTTCCATCTCACTAACCACCCACCCCTACCTGGAATGG
AGGCTGGGAGATGTGGCTTATTTGCTGGGTACGTGACTATCCCTAATAACAAAGGGGTTT
TGACACTAAGACATTAGGGGAGAATGTTGGGTAGGCAGCCAGCACTCTTTTACCAGAGGG
CCTCCTGGTGTGTTGGATTTTGATCTCAATGTGTAAATGACAGAGATGTAACAAGCTCAT
AGGGTATCAATATCTCTTATTGTTCT

SEQ ID NO: 21_AA887783_H

CGGATGCATTTNTTGGTGTGCTCTTGAGGGATTAAATGCAAAGAGATCACACCATGGACT
ACAAGGAAAGCTGCCCAAGTGTAAGNATTCACAGCTCCGATGAACACAGAGAGAAAAAGA
AGAGGTTTACTGTTTATAAAGTTCTGGTTTTCAGTGGGAAGAAGTGAATGGTTTGTCTTCA
GGAGATATGCAGAGTTTGATAAACTTTATAACACTTTAAAAAAACAGTTTCCTGCTANGG
CCCTGAAGATTCTGCCAAGAGAATATTTGGTGATAATTTTGATCCAGATTTTATTAAAC
AAAGACGAGCAGGACTAAACGAATTCATTTCAGAACCTAGTTAGGTATCCAGAACTTTATA
ACCATCCAGATGTCAGAGCATTCTTCAAATGGACAGTCCAAAACACCAGTCAGATCCAT
CTGAAGATGAGGATGAAAGAAGTTCTCAGAAGCTACACTCTACCTCACAGAACATCAACC
TGGGACCGTCTGGAAATCCTCATGCCAAACCAACTGACTTTGATTTCTTAAAAGTTATTG
GAAAAGGCAGCTTTGGCAAGGTTCTTCTTGCAAAACGGAAACTGGATGGAAAATTTTATG
CTGTCAAAGTGTTACAGAAAAAATAGTTCTCAACAGAAAAGAGCAAAAACATATTATGG
CTGAACGTAATGTGCTCTTGAAAAATGTGAAACATCCGTTTTTGGTTGGATTGCATTATT
CCTTCCAAACAACTGAAAAGCTTTATTTTGTCTGGATTTTGTAAATGGAGGGGAGGGAC
ATGTTGTCTTAACAGATTTTGGGCTTTGTAAAGAAGGAATTGCTATTTCTGACACCACTA
CCACATTTTGTGGGACACCAGAGTATCTTGACCTGAAGTAATTAGAAAACAGCCCTATG
ACAATACTGTAGATTGGTGGTGCCCTTGGGGCTGTTCTGTATGAAATGCTGTATGGATTGC
CTCCTTTTTTATTGCCGAGATGTTGCTGAAATGTATGACAATATCCTTCACAAACCCCTAA
GTTTGAGGCCAGGAGTGAGTCTTACAGCCTGGTCCATTCTGGAAGAACTCCTAGAAAAAG
ACAGGCAAAATCGACTTGGTGCCAAGGAAGACTTTCTTGAAATTCAGAAATCATCCTTTTT
TTGAATCACTCAGCTGGGCTGACCTTGTACAAAAGAAGATTCCACCACCATTTAATCCTA
ATGTGGCTGGACCAGATGATATCAGAACTTTGACACAGCATTTACAGAAGAAACAGTTC
CATATTCTGTGTGTATCTTCTGACTATTCTATAGTGAATGCCAGTGTATTGGAGGCAG
ATGATGCATTTCGTTGGTTTCTCTTATGCACCTCCTTCAGAAGACTTATTTTGTGAGCAG
TTTGCCATTTCAGAAACCATTTGAGCAAAAATAAGTCTATAGATGGGACTGAAACTTCTATTT
GTGTGAATATATTCAAATATGTATAACTAGTGCCTCATTTTATATGTAATGATGAAAAC
TATGAAAAAATGTATTTCTTCTATGTGCAAGAAAAATAGGGCATTTCAAAGAGCTGTTT
TGATTAAAATTTATATTCTTGTTTAATAAGCTTATTTTAAACAATTTAAAGCTATTAT
TCTTAGCATTAACTATTTTAAAGAAACCTTTTTTGCTATTGACTGTTTTTCCCTCTA
AGTTTACACTAACATCTACCCAAGATAGACTGTTTTTAAACAGTCAATTCAGTTCAGCT
AACATATATTAATACCTTTGTAACCTTTTGCTATGGCTTTTGTATCACACCAAACTAT
GCAATTGGTACATGGTGTGTTAAGAAGAAACCGTATTTTCCATGATAAATCACTGTTTG
AAATATTTGGTTCATGGTATGATCGAAATGTAAAAGCATAATTAACACATTGGCTGCTAG
TTAACAATTGGAATAACTTTATTCTGCAGATCATTTAAGAAGTAACAGGCCGGGCGCGGT
GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACCTGAGGTCA

FIGURE 2P

GGAGTTGGAGACCAGCCTGACCAACATGGACAAACCCCGTCTCTACTAAAAATACAAAAT
TGGCAGGGTGTGGTGGCACATGCCTATAATCCCAGCTACTTGGGAGGCTAAGGCAGGAGA
ATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCATTGCACTCCTG
CCTGGGCAACAAGAGTGAAACTCCATCTCC

SEQ ID NO: 22_R47805_H

ATGGCGCACCAAACGGGCATCCACGCCACGGAAGAGCTGAAGGAATTCTTTGCCAAGGCA
CGGGCTGGCTCTGTGCGGCTCATCAAGGTTGTGATTGAGGACGAGCAGCTCGTGCTGGGT
GCCTCGCAGGAGCCAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGTGCTGCCACTG
CTGGACGCCCAGCAGCCCTGCTACCTGCTCTACCGCTCGACTCACAGAATGCTCAGGGC
TTCGAATGGCTCTTCCTCGCCTGGTCGCCTGATAACTCCCCCGTGGGCTGAAGATGCTG
TACGCGGCCACGCGGGCCACAGTGAAAAAGGAGTTTGGAGGTGGCCACATCAAGGATGAG
CTCTTCGGGACTGTGAAGGATGACCTCTCTTTTGCTGGGTACCAGAAACACCTGTCTGCTCC
TGTGCGGCACCTGCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAAC
GAGGTGAAGACAGAGATCAGTGTGAAAGCAAGCACCAGACCCTGCAGGGCCTCGCCTTC
CCCCTGCAGCCTGAGGCCAGCGGGCACTCCAGCAGCTCAAGCAGAAAATGGTCAACTAC
ATCCAGATGAAGCTGGACCTAGAGCGGGAACCATTGAGCTGGTGCACACAGAGCCCACG
GATGTGGCCAGCTGCCCTCCCGGGTGCCCCGAGATGCTGCCCGCTACCACTTCTTCCTC
TACAAGCACACCCATGAGGGCGACCCCTTGAGTCTGTAGTGTTCATCTACTCCATGCCG
GGGTACAAGTGCAGCATCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCCTCCTC
GACTCCGTGGAGCAGGACTTCCATCTGGAGATCGCCAAGAAAATTGAGATTGGCGATGGG
GCAGAGCTGACGGCAGAGTTCCTCTACGACGAGGTGCACCCCAAGCAACACGCCTTCAAG
CAGGCCTTCGCCAAGCCCAAGGGCCAGGGGGCAAGCGGGGCCATAAGCGCCTCATCCGC
GGCCCGGGTGAAAATGGGGATGACAGCTAG

SEQ ID NO: 23_H60215_H

CCACGCGTCCGGCGCCGCAGCCATGGAGGGAGGCGGCGGCGGCGGCGGCGGCTCGGG
TGGCTGCGCTGGGAGGCGGCGGTGAGAGGCTCGCACGCCTCCAGCCCGGCCCCGGCCCCC
CGGGAGGGAGAGCCGAGCAGCCCCGGCTCTGGGCTACGGACTATGGGCGAATAGCTCTGA
CCACCCGGCGAAGTGCACACACCCAGAAGCTATGTCCTTCGGCAGTAAAAGTTTTACAGC
ACAATATATGTGCTCTGCTCTCCTCCCGCAATCCTGCTCCAAGAGATCTTAAGCTGGAGG
CACCAGGTCTGAATTCAGACTCCTCCCCACCACCCACACTTCACCTCCAAGTGGAGCAT
GACCACAGACCCATTGAGGAGGCTGGCGGACTCTTCATCCTGGACAGTCCCTTACTGTA
TGTCAAAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCCGCCA
GGGCCAAGGCTCTAGGAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTC
TCCTTGGTCCCCGTCTGGGCAACTCACCGGTGCCAAGCATAGTGCAGTGTTTGGCGAGGA
AAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCTGGAGGAGAGGGGGGACC
AAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCGAGTACTCAC
TGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACC
GCACCTGTGAAATCGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGC
GCATCTGCCTCGTCTGGACTGCCTCTGTGCTCATGACTTCAGCGATAAGACCGCTGACC
TCATCAACCTGCAGCACTACGTCAATCAAGGAGAAGAGGCTCAGCGAGAGGGAGACTGTGG
TAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGCACA
GAGACCTGAAGCTGGGGAACATGGTGTCTCAACAAGAGGACACATCGGATAACCATCACCA
ACTTCTGCCTCGGGAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGA
GCCCTGCCTACATCAGTCCCGACGTGCTCAGCGGCCCGGCCGTACCGTGGCAAGCCCAGTG
ACATGTGGGCCCTGGGCGTGGTGTCTTTCACCATGCTGTATGGCCAGTTCCTTCTACG
ACAGCATCCCCGAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATAACCATTCCTGAGG
ATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCTTGAACCCC
AGCAGCGCCTGGCCGCCGCCGACGTCTGGAGGCCCTCAGTGCCATCATTGCATCATGGC

FIGURE 2Q

AGTCCCTGTCATCTCTGAGTGGGCCTTTGCAAGTGGTTCCTGACATTGATGACCAAATGA
GCAATGCGGATAGCTCCCAGGAGGCGAAGGTGACGGAGGAGTGCTCCCAGTACGAGTTTG
AGAACTACATGCGTCAGCAGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACACCC
GGAGCTGGGTACCCAAGCGGCAGTTTCGGCAGCGCACACCACCGGTGCGACGGCTGGGCCACG
ACGCACAGCCCATGACCTCCTTGACACGGCCATCCTGGCGCAGCGCTACCTGCGGAAAT
AACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCG
TGGCTGTGAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGC
AGGGACAGGGACAGCCAGGTCACACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTT
TGGGATGATTGCTCGATTGTTTGGTTTTTAAATCTGAGAAGCCTAGATAACTAATCTGCT
TTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTCTCTGGACTGAGC
AAGAGGGAGGAGGGAGCCTGCTCACCCCACTCCAGGGCCTTCCCCAGCGGCCACCAACTG
ACCTGGGGCGCTGCTCCCCACAGTCAAATAAGCTGAAAGTGACGCTCGCTGCAGGCCCC
AGAGCGAGCTTCCCCTCCTCCTGCTCTCCAGGCCCCCTGCCACAGCCTCTTCCGTCCC
TCTCTTTCTGATCCAGGCCCTCAGTCCAAGCTTTGGAAAACCTTCACCTCATCTTAAAC
CAAAC TCAAATATATTTATTTTTTTTACCAT

SEQ ID NO: 24_SGK324_H

GCCGCGATGGCCAGCACCAGGAGTATCGAGCTGGAGCACTTTGAGGAACGGGACAAAAGG
CCGCGGCCGGGGTCGCGGAGAGGGGCCCCCAGCTCCTCCGGGGGCAGCAGCAGCTCGGGC
CCCAAGGGGAACGGGCTCATCCCCAGTCCGGCGCACAGTGCCCACTGCAGCTTCTACCGC
ACGCGGACCCTGCAGGCCCTCAGCTCGGAGAAGAAGGCCAAGAAGGCGCGCTTCTACCGG
AACGGGGACCGCTACTTCAAGGGCCTGGTGTTTGCCATCTCCAGCGACCGCTTCCGGTCC
TTCGATGCGCTCCTCATAGAGCTCACCCGCTCCCTGTGCGACAACGTGAACCTGCCCCAG
GGTGTCGCGCACTATCTACACCATCGACGGCAGCCGGAAGGTCACCAGCCTGGACGAGCTG
CTGGAAGGTGAGAGTTACGTGTGTGCATCCAATGAACCATTTTCGTAAAGTCGATTACACC
AAAAATATTAATCCAACTGGTCTGTGAACATCAAGGGTGGGACATCCCGAGCGCTGGCT
GCTGCCTCCTCTGTGAAAAGTGAAGTAAAAGAAAGTAAAGATTTTCATCAAACCCAAGTTA
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AAGACTGCTCATTCTTTGAACAAGTCTTAACAGATATCACCGAAGCCATTAAACNAGCC
TCAGGAGTCGTCAAGAGGCTCTGCACCTGGATGGAAAGCAGGTGAGAGTTACGTGTGTG
CATCTGCCAGACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTT
CGTTATGCCCAAGATGACTTTGTCTGGATCATAGTGAATGTCGTGTCTGAAGTCATCT
TATTCTCGATCCTCAGCTGTTAAGTATTCTGGATCCAAAAGCCCTGGGCCCTCTCGACGC
AGCCAGATTTCTGCTCATGGCAGATCTTCTTCCAATGTAAACGGTGGACCTGAGCTTGAC
CGTTGCATAAGTCTGAAGGTGTGAATGGAAACAGATGCTCTGAATCATCAACTCTTCTT
GAGAAATACAAAATTGGAAAGGTCATTGGTGATGGCAATTTTGCAGTAGTCAAAGAGTGT
ATAGACAGGTCCACTGGAAAGGAGTTTGCCCTAAAGATTATAGACAAAGCCAAATGTTGT
GGAAAGGAACACCTGATTGAGAATGAAGTGTCAATACTGCGCCGAGTGAAACATCCCAAT
ATCATTATGCTGGTTCGAGGAGATGGAAACAGCAACTGAGCTCTTCTGGTGATGGAATTG
GTCAAAGGTGGAGATCTCTTTGATGCAATTACTTCGTGACCAAGTACACTGAGAGAGAT
GGCAGTGCCATGGTGTACAACCTAGCCAATGCCCTCAGGTATCTCCATGGCCTCAGCATC
GTGCACAGAGACATCAAACCAGAGAATCTCTTGGTGTGTGAATATCCTGATGGAACCAAG
TCTTTGAAACTGGGAGACTTTGGGCTTGCGACTGTGGTAGAAGGCCCTTTATACACAGTC
TGTGGCACACCCACTTATGTGGCTCCARAAATCATTGCTGAAACTGGCTATGGCCTGAAG
GTGGACATTTGGGCAGCTGGTGTGATCACATACATACTTCTCTGTGGATTCCCACCATTC
CGAAGTGAGAACAATCTCCAGGAAGATCTCTTCGACCAGATCTTGGCTGGGAAGCTGGAG
TTTCCGGCCCCCTACTGGGATAACATCACGGA CTCTGCCAAGGAATTAATCAGTCAAATG
CTTCAGGTAAATGTTGAAGCTCGGTGTACCGCGGGACAAATCCTGAGTCACCCCTGGGTG
TCAGATGATGCCTCCCAGGAGAATAACATGCAAGCTGAGGTGACAGGTAAACTAAAACAG
CACTTTAATAATGCGCTCCCCAAACAGAACAGCACTACCACCGGGTCTCCGT CATCATG

FIGURE 2R

GTGAGTGGAAGGCGGCAGGTCTGGCCTGACTGCGGAGCCGGCCTTGAAGTTTTTGAATTA
GGTAGCCGGGAGCTGCCCTCACATGGAAGTTGGTGCCCTCCGTAAGTCTATTTTCATATGA
AGATTGGCTTGGCATGTGGAGGGCACTCATTGCGCAACTCCCAGGCTTTGGGCACTGTGT
GGAGGGGCTTGTGTAGGGACCAGCAGGCCTGGTGTGAGGGGTCCAGGCGTCAAGGAGCTC
CTGGCTGGGCCCTCTGGGCAGCTGCTTCCACTCTTGTCTCTGCCTTCTCATCTAGAGAGA
CTCCCAAGCCCTGGAGGGGTGTGTTGTGTTAGGAATTAACTCCCTGCCTACCCCAAGGCC
TCAGAAATAGATTATTAGAGATGTGAATTATTCTTTGAGACTTGGGATAAGAAACAGCCA
AAGCTAAACATATTTTCAAGTTTTAAAAAATCAGTGTTTTATAAAACACAGTTTGGGGCTTT
TAAAGGTACATAATCAAGGAAAAAATATATATTTCATTTTTTCAAGGTTGGTAACATTTTA
TGAGATGTCAGTGACAACGATGGCCTTATTTTTTTTCAGCCTTTTCTTCTTCCAAAATGTT
TCTTAAGGCAACTCTCCTAAATACATAAACACAACAAATTTAAATGAAAAGTGACATGAG
AGTAAATGAATCAAAAGGAAAAAATATTGAACCAGAGGTGAGGGCAGCACACCCCGCAGCA
GCTGTCCAGGCCTGAGCCAATGCAACCCCTGGGCGGGAAGGCCAGCTCACCGTGAGCAGGT
AGAAGCCAGCCAGCCACCCAGGCAGGGACCTTGGTTCTCCCCACACACTCCCAGGAGCAG
GGAACAGGGGTGGAGTGGCCTTTCCAGAGCTGGAGTTGGCTGCAGCAGCTTTCGAATCA
GACCTGCCAAGGTGATGGGCGTCTGAGTTTACATCTGGGCCCCCGTGACCCCACTGAG
TCCTGACAGCTAAGGATGGGCCACCTCCACAGCTCCGTCACTCGTACTTGGGACAGGCCT
CTCATCTCTGGGAAGGTCTCTCTTGTCTTCTTACCCAACTAGAAGGGAAACAGTGGCATA
TTCTCATGGTACATGGTTGTCTGAAAGCCTTACCTAGGAAGACGCAGGGTCTAGATAGAA
GCTATAAGGAAGCCACACACATAACCCACATCCCCACACCCCAACATCCCCCACACTCC
CCACACCCCCCACACCCCCACATCCCCACCATAATTACCCCCACCTCCAAATATCTCAT

SEQ ID NO: 25_W30246_M SGK324_M

ACCAAGTCTCTCAGCTCCTCTCCAACCAGCCCGGAAGTTTCAGAGGATTGAAGATTTCT
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CCTGAAGGTGTGAATGGAAACCGGTGCTCCGAGTCGTTCCCCCTTCTGGAGAAATACAGA
ATAGGGAAGGTTCATCGGGGACGGCAACTTCGCGGTAGTTAAGGAGTGCCTGGACAGGTAC
ACTGGAAGAGATTTGCATTAAAGATTATAGACAAAGCCAAATGCTGTGGAAAGGAGCAT
CTGATTGAGAACGAAGTGTCAATCCTGCGCGAGTGAAGCACCCCAACATCATCATGTTG
GTTGAAGAGATGGAAACAGCAACTGACCTCTTCTAGTGATGGAAGTGGTCAAAGGTGGA
GATCTCTTTGATGCGATTACCTCTTCAACCAAGTACACTGAGAGAGATGGAAGCGCCATG
GTGTACAACCTAGCCAATGCCCTCCGGTACCTGCACAGCCTCAGCATCGTCCACAGGGAC
ATCAAGCCTGAGAATCTGCTGGTGTGCGAATACCCAGATGGAACCAAGTCTTTGAAGCTG
GGAGACTTTGGGCTGGCGACGGTGGTTGAAGGCCCGTTGTACACGGTCTGTGGCACGCCA
ACTTATGTGGCACCAGAGATCATAGCTGAAACAGGTTATGGCCTGAAGGTGGATGTTTGG
GCAGCTGGTGTGATTACATACATACTTCTCTGTGGATTCCCACCATTCGGGAGTGAGAAC
AATCTCCAGGAAGATCTCTTTGACCAGATCTTGGCTGGAAAGCTGGAATTCACAGCCCCC
TACTGGGACAACATTACAGACTCTCCTTGTGTGTGTTTTAGGAAATGCTTATGAAGCTGG
CCCGTGGGCTTCCAGTGGGACGTGCAGCAGTTCTTGGCAGAGCAGGGCCAGCTCTGCTG
TGTCATCTCCAGGGTCTCCCATCACCTCTGCTCTTTGCCATGGCAGGTCTGCTGAGACCC
CGCGGGGACGGGGGCATGGTGTCTCCCTGATTGGCCTGTGACCAACCTTCTGGAAGGCTGC
TGGCAGTTTTCCCTGTTTTCCACCACCCCACTCTTTTAAATAATTGTATATAACTGTACT
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SEQ ID NO: 26_AA383293_H

CCAGCAGCCAAGGGTAGTGGTGTACCGGAATGGGGACCCATTCTTCCCAGGCTCCCAG
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GCTGTGCAGGCCCCACTGGCTGTGCGTGGCCTCTACACACCTTGTTCATGGCCACCCTGTC
ACCAACCTGGCAGACTTGAAGAACAGAGGGCAGTATGTGGCCGCTGGATTTGAACGATTC

FIGURE 2S

CACAAGCTCCCCCTTACCAGGCTTTTTGTCTCAGTGTGTTTTCAGGAATGGGGACCTGGTA
AGTCCCCCATTTAGTCTGAAGCTGTCCCAGGCTGCCAGCCAGGACTGGGAAACTGTGTTG
AAGCTCCTGACTGAGAAGGTCAAGTTGCAGAGTGGGGCTGTGAGACTCTGCACCCTAGAG
GGGCTCCCACTGTTCAGCAGGGAAGGAGCTGGTAACTGGCCATTACTATGTGGCTGTCCGA
GAGGATGAGTTCAAGGACCTTCCCTATCCAGCTCTGTCCACAAGAGGGCTCCTGGCAGCA
GGCAATGAAGCCCACCTGAGGAGTGGAGTGGGGACTGTGCTGGTTCCCCAAGCCTCTT
GGAAGGAAGGCTAAGAAGGAGACATGCCTAATCGTGACCCTGACCCTGAAATACCAGCAG
TCAGAAACAAGCAGAGACGGGCAATCATTCCCATCAGGAGTTATAGGAGTATATGGAGCT
CCCCACCGAAGGAAGGAGACAGCGGGGGCCCTGGAAGTAGCAGATGATGAAGACACTCAG
ACAGAGGAGCCCTTGGATCAGAGGGCAGCACAGATAGTGAACAGGTTACTTGTCTGCAA
GACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTTTCGTTATGCC
CAAGATGACTTTGTCTGGATCATAGTCGTCGACGGCTCCTGAGAGAGCACCAGGCGGGC
TTTGAGAAGCTCCGCAGGACCCGAGGAGAAGAGAAGGAGGCAGAGAAGGAGAAAAAGCCA
TGTATGTCTGGAGGCAGAAGGATGACTCTCAGAGATGACCAACCTGCAAAGCTAGAAAAG
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CCCATGGGCATCATTGCCGCCAATGTGGAAGCAATTATGAGACTGGCCGGGTGCTTGGG
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GACATGGAATCTACCTGATCCTGGAGTACGTGCAGGGAGGAGACCTTTTTGACGCCATC
ATAGAAAGTGTGAAGTTCCCGGAGCCCGATGCTGCCCTCATGATCATGGACTTATGCAAA
GCCCTCGTCCACATGCACGACAAGAGCATTGTCCACCGGGACCTCAAGCCGGAACCTT
TTGGTTCAGCGAAATGAGGACAAATCTACTACCTTGAAATTGGCTGATTTTGGACTTGCA
AAGCATGTGGTGAGACCTATATTTACTGTGTGTGGGACCCCAACTTACGTAGCTCCCGAA
ATTCTTTCTGAGAAAGGTTATGGACTGGAGGTGGACATGTGGGCTGCTGGCGTGATCCTC
TATATCCTGCTGTGTGGCTTTCCCCCATTCCGCAGCCCTGAXXGAGGGGACCAGGACGAG
CTCTTTAACATCATCCAGCTGGGCCACTTTGAGTTTCTCCCCCTTACTGGGACAATATC
TCTGATGCTGCTAAAGATCTGGTGAGCCGGTTGCTGGTGGTAGACCCCAAAAAGCGCTAC
ACAGCTCATCAGGTTCTTCAGCACCCCTGGATCGAAACAGCTGGCAAGACCAATACAGTG
AAACGACAGAAGCAGGTGTCCCCCAGCAGCGATGGTCACTTCCGGAGCCAGCACAAGAGG
GTTGTGGAGCAGGTATCATAGTCACCACCTTGGGAATCTGTCCAGCCCCCAGTTCTGCTC
AAGGACAGAGAAAAGGATAGAAGTTTGAGAGAAAAACAATGAAAGAGGCTTCTTCACATA
ATTGGTGAATCAGAGGGAGAGACACTGAGTATATTTTAAAGCATATTAAAAAATTAAGT
CAATGTTAAATGTCAACATATTTTTAGATTTGTATATTTAAAGCCTTTAATACATTTT
TGGGGGGTAAGCATTGTCTCAGTGAGGAATTTTGGTAATAATGATGTGTTTTGCTTCCC
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CTGTGAGATTAATAAGGTGCATTG

SEQ ID NO: 28_AA197883_M

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TGCTTAAGCTCGAAGATCTCTGAGAGAAAGCTGCCAGGCCCTGGTTACCTGCGGGACGA
GGACCTCTGGAGAAGCCAGTTCTGGGGCCACGTGGTGCCGTCATGCCGCTGTTACGCCCT
CAGAGCAGCCTCCACTCAGTCCGCGCAGAGCACAGCCCACTGAAGCCCAGGGTGGTGACG
GTGGTGAAGCTGGGTGGGCAGCCCTCCGTAAGGCCACCCCTGCTCCTCAACCGGCGCTCA
GTGCAGACCTTTGAGCAGCTCCTATCAGACATCTCCGAAGCCTTGGGCTTCCCACGCTGG
AAGAACGACCGTGTGCGGAAGCTGTTACCCCTCAAGGGCAGGGAGGTGAAGAGTGTGTCT
GACTTCTTCCGGGAGGGTGTGCTTTTATAGCTATGGGCAAAGAGCCGCTGACATTGAAG
AGTATCCAGTTGGCCATGGAGGAGCTGTATCCTAAGAACCGGGCTCTTGCCCTGGCCCT
CACAGTAGAGTCCCCTCCCCAAGGCTGAGAAGCAGACTTCCCAGCAAGCTTCTGAAAGGA

FIGURE 2T

AGTCACCGCTGTGGGGAGGCAGGAAGCTATAGCGCGGAAATGGAGAGTAAGGCAGTCTCT
AGGCATCAGGGCAAGACTTCCACAGTGCTGGCCCCAGAAGACAAGGCGAGGGCCCAGAAG
TGGGTAAGAGGGGAAACAGGAGTCAGAACCTGGTGGCCCGCCTTCACCCGGGGCAGCCACT
CAGGAGGAGACTCATGCAAGTGGAGAGAAACATCTGGGGGTGGAGATCGAAAAGACCTCC
GGGGAGATTGTGAGATGTGAGAAGTGTAAGAGAGAAAGAGAGCTGCAGTTGGGCCTGCAG
AGGGAGCCGTGCCCCGCTGGGAACCAAGTGCAGTGGACCTGGGGAGAGCTCAGAAGAGGGAT
TCCGAGAAGTTGGTGAGGACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT
GGAGAGGAAGGGTGGAAAGGTGACAGCCATCGGGGCAGTCCCAGGGACCCCCCTCAGGAA
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AGTTATCCTCAGGGGGCACCCAAGGCCCAGAAGGACTTCGTGGAAGGGCCACCAGCTGTA
GAGGAGGGGCCGATAGACATGAGGAGAGAGGACCGGCACACATGCAGGAGCAAGCATGCC
GCCTGGCTCCGGAGAGAGCAGCAGGCCGAACCCCCACAGCTCCCAGAACCCGAGGGGAG
GAGAAGCAAGCAGAGCACGAGAAGAAGCCAGGCGGCTTAGGAGAGAGGAGGGCGCCAGAG
AAGGAGTCTAAGAGGAAGCTAGAAGAGAAGAGGCCAGAACGACCCAGTGGCCGGAAGCCG
AGGCCCAAGGGCATCATCTCAGCGGATGTGGAGAAGCACTATGACATAGGTGGGGTCATT
GGGGATGGCAACTTTGCCACCGTGAAGGAATGCAGGCACCGAGAGACCAAGCAGGCTTAC
GCCATGAAGATGATTGACAAGTCCCAGCTGAAGGGTAAGGAGGACATTGTGACAGTGAG
ATTTTAATCATCCAGAGTCTCTCTCATCCCAACATTGTGAACTGCATGAGGTCTACGAA
ACGGAGGCGGAGATCTACCTGATCATGGAGTATGTGCAGGGAGGGGACCTTTTTGTATGCC
ATCGTTGAAAATGTGAAGTTTCCAGAGCCCGAGGCTGCAGTTATGATCACAGACTTGTGT
AAGGCCCTTCGTCCACATGCACGACAAGAATATCGTCCACCGGGACGTGAAACCAGAAAAC
CTCCTGGTTCAGCGAAATGAAGACAAGTCTATCACCTTGAAGCTGGCTGATTTTGGCTTG
GCCAAATATGTGGTGAGGCCTATATTTACTGTGTGTGGGACGCCAACATATGTAGCTCCT
GAAATTCTTTCTGAGAAAGGTTACGGCCTGGAGGTGGACATGTGGGCGGCAGGTGTGATC
CTATACATCCTCTTGTGTGGCTTCCCCCTTTCCGAAGTCTTGAGAGGGACCAAGACGAG
CTCTTCAACATCATCCAAGTGGGCCAGTTTGAGTTCCCTCTCTCCTTACTGGGACAACATT
TCTGATGCTGCCAAAGATCTGGTGAGAAATTTGCTGGAGGTGGACCTAAGAAGCGGTAC
ACGGCCGAACAGGTCTTACAGCATCCCTGGATTGAGATGGTTGGGCATACCAACACAGGG
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GTTGCAGAGCAGATGCCATAA

SEQ ID NO: 29_DRAK2_H

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GAGCTAGAGAACTCGTCCTGTGGCGGCCCCCGGCGTGGGGCGGGACAGCGGCCCCCTGGA
GGGGGCAGTCCCGGGAGAACCTGCGGCGGCGGAGCGGTAAAAATAAGTGACTAAAGAAG
CAGACCTGGGAATCACCTAACATGTGAGGAGGAGATTTGATTGCCGAAGTATTTACAGGC
CTACTAACTACAACCTCTCAAATTTCAATAAAAAATGGAAAACTTTAATAATTTCTATATA
CTTACATCTAAAGAGCTAGGGAGAGGAAAATTTGCTGTGGTTAGACAATGTATATCAAAA
TCTACTGGCCAAGAATATGCTGCAAAAATTTCTAAAAAAGAGAAGAAGAGGACAGGATTGT
CGGGCAGAAATTTTACACGAGATTGCTGTGCTTGAATTGGCAAAGTCTTGTCCCCGTGTT
ATTAATCTTCATGAGGTCTATGAAAATACAAGTGAAATCATTTTGATATTGGAATATGCT
GCAGGTGGAGAAAATTTTACGCCTGTGTTTACCTGAGTTGGCTGAAATGGTTTCTGAAAAT
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ATTGTACACCTTGATTTAAAGCCACAGAATATATTACTGAGCAGCATATACCTCTCGGG
GACATTAAATAGTAGATTTTGGAAATGTCTCGAAAATAGGGCATGCGTGTGAACCTTCGG
GAAATCATGGGAACACCAGAATATTTAGCTCCAGAAATCCTGAACCTATGATCCATTACC
ACAGCAACAGATATGTGGAATATTGGTATAATAGCATATATGTTGTTAACTCACACATCA
CCATTTGTGGGAGAAGATAATCAAGAAACATACCTCAATATTTCTCAAGTTAATGTAGAT
TATTCGGAAGAACTTTTTCATCAGTTTACAGCTGGCCACAGACTTTATTCAGAGCCTT

FIGURE 2U

TTAGTAAAAAATCCAGAGAAAAGACCAACAGCAGAGATATGCCTTTCTCATTCTTGGCTA
CAGCAGTGGGACTTTGAAAACCTTGTTTCACCCTGAAGAACTTCCAGTTCCTCTCAAAC
CAGGATCATTCTGTAAGGTCCTCTGAAGACAAGACTTCTAAATCCTCCTGTAATGGAACC
TGTGGTGATAGAGAAGACAAAGAGAATATCCCAGAGGATAGCAGCATGGTTTCCAAAAGA
TTTCGTTTTCGATGACTCATTACCCAATCCCATGAACCTGTTTCAGATTTGCTCTGTTAG
CACTTTTTTCTTTGACTCATTGACTGAATTTGAAATTTTATATCCACTCCAGTGAGAT
TATGATTTGTAGCTTCATATATGACATGTTTATATTGTAAATGCACTTTTCCATGGAATA
ATTTAGGGAAGTGTTTAAATGTTAAATTACTAGTTGCTAGCATGTTATGATTTTCATATCC
TGAGATAGCTCTGCAGATAAGAAAATATTTAAATATATGACAAAAAGTAAATTTGTACAT
GTGAAAG

SEQ ID NO: 30_W44160_M_DRAK2_M

CCAGACGCGGCTGCACCTTTCAAACCTCAACTGTAAGAAGCGTCGGTCAGCGTCTGTGCG
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GAGTGCGAGGTAAGAGTCTGCCCTAGAGAAGCAGGTCTGGCAGTCATCAACATGTCTCGGA
GGAGATTCGATTGCCGAAGTGCTCAGGCTTGCTAACTACAACCCCTCAAACGCCGATTA
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TTGCTGTGGTTAGACAATGTATATCAAAATCAACTGGACAAGAGTATGCTGCCAAATCCC
TGAAAAAGAGGAGAAGAGGGCAGGATTGCCGGGCGGAAATCTGCATGAGATAGCTGTGC
TGGAGCTGGCCAGGTCTTGTCGCCACGTGATTAATCTGCATGAGGTCTACGAAAATGCAA
CGGAAATCATTTTGGTGTTAGAATATGCTGCGGGTGGAGAAATTTTCAACCTGTGTTTAC
CTGAGTTAGCCGAAATGGTATCTGAAAATGATGTTATCAGACTCATTAAACAAATCCTTG
AAGGAGTTCATTATCTACATCAGAATAACATTGTTACCTTGATTAAAGCCACAGAATA
TACTTTTGAGCAGTATATACCCACTCGGGGACATAAAAATTGTAGATTTTGAATGTCTC
GAAAAATTGGGAATGCAAGTGAGCTTCGGGAAATCATGGGAACACCTGAATACTTAGCTC
CAGAAATCCTCAACTATGATCCCATACCACAGCAACAGATATGTGGAATATTGGCATAA
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ATCTGAATATTTCTCAAGTGAATGTAGATTATTCAGAAGAAATGTTTTCATCAGTTTCAC
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CAGAATCCTGCCTATCCCACTCATGGCTGCAGCAGTGGGACTTTGGAAGCTTGTTTCATC
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AGACCTCCAAGTCCCTCTGTAATGGGAGCTGTGGAGCCCGGGAGGACAAGGAGAACATCC
CTGAAGATGGCAGCTTAGTTTCTAAAAGATTTGATTGATGACTCCTTGCCAGCCCCC
ATGAACCTGTTCCAGATTTGTTCTGTTAGCATTTTCTCTGTGACTCATCTGGACTGACT
CGGAAATTTGAAATCTCTGGTGTGAGATTGTGTTTGTAGCTTCATATATTATGTTTATAT
TATAAATGCACTTCTGCTTAGAAGAACCTTAAGGAACAGTTTAAATGCTAGGCTTCTGTTG
GCTAGCATATCATTTCTTGTCCTGAAATTGTTTTGCAGAGGAAAATATTTAAGTATATGA
CAAAAAATGTAAATTGTGTTTAAAGAGAACACATGCAACTGAAAGAATCAAGTTCAGTCA
GACTTATAAAATGGGTTATATTATGGTTAGTAAAAGTTGAAAAAAATGAAAACAGGAAT
TTAGTAGGTTCTAAGGTAAGCCCTATACCATAACTCTATTACAGAGAATCTGTTTGGGGA
AATGCTGTCAAGGGTAAACCACAACATATACTGCTTTATAAATACTCCAGAGAGAGTTTA
TAGTTGAAAGTATTTCCAGTTACCAATAATAGCTTGAAACTGTAAGATTTTCTTTGTGT
GCCATGTGCTCGGTGAGAGGACACAGTCAACCAGAGCAGGGTTGATCCAGGCTGTTTCTC
TGCAACCGAGTCAAACTCGACATCATTTCCAGCTCATGTATTTGTACGTGCATCATA
TATCAGATCTAATAAGATCTGGAAGATGGATATGCAATAAGAGGCCTTTGTCTTCTAGA
ATGATTAGAGTAGAGGAGAATTGGATAGTACAGAATATGCTCTAGTTTCAGTCAGACATA
TTCATAAAGGGAAATGTTAAGTTCTGGCAGCTGACTTAGTGTGGATGTCTCCTAAGTCT
CAGGATAGAAGCCCATCATTAGAGCATAGGCACCTCAGGAATCTTGTGTGAAATCTAG
TGAGTGAGGAGGTGTGACATGCAGCTATCTTTGGGCTCCTTTTGTGTGTGTTCTGCTGGA
CAACACATGGGAGTGTTCAAGTGTGTCGGTGGTCAATATCTATGTTCAAGTCCTGATGG

FIGURE 2V

GAGGGGCCTAGGGACTGCTTTGGAGATTTCCCACTGGTGTCCATTTTAAAGGTCTGTAATA
ATGTCATGTTAAGATAACAGATCTCATAAATATGCTACTCTATCAGACTCCGTTGCCAAA
ACAAATTAAAAGCCTGTGTATTGAAGTGGGTGTTAGTCTAACAACCTGTAAATTCTTGAA
ATTGTTACTAAAATTCCAAATTCCTTTAGATAAATTTAACTATTTAAATTGAGCATTGCT
GTCTTTGTTTGATTAAAGGTTGAGTTCCTTTATATCTGTTATTTTAAAGGAAAAGTTGT
TTGCCCTTTTGTATATGTGTGTGCATATGTGTATGTGTACAGGTATATGTATATATGTATT
GATAGATAAAATACAGCCTTTAAACAACCTTC

SEQ ID NO: 31_H01248_H, DRK1_H

ATGATCCCTTTGGAGAAGCCAGGCAGCGCGGCTCCTCCCCAGGCGCCACCTCAGGCTCG
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CTGTGCCCGGGCCGGGAGCTGGGCAGGGGGAAATTTGCAGTGGTGAGAAAATGTATAAAG
AAAGATTCTGGGAAAGAATTTGCTGCAAAGTTCATGAGAAAAAGAAGAAAAGGCCAAGAT
TGTCGGATGGAAATAATTCATGAGATTGCTGTACTTGAAGTAGCACAAGACAATCCTTGG
GTCATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTAGTTCTGGAATAT
GCTGCTGGGGTGAAATCTTTGACCAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAA
AAAGATGTTCAAAGACTTATGCGACAGATTTTAGAAGGTGTTCACTTTTTACACACTCGT
GATGTAGTTCATCTTGATTTGAAGCCTCAGAATATCTGTTGACAAGTGAATCTCCATTG
GGTGACATTAAGATTGTTGATTTTGGCCTTTCAAGAATATTGAAGAACAGTGAAGAGCTC
CGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATCTTAGTTATGATCCTATA
AGCATGGCAACAGATATGTGGAGCATTGGAGTGTAAACATATGTCATGCTTACAGGAATA
TCACCTTTCTTAGGCAATGATAAACAAGAAACATTCTTAAACATCTCACAGATGAATTTA
AGTTATTCTGAGGAAGAATTTGATGTTTTGTCTGAGTCGGCTGTTGATTTTCATCAGGACA
CTTTTAGTTAAGAAACCTGAAGATCGAGCCACTGCTGAAGAATGTCTAAAGCACCCCTGG
TTGACACAGAGCAGTATTCAAGAGCCTTCTTTCAGGATGGAAAAGGCACTAGAAGAAGCA
AATGCCCTCCAAGAAGGTCAATCTGTGCCTGAAATTAATTCGGATACCGACAAATCAGAA
ACCGAGGAATCCATTGTAACCGAAGAGTTAATTGTAGTTACTTCATATACTCTAGGACAA
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SEQ ID NO: 32_AA021445_H

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CACCATCGGCAAGGGCAACTTCGCGGTGGTCAAGCGGGCCACGCACCTCGTCACCAAGGC
CAAGGTTGCTATCAAGATCATAGATAAGACCCAGCTGGATGAAGAAAACCTGAAGAAGAT
TTTCCGGGAAGTTCAAATTATGAAGATGCTTTGCCACCCCCATATCATCAGGCTCTACCA
GGTTATGGAGACAGAACGGATGATTTATCTGGTGACAGAATATGCTAGTGGAGGGGAAAT
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ACAGATCGTCACAGCTGTCTATTTTTGTCACTGTGCGAACATTGTTTCATCGTGATTTAAA
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ACCTGAACTCTTTGAAGGAAAAGAATATGATGGGCCCCAAAGTGACATCTGGAGCCTTGG
AGTTGTCTCTACGTGCTTGTGTGCGGTGCCCTGCCATTTGATGGAAGCACACTGCAGAA
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GATCTGCAAGCACAAGTGGATGAAGCTAGGGGACGCCGATCCCAACTTTGACAGGTTAAT
AGCTGAATGCCAACAATAAGGAAGAAAGACAGGTGGACCCCTGAATGAGGATGTCTCT
CTTGCCCATGGAGGACATGGGACTGGACAAAGAACAGACACTGCAGTCATTAAGATCAGA

FIGURE 2W

TGCCTATGATCACTATAGTGCAATCTACAGCCTGCTGTGTGATCGACATAAGAGACATAA
AACCCTGCGTCTCGGAGCACTTCCTAGCATGCCCGAGCCCTGGCCTTTCAAGCACCAGT
CAATATCCAGGCGGAGCAGGCAGGTACTGCTATGAACATCAGCGTTCCCCAGGTGCAGCT
GATCAACCCAGAGAACCCTTGTGGAGCCGGATGGGACACTGAATTTGGACAGTGATGA
GGGTGAAGAGCCTTCCCCGAAGCATTGGTGCCTATTTGTCAATGAGGAGGCACACAGT
GGGTGTGGCTGACCCACGCACGGAAGTTATGGAAGATCTGCAGAAGCTCCTACCTGGCTT
TCCTGGAGTCAACCCCGAGGCTCCATTCTGCAGGTGGCCCCCTAATGTGAACCTCATGCA
CAACCTGTTGCCTATGCAAACTTGCAACCAACCGGGCAACTTGAGTACAAGGAGCAGTC
TCTCCTACAGCCGCCCACGCTACAGCTGTTGAATGGAATGGGCCCCCTTGGCCGGAGGGC
ATCAGATGGAGGAGCCAACATCCAACCTGCATGCCAGCAGCTGCTGAAGCGCCACGGGG
ACCTCTCCGCTTGTCAACCATGACACCAGCAGTGCCAGCAGTTACCCCTGTGGACGAGGA
GAGCTCAGACGGGGAGCCAGACCAGGAAGCTGTGCAGAGGTACTTGGCAAATAGGTCCAA
AAGACATACTGGCCATGACCAACCCCTACAGCTGAGATCCACCCGACCTACAACGGCA
GCTAGGACAGCAGCCTTCCGTTCCCGGGTCTGGCCTCCTCACCTGGTACCTGATCAGCA
TCGCTCTACCTACAAGGACTCCAACACTCTGCACCTCCCTACGGAGCGTTTCTCCCCTGT
GCGCCGGTTCTCAGATGGGGCTGCGAGCATCCAGGCCTTCAAAGCTCACCTGGAAAAAAT
GGGCAACAACAGCAGCATCAAACAGCTGCAGCAGGAGTGTGAGCAGCTGCAGAAGATGTA
CGGGGGGAGATTGATGAAAGAACCCTGGAGAAGACCCAGCAGCAGCATATGTTATACCA
GCAGGAGCAGCACCATCAAATTCTCCAGCAACAAATTCAAGACTCTATCTGTCTCTCTCA
GCCATCTCCACCTCTTCAGGCTGCATGTGAAAATCAGCCAGCCCTCCTTACCCATCAGCT
CCAGAGGTTAAGGATTAGCCTTCAAGCCCACCCCCCAACCACCCCAACAACCATCTCTT
CAGGCAGCCAGTAATAGTCTTCCCCCATGAGCAGTGCCATGATCCAGCCTCACGGGGC
TGCATCTTCTTCCAGTTTCAAGGCTTACCTTCCCGCAGTGCAATCTTTCAGCAGCAACC
TGAGAACTGTTCTCTCTCTCCCAACGTGGCACTAACCTGCTTGGGTATGCAGCAGCCTGC
TCAGTCACAGCAGGTACCATCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC
AGGCACAGCTGCAGGCTCCAGTGGGCGCGGCATCTCCATCAGCCCCAGTGCTGGTCAGAT
GCAGATGCAGCACCCTACCAACCTGATGGCCACCCTCAGCTATGGGCACCCTCCCTTGTCT
CAAGCAGCTGAGTGCTGACAGTGACAGGCTCACAGCTTGAACGTGAATCGGTTCTCCCC
TGCTAACTACGACCAGGCGCATTTACACCCCCATCTGTTTTTCGGACCAGTCCCGGGGTTCT
CCCCAGCAGCTACAGCCCTTCAACAGGAGTGGGGTTCTCTCCAACCCCAAGCCCTGAAAAGT
CCCTCCACTTGACCAATTCCCCACCTTCCCTCCCAGTGACATCAGCAGCCGCCACACTA
TACCACGTCGGCACTACAGCAGGCCCTGCTGTCTCCACGCGCCAGACTATAACAAGACA
CCAGCAGGTACCCACATCCTTCAAGGACTGCTTTCTCCCGGCATTGCTCACCGGCCA
CTCGGACATCCGGCTGCCCCCAACAGAGTTTGCACAGCTCATTAAGGAGCAGCAGCAACA
ACGGCAGCAGCAGCAGCAACAGCAGCAACAGCAAGAATACCAGGAACCTGTTACGGCACAT
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CCAGGCTTTATCTTATCAAAATGCTGACTCTTATCACCATCACACCAGCCCCCAGCATCT
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GTATGCTCACCAGCCGGCACTGATGCATTAGAGAGCATGGAGGAGGACTGCTCGTGTGA
GGGGGCCAAGGATGGCTTCCAAGACAGTAAGAGTTCAAGTACATTGACCAAGGTTGCCA
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TGTGAGTCATGCCAAGAATTGGGGATACATCCCTATGGTCATCAGCCAACCTGCTGCATT
CAGTAAAAATAAGGTGCCAGCAGAGAGCCTGTCATAGGGAAGTGCATGGATAGAAGTTC
TCCAGGACAAGCAGTGGAGCTGCCGGATCACAATGGGCTCGGGTACCCAGCACGCCCCCTC
CGTCCATGAGCACCACAGGCCCGGGCCCTCCAGAGACACCACACGATCCAGAACAGCGA
CGATGCTTATGTACAGCTGGATAACTTGCCAGGAATGAGTCTCGTGGCTGGGAAAGCACT
TAGCTCTGCCCCGATGTGCGATGCAGTTCTCAGTCAGTCTTCGCTCATGGGCAGCCAGCA
GTTTCAGGATGGGGAAAATGAGGAATGTGGGGCAAGCCTGGGAGGTATGAGCACCAGCA
CCTGAGTGATGGCAGCCAGCATTTAACTCCTCTTGCTATCCATCTACGTGTATTACAGA
CATTCTGCTCAGCTACAAGCACCCCGAAGTCTCCTTCAGCATGGAGCAGGCAGGCGTGTA

FIGURE 2X

ACAAGAAACAGAGAGTTTTGTGTACAGCTTGGGAATGAAAAGGTTGATTGTAAACCCACA
GTATCTAGCAGCGTTGTGCCAAATTGCCCTTGTGTTTCTCTCCACCCAAAATATCACAGC
TGCTTTTCTCACATTTGGTTCATCCGTGTGCTGTTCTTTTGGGTTCTGAGAGGGTTTTGC
CATGTTTGCCTTGATGACCAAGTCACCAAGGAAATAAACAGGAAGGAAATCCATGTTCTC
C

SEQ ID NO: 33_2R22-5-11_H

CTGGGCGCGTGCCTGAGTCCGCGCCCTGACAGCTCCGGGAGCCTCAAGCGCGACA
GGGCGCCCTCACCTCGGGACATCCACACACCGACCGCTCCTGCTCCAGAGGCAACAACCC
AGCGCGCCTAGCCTGGCGCCGTGCAGCGAAGCCCAAGAGCTGGCCTCGCCACGAAGGTTG
AACCAGCCAAATTTTCGAGACAGCTCACGGCTTAGAGGAAGGTTTCTCTAAATAAAGGCC
GGCTAAAGTGACATTGCAGGGATTAAATCCTTCTTTGGCTGCCTGTGTGACCAGAAGGCT
TATTTGCAAGTTTCTTCTTTCTGGGGTCCAGATTATTAGGCTCTCCAGCGCCCTGCAGCT
TGACAGAAAGAGAAGCATGAAATGAAGGTCAGAGATGAGATCCCGCAGCAGGGACGTGGG
GGCCTCCAGGGGCATTTACGCACCAGAGTGCAAGATTCTCTGGCCATCAAGGGAAATAG
CAAACAGAAGCCTTTGTCTTGGGGCAGCCACCTACCACAAAGCATCAGACTCCACGTC
TGCCAGAAAGTTCTTGAGTCCCATCAGGCCAGTGGGTATGTAACATGTGCCTAATTGT
ACAGCTAGAGCCTGCAAGTTCAACGTGAGGGAAGGTGGGAAATGTCTTGAGTGAGGCGAG
CAGCTCCTGGCTGGGCTGGGCAGACTCAGCTACCACGTTCACTGCCTTCTCTCACTAAA
GCCGAGAGGGAGGCTGCTCAGCTCTCAGGAAAACCTTTTTGAACCCTGGGCACCTGCTGT
CCTCAGTTGGCATCTCCACCCCTCTGAGCCTCTTCTGCTCCTGCACAACCTGCCTCTTCG
CTGAGATGGAGACGTGAGCCCCGTGGACGATGACTGCAGTGTATATGAATGGAGGTGGC
CTGGTGAACCCCCACTATGCCCGGTGGGATCGGCGCGACAGTGTAGAAAGTGGCTGTGAG
ACCGAGAGTAGCAAGGAGGGTGAGGAGGGACAGCCCCGCCAGCTGACGCCCTTCGAGAAA
CTGACACAGGACATGTCCAGGATGAGAAGGTGGTGAGGGAGATCACGCTGGGGAAACGG
ATAGGCTTCTACCGAATTCGAGGGGAAATCGGAAGTGGAAACTTCTCCCAAGTGAAGCTT
GGGATTCACCTCCCTAACCAAGAAAAGGTGGCCATTAAGATCCTGGACAAGACCAAGTTA
GACCAGAAAACCCAGAGGCTACTATCCCAGAAAATCTCCAGCATGGAAAAGCTGCACCAT
CCCAACATCATCCGCCTTTACGAAGTGGTGGAGACCCTATCCAAGCTGCACTTGGTGATG
GAGTATGCAGGGGGTGGGGAGCTCTTCGGAAAAATTAGCACTGAGGGGAAGCTCTCTGAA
CCAGAAAGCAAGCTCATCTTCTCCAGATTGTGTCTGCCGTGAAGCACATGCATGAAAAC
CAAATTATTCATAGAGATCTGAAAGCAGAAAATGTATTCTATACCAGTAATACTTGTGTG
AAGGTGGGCGATTTTGGATTGAGCACAGTAAGCAAAAAAGGTGAAATGCTGAACACTTTC
TGTGGGTCTCCTCCCTACGCTGCGCCTGAACTCTTCCGGGACGAGCACTACATCGGCATT
TACGTGGATATCTGGGCCTTGGGGGTGCTTTTGTACTTCATGGTGAAGTGGCACCATGCCA
TTTCCGGCAGAAACCGTGGCCAACTAAAAAAGAGCATCCTCGAGGGCACATACAGTGTA
CCGCCGCACGTGTGAGAGCCCTGCCACCGACTCATCCGAGGAGTCCCTTCAGCAGATCCCC
ACGGAGAGGTACGGAATCGACTGCATCATGAATGATGAATGGATGCAAGGGGTGCCATAC
CCTACACCTTTGGAACCTTTCCAACCTGGATCCCAACATTTGTTCGGAAACAGCACTCTC
AAGGAAGAAGAAAATGAGGTCAAAAGCACTTTAGAACATTTGGGCATTACAGAAGAGCAT
ATTGCAAAATAACCAAGGGAGAGATGCTCGCAGCTCAATCACAGGGGTCTATAGAATTATT
TTACATAGAGTCCAAAGGAAGAAGGCTTTGGAAAGTGTCCCAGTCATGATGCTACCAGAC
CCTAAAGAAAGAGACCTCAAAAAAGGGTCCCGTGTCTACAGAGGGATAAGACACACATCC
AAATTTTGCTCGATTTTATAAATTGCACTAGACTGCTTGTAACCTAACCAAGATGATTGTT
GCTGCTTCTAAATTTTTTTTCAAGGACAACTTGAGTGGAGACATTTTTTGTAATTTTTAAAT
AAACTTAAATTTGAGATATGCAAAAAA

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ATGTCCACTAGGACCCCATTTGCCAACGGTGAATGAACGAGACACTGAAAACCACACGTCA
CATGGAGATGGGCGTCAAGAAGTTACCTCTCGTACCAGCCGCTCAGGAGCTCGGTGTAGA

FIGURE 2Y

AACTCTATAGCCTCCTGTGCAGATGAACAACCTCACATCGGAACTACAGACTGTTGAAA
ACAATCGGCAAGGGGAATTTTGCAAAAGTAAATTTGGCAAGACATATCCTTACAGGCAGA
GAGGTTGCAATAAAAAATAATTGACAAAACCTCAGTTGAATCCAACAAGTCTACAAAAGCTC
TTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATCCCAATATAGTGAAGTTATTCGAA
GTCATTGAAACTGAAAAAACACTCTACCTAATCATGGAATATGCAAGTGGAGGTGAAGTA
TTTGAATTTTGGTTGCACATGGCAGGATGAAGGAAAAAGAAGCAAGATCTAAATTTAGA
CAGATTGTGTCTGCAGTTCAATACTGCCATCAGAAACGGATCGTACATCGAGACCTCAAG
GCTGAAAATCTATTGTTAGATGCCGATATGAACATTAAATAGCAGATTTCCGTTTGTAGC
AATGAATTTACTGTTGGCGGTAAACTCGACACGTTTGTGGCAGTCCTCCATACGCAGCA
CCTGAGCTCTTCCAGGGCAAGAAATATGACGGGCCAGAAGTGGATGTGTGGAGTCTGGGG
GTCATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGGGCAAAACCTAAAGGAA
CTGAGAGAGAGAGTATTAAGAGGGAAATACAGAATTCCTTCTACATGTCTACAGACTGT
GAAAACCTTCTCAAACGTTTCTGGTGCTAAATCCAATTAAACGCGGCACTCTAGAGCAA
ATCATGAAGGACAGGTGGATCAATGCAGGGCATGAAGAAGATGAACTCAAACCATTGT
GAACCAGAGCTAGACATCTCAGACCAAAAAAGAATAGATATTATGGTGGGAATGGGATAT
TCACAAGAAGAAATTCAAGAATCTCTTAGTAAGATGAAATACGATGAAATCACAGCTACA
TATTTGTTATTGGGGAGAAAACTTTCAGAGCTGGATGCTAGTGATTCCAGTTCTAGCAGC
AATCTTTCACTTGCTAAGGTTAGGCCGAGCAGTGATCTCAACAACAGTACTGGCCAGTCT
CCTCACCAAAAGTGCAGAGAAGTGTCTTCAAGCCAAAAGCAAAGACGCTACAGTGAC
CATGCTGGACCAGCTATTCTTCTGTTGTGGCGTATCCGAAAAGGAGTCAGACAAGCACT
GCAGATGGTGACCTCAAAGAAGATGGAATTTCTCCCGGAAATCAAGTGGCAGTGCTGTT
GGAGGAAAGGGAATTGCTCCAGCCAGTCCCATGCTTGGGAATGCAAGTAATCCTAATAAG
GCGGATATTCTGAACGCAAGAAAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT
GGAATGACACGACGAAATACTTATGTTTGCAGTGAGAGAACTACAGCTGATAGACACTCA
GTGATTGAGAATGGCAAAGAAAACAGCACTATTCTGATCAGAGAACTCCAGTTGCTTCA
ACACACAGTATCAGTAGTGACGCCACCCAGATCGAATCCGCTTCCCAAGAGGCACTGCC
AGTCGTAGCACTTTCACGGCCAGCCCCGGGAACGGCGAACCAGCAACATATAATGGCCCT
CCTGCCTCTCCAGCCTGTCCCATGAAGCCACACCATTGTCCAGACTCGAAGCCGAGGC
TCCACTAATCTCTTTAGTAAATTAACCTCAAACTCACAAGGAGTCGCAATGTATCTGCT
GAGCAAAAAGATGAAAACAAGAAGCAAAGCCTCGATCCCTACGCTTACCTGGAGCATG
AAAACCACTAGTTCAATGGATCCCGGGGACATGATGCGGGAAATCCGCAAAGTGTTGGAC
GCCAATAACTGCGACTATGAGCAGAGGGAGCGCTTCTTGCTCTTCTGCGTCCACGGAGAT
GGGCACGCGGAGAACCCTCGTGAGTGGGAAATGGAAGTGTGCAAGCTGCCAAGACTGTCT
CTGAACGGGGTCCGGTTTAAGCGGATATCGGGGACATCCATAGCCTTCAAAAATATTGCT
TCCAAAATTGCCAATGAGCTAAAGCTGTAA

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AAAGGGCCGTCCTGGTCCAGCCGTTCCCTGGGTGCCCGTTCGCGGAACTCTATCGCTTCC
TGCCCTGAGGAACAACCCCATGTGGGCAACTATAGGCTGCTAAGGACCATCGGGAAGGGC
AACTTCGCCAAAGTCAAGCTGGCTCGGCATATCCTCACGGGCCGGGAGGTGCTATTAAAG
ATCATTGATAAGACCCAGCTGAACCCAGTAGCTTGCAAGAGCTGTTTCAAGAGAAGTCCGA
ATTATGAAGGGACTCAACCACCCCAACATCGTGAAGCTTTTTGAGGTGATAGAGACGGAG
AAGACGCTATACCTGGTGATGGAATACGCTAGCGCAGGAGAAGTGTGTTGACTACCTCGTG
TCGCACGGCCGATGAAGGAGAAGGAGGCTCGAGCCAAGTTCCGGCAGATCGTGTACGCC
GTGCACTACTGTATCAGAAGAACATTGTACACAGGGATCTAAAGGCTGAAAACCTGTTG
CTGGATGCCGAGGCCAACATCAAAATCGCCGACTTCGGCTTCAGCAATGAGTTCACGCTG
GGCTCCAAGCTGGACACCTTCTGTGGGAGCCCCCATACGCCGCCAGAGCTGTTCCAG
GGCAAGAAGTATGATGGGCCAGAGGTGGACATCTGGAGCCTGGGTGTATCCTGTACACG
CTGGTCAGCGGCTCCCTGCCCTTCGATGGGCACAACCTCAAGGAGCTGCGGGAGCGAGTC
CTCAGAGGAAAGTACCGGGTCCCTTCTACATGTCTACAGACTGCGAGAGCATTCTGCGG

FIGURE 2Z

AGATTTCTGGTGTGAACCCCGCAAAACGCTGTACTCTGGAGCAAATCATGAAAGACAAA
TGGATCAACATCGGCTATGAGGGTGAGGAGCTGAAGCCAGACACGGAGCTCAAAGAAGAG
CGGATGCCGGGTTCGGAAAGCGAGCTGCAGTGCAGTGGGCAGTGGGAAGTCGAGGCTTGCCC
CCCTCCAGCCCCATGGTCAGCAGTGGCCACAACCCCAATAAGGCAGAGATCCCTGAGCGG
CGGAAGGACAGCACTAGCACCCCTAACAACCTCCCCCCCAGCATGATGACCCGAAGAAAC
ACCTATGTGTGCACAGAGCGACAGGATCTGAACGCCCCGTCTTGTGTCCAAATGGCAAA
GAAAATAGCTCCGGTACCTCGCGGGTGCCCCCTGCCTCGCCTTCAGTCATAGCCTGGCT
CCCCCGTCAGGCGAGCGGAGCCGCTGGCTCGGGGCTCCACCATCCGCAGCACCTTCCAT
GGGGGCCAGGTCCGAGACCGGCGGGCAGGGAGCGGGAGTGGCGGGGGTGTGCAGAATGGA
CCCCCAGCCTCACCCACGCTTGCCACGAGGCCGACCCCTGCCCTCCGGGCGGCCTCGC
CCCACCACCAACCTCTTACCAAGCTGACCTCCAACTGACCCGAAGGGTCACAGACGAA
CCTGAGAGAATCGGGGGACCTGAGGTACAAGTTGCCATCTACCTTGGGATAAAACGGAA
ACCGCCCCCAGGCTGCTCCGATTCCCCTGGAGTGTGAAGCTGACCAGCTCGCGACCTTCC
TGAGGCCCTGATGGCTGCCCTGCGACAGGCCACA

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GTAGCCGGCTTGCGCTGACCGTCGCTGATCCAGTTGTTAGAGGTGGAAGCTTGGCAGTT
GGCCTCCCTTCTTCCCATGGAGGTGCGGGGCTTAACAGTCTTTGAAGAGGACCAGAGATG
CCTTTCCAGAGCCTCCCCCTTGCCAGTGTGAGCAGAGGGCCAGCTGCACAGACCACTGC
TGAGCCCAGCAGGTGCTTTTCTCAGCCACAGACACCTGAGCAGAAGGAATGGGCTTTC
CAGACTCTGCCAGAGCAGGACGGCGCTCTCTGAAGACAGATGGAGCTCCTATTGTCTATC
ATCACTGGCTGCCAGAATATTTGTACAAGTAACTGCACTGCCCTGCTGCCCCTGAGCA
CACGGACCCGTCCGAACCGCGGGGCAGTGTGTCTGCTGCTCCCTGCTGCGGGGACTGTC
CTCAGGGTGGTCTCCTCTGCTTCCGGCCCCCTGTGTGCAACCCTAACAAGGCCATCTT
CACGGTGGATGCCAAGACCACAGAGATCCTCGTTGCTAACGACAAAGCTTGCGGGCTCCT
GGGGTACAGCAGCCAGGACCTGATTGGCCAGAAGCTCACGCAGTTCTTTCTGAGGTGAGA
TTCTGATGTGGTGGAGGCCCTCAGCGAGGAGCACATGGAGGCCGACGGCCACGCTGCGGT
GGTGTGTTGGCACGGTGGTGGACATCATACCCGTAGTGGGGAGAAGATTCCAGTGTCTGT
GTGGATGAAGAGGATGCGGCAGGAGCGCCGCTATGCTGCGTGGTGGTCTGAGCCCGT
GGAGAGGGTCTCGACCTGGGTGCTTTCCAGAGCGATGGCACCATCACGTGATGTGACAG
TCTCTTTGCTCATCTTCACGGGTACGTGTCTGGGGAGGACGTGGCTGGGCAGCATATCAC
AGACCTGATCCCTTCTGTGCAGCTCCCTCCTTCTGGCCAGCACATCCCAAAGAACTCTCAA
GATTCAGAGGTCTGTTGGAAGAGCCAGGGACGGTACCACCTTCCCTCTGAGCTTAAAGCT
GAAATCCCAACCCAGCAGCGAGGAGGCGACCACCGGTGAGGCGGCCCTGTGAGCGGCTA
CCGGGCATCTGTCTGGGTGTTCTGCACCATCAGTGGCCTCATCACCTCCTGCCGGATGG
GACCATCCACGGCATCAACCACAGCTTCGCGCTGACACTGTTTGGTTACGGAAAAGACGGA
GCTCCTGGGCAAGAATATCACTTTCCTGATTCTGTTTCTACAGCTACATGGACCTTGC
GTACAACAGCTCATTACAGCTCCCAGACCTGGCCAGCTGCCTGGACGTGCGCAATGAGAG
TGGGTGTGGGGAGAGAACCCTTGACCCGTGGCAGGGCCAGGACCCAGCTGAGGGGGGCCA
GGATCCAAGGATTAATGTGCTGCTTGTGCTGGTGGCCACGTTGTGCCCCGAGATGAGATCCG
GAAGCTGATGGAAAGCCAAGACATCTTACCGGGACTCAGACTGAGCTGATTGCTGGAGG
CCAGCTCCTTTCTGCTCTCACCTCAGCCTGCTCCAGGGGTGGACAATGTCCCAGAAGG
AAGCCTGCCAGTGCACGGTGAACAGGCGCTGCCCAAGGACCAGCAAATCACTGCCTTGGG
GAGAGAGGAACCTGTGGCAATAGAGAGCCCCGGACAGGATCTTCTGGGAGAAAGCAGGTC
TGAACCAAGTGGATGTGAAGCCATTTGCTTCTGCGAAGATTCTGAAGCTCCAGTCCCAGC
TGAGGATGGGGGCAGTGATGCTGGCATGTGTGGCCTGTGTGAGAAGGCCAGCTAGAGCG
GATGGGAGTCAGTGGTCCCAGCGTTTACAGCTTGGGCTGGGGCTGCCGTGGCCAAGCC
CCAGGCCAAGGGTCAGCTGGCGGGGGGACGCTCCTGATGCACTGCCCTTGCTATGGGAG
TGAATGGGGCTTGTGGTGGCGAAGCCAGGACTTGCCCCCAGCCCCCTTGGGATGGCAGG
CCTCTCGTTTGGGACACCTACTCTAGATGAGCCGTGGCTGGGAGTGGAACGACCCGAGA

FIGURE 2AA

AGAGCTGCAGACCTGCTTGATTAAGGAGCAGCTGTCCCAGTTGAGCCTTGACAGGAGCCCT
GGATGTCCCCACGCCGAACCTCGTTCCGACAGAGTGCCAGGCTGTCACCGCTCCTGTGTC
GTCCTGCGATCTGGGAGGCAGAGACCTGTGCGGTGGCTGCACGGGCAGCTCCTCAGCCTG
CTATGCCTTGGCCACGGACCTCCCTGGGGGCTGGAAGCAGTGAGGGCCAGGAGGTTGA
TGTGAATTCGTTTTCTGGAACCTCAAGGAACTCTTTTTCAGTGACCAGACAGACCAAAC
GTCATCAAATTGTTCTGTGCTACGTCTGAACTCAGAGAGACACCCTCTTCTTGGCAGT
GGGCTCCGATCCAGATGTAGGCAGTCTCCAGGAACAGGGGTGCTGTGTCTTGGATGACAG
GGAGCTGTTACTACTGACCGGCACCTGTGTTGACCTTGGCCAAGGCCGACGGTTCGGGA
GAGCTGTGTGGGACATGATCCAACAGAAACCGCTTGAGGTTTGTGTTGGTGTCTCTGAGCA
TTATGCAGCAAGCGACAGAGAAAGCCCAGGACACGTTCTTCCACGTTGGATGCTGGCCC
TGAGGACACGTGCCCATCAGCAGAGGAGCCAAGGCTGAACGTCCAGGTCACCTCCACGCC
CGTGATCGTGATGCGCGGGGCTGCTGGCCTGCAGCGGGAGATCCAGGAGGCTGCTACTC
CGGGAGCTGCTACCATCGAGATGGCTTACGGCTGAGTATACAGTTTGAGGTGAGGCGGGT
GGAGCTCCAGGGCCCCACACCTCTGTTCTGCTGCTGGCTGGTGAAGACCTCCTCCACAG
CCAACCGGACTCAGCCGCCAGGACCCGCTGTCTTGGCAGCCTGCCCGGCTCCACCCA
CTCTACCGCTGCTGAGCTCACCGGACCCAGCCTGGTGAAGTGCTCAGAGCCAGACCCTG
GTTTGAGGAGCCCCCAAGGCTGTGGAAGTGGAGGGGTGGCGGCTGTGAGGGCGAGTA
CTCCCCAAAGTACAGTACCATGAGCCCGCTGGGCAGTGGGGCCTTCGGCTTCGTGTGGAC
TGCTGTGGACAAGGGAAAAACAAGGAGGTGGTGGTGAAGTTTATTAAGAAGGAGAAGGT
CTTGAGGATTGTTGGATTGAGGATCCCAAAGTTGGGAAAGTTACTTTAGAGATCGCAAT
TCTATCCAGGTTGGAGCACGCCAATATCATCAAGGTATTGGATATATTGAAAACCAAGG
GTTCTTCCAGCTTGTGATGGAGAAGCACGGCTCCGGCCTAGACCTCTTCGCTTTCATCGA
CCGCCACCCAGGCTGGATGAGCCCTGGCGAGCTACATCTTCCGACAAGTGAGAGCAGG
CCAGAGCCGTCTAGTGTGAGCAGTGGGATACCTGCGCTTGAAGGACATCATCCACCGTGA
CATCAAGGATGAGAACATCGTGATCGCTGAGGACTTCACAATCAAGCTGATAGACTTTGG
CTCGGCCGCTACTTGGAAAGGGGAAAATTATTTTATACTTTTTGTGGGACCATCGAGTA
CTGTGCACCCGAAGTTCTCATGGGGAATCCCTACAGAGGGCCGAGCTGGAGATGTGGTC
TCTGGGAGTCACTCTGTACACGCTGGTCTTTGAGGAGAACCCTTCTGTGAGCTGGAGGA
GACCGTGGAGGCTGCCATACACCCGCCATACCTGGTGTCCAAAGAACTCATGAGCCTTGT
GTCTGGGCTGCTGCAGCCAGTCCCTGAGAGACGCCACCTTGGAGAAGCTGGTGACAGA
CCCGTGGGTAACACAGCCTGTGAATCTTGTGCTGACTATACATGGGAAGAGGTGTTTCGAGT
AAACAAGCCAGAAAGTGGAGTTCTGTCCGCTGCGAGCCTGGAGATGGGGAACAGGAGCCT
GAGTGATGTGGCCAGGCTCAGGAGCTTTGTGGGGCCCCGTTCCAGGCGAGGCTCCTAA
TGGCCAAGGCTGTTTGCATCCCGGGGATCCCCGTCTGCTGACCAGCTAAACACCAATTTCT
TCCTGCTTTTCTCCACTTGGTTTGGAAATCACACAGTTTTTCAGGCTCCATCTGTTTG

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CCACGCGTCCGCATCCCTGCTTGGATGAGCCCTGGCGAGTTTCATCTTTTCGACAACCTAG
TGTCTGCTGTAGGATACCTGCACTCCCAAGGCATCATCCATAGAGACATCAAGGATGAGA
ACATTGTGATTGCTGAGGACTTCACAATTAAGCTGATAGATTTTGGCTCAGCTGCCTACT
TAGAGAGGGGCAAACTATTTTATACCTTTTGTGGAACAATCGAATACTGTGCACCTGAGG
TTCTCATTGGAAATCCCTACAGAGGGCCAGAGCTGGAGATGTGGTCTCTGGGGGTCAACC
TGTACACGCTCATCTTCGAGGAGAATCCCTTCTGTGAGGTGGAGGAGACCATGGAGGCAG
TTATTCATCCCCCATTCCTGGTTTCCCAAGAACTTATGAGTCTTCTGTCTGGACTGCTGC
AGCCTTGGCCTGAGCAGCGGACCCTTTGGAGAAGCTGATCAGGGACCCCTGGGTGACAC
AGCCTGTGAACCTTGCTAGCTATACTTGGGAAGAGGTGTGTAGGACCAACCAGCCAGAAA
GTGGCCTGCTGTGAGCTGCAAGTCTGGAGATTGGGAGTAGGAGTCCAAGTGAAATGGCTC
AGAGAGAGGGTCTCTGTGGGCCTCCTGCTCCAGGGAGACTCGTGGTGACCAGCACTGCT
TGCATCTTAAGGACCCCTCTTGGCAGTCAGCTGAGCAAGCTCTCCTGCTCTTTGGTTTG
GGCAGTTGTATGGATTTAGGGCTTTCTACCTGGAGAAAGGAAGTTGTGAAGGATTGGGA

FIGURE 2BB

TGACTTCTGCTTCTAGATTCTATGCAAATGCTACAAGAGCCTGCGATGCTAGTTTTCTT
AGGTTTATGATATAGACTTGTAATTCATGTTTTTTTATAACCTTGAAAATCATTCTAATG
TTCAGTTATACTGTACTATTAAAGGGCTTTAAGTTGTAAGCCTCAGAAAGACACAAGGAG
TGTTTAAGTTCTCTATTTTTTGTGTTGTTTTTGTCTGTAAGTTTTTGAGACAGGATCTC
ACCATGTAACCTTTGGCTGGCCTGGAACCTCAACTATGTAGACCAGGTAGACCTTAAACTGA
CAGATCTGCCTGCGCTTGCCCTCCAAGCATTAGGACTGATGGTGTGTGTCACCATGCCCA
GTTCTTCCTGGTTTTGTGTGTAGGTTTCTTTCCCACTGACTTGGTACATGTGACATGTGA
CAGATGTATGGAGTCTATAGAAGTGGCCAGACAAAATGGCCAGAATATTTATTTATTTT
CTTAAAAATTTTCCAAATTAAAGCTACTTAGTTAACAGTTAAACTGGCCAGGACTATATG
AGATAAACTTGTTTTCTATTTCTTTTGT

SEQ ID NO: 38_AA785735_H

GGCACGAGGCGCGCTGGCTGGGCCCTGCGGAGGANGGGAAGGAGCGAAGGAGCGAAGGA
GCAAGCGGAGCGCAGTTCCGCCAAGCCAAGCCGCGCTGCCAACCTCCCGCCCGCCCGCG
CTCCTGTCCGCCGTGTCTAGCAGCGGGGCCAGCATGGTCATGGCGGATGGCCCGAGGCA
CTTGACGCGCGGGCCGGTCCGGGTGGGGTTCTACGACATCGAGGGCACGCTGGGCAAGGG
CAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGGATCACCAAGACGGAGGTGGCAATAAA
AATAATCGATAAGTCTCAGCTGGATGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACA
AATAATGAAAATGTTAGACCACCCTCACATAATCAAACCTTTATCAGGTAATGGAGACCAA
AAGTATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAAATTTTTGACTATCTTGC
TAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATTTCTGGCAAATCCTGTCTGC
TGTTGATTATTGTCTATGGTCGGAAGATTGTGCACCGTGACCTCAAAGCTGAAAATCTCCT
GCTGGATAACAACATGAATATCAAAATAGCAGATTTCCGTTTTGGAAATTTCTTTAAAG
TGGTGAACCTGCTGGCAACATGGTGTGGCAGCCCCCTTATGCAGCCCCAGAAGTCTTTGA
AGGGCAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCTTTATGT
CCTTGCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAATTTTGAGGCAGAGGGT
TCTGGAAGGAAGATTCCGGATTCCGTATTTTCATGTCAGAAGATTGCGAGCACCTTATCCG
AAGGATGTTGGTCCTAGACCCATCCAAACGGCTAACCATAGCCCAAATCAAGGAGCATAA
ATGGATGCTCATAGAAGTTCCTGTCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAA
TGAGCCATCCATCGGGGAGTTTAATGAGCAGGTTCTGCGACTGATGCACAGCCTTGGAAAT
AGATCAGCAGAAARCCATTGAGTCTTTGCAGAACAGAGCTATAACCACTTTGCTGCCAT
TTATTTCTTGTTGGTGGAGCGCCTGAAATCACATCGGAGCAGTTTCCCAGTGGAGCAGAG
ACTTGATGGCCGCCAGCGTCGGCCTAGCACCATTGCTGAGCAAACAGTTGCCAAGGCACA
GACTGTGGGGCTCCCAGTGACCATGCATTACCGAACATGAGGCTGCTGCGATCTGCCCT
CCTCCCCCAGGCATCCAACGTGGAGGCCTTTTCATTTCCAGCATCTGGCTGTGAGGCGGA
AGCTGCATTTCATGGAAGAAGAGTGTGTGGACACTCCAAAGGTCAATGGCTGTCTGCTTGA
CCCTGTGCCTCCTGTCTGGTGCAGGAAGGGATGCCAGTCACTGCCCAGCAACATGATGGA
GACCTCCATTGACGAAGGGCTGGAGACAGAAGGAGAGGCCGAGGAAGACCCCGCTCATGC
CTTTGAGGCATTTTCAGTCCACACGCAGCGGGCAGAGACGGCACACTCTGTCTAGAAGTGAC
CAATCAACTGGTCGTGATGCCTGGGGCAGGGAAAATTTTCTCCATGAATGACAGCCCCCTC
CCTTGACAGTGTGGACTCTGAGTATGATATGGGGTCTGTTTCAGAGGGACCTGAACTTTCT
GGAAGACAACCTTCCCTTAAGGACATCATGTTAGCCAATCAGCCTTCACCCCGCATGAC
ATCTCCCTTCATAAGCCTGAGACCTACCAACCCAGCCATGCAGGCTCTGAGCTCCCAGAA
ACGAGAGGTCCACAACAGGTCTCCAGTGAGCTTCAGAGAGGGCCGAGAGCATCAGATAC
CTCCCTCACCCAGGGAATTGTAGCATTTAGACAACATCTTCAGAATCTGGCTAGAACCAA
AGGAATTCTAGAGTTGAACAAAGTGCAGTTGTTGTATGAACAAATAGGACCGGAGGCAGA
CCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAGGACCTTGCTAGCAGCTGCCCTCAGGA
AGAAGTTTCTCAGCAGCAGGAAAGCGTCTCCACTCTCCCTGCCAGCGTGCATCCCCAGCT
GTCCCCACGGCAGAGCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCCAGCCT
TCTGTCAAAGGCCAGAACACCTGTGAGCTTTATTGCAAAGAACCACCGCGAGCCTTGA

FIGURE 2CC

GCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTCTTCAGAAGCAGTCTCA
ACTGCAGGCCTATTTTAAATCAGATGCAGATAGCAGAGAGCTCCTACCCACAGCCAAGTCA
GCAGCTGCCCCCTTCCCGCCAGGAGACTCCACCGCCTTCTCAGCAGGCCCCACCGTTTCAG
CCTGACCCAGCCCCCTGAGCCCCGTCTGGAGCCTTCCCTCCGAGCAGATGCAATACAGCCC
TTTCCTCAGCCAGTACCAAGAGATGCAGCTTCAGCCCCCTGCCCTCCACTTCCGGTCCCCG
GGCTGCTCCTCCTCTGCCCACGCAGCTACAGCAGCAGCAGCCGCCACCGCCACCACCCCC
TCCACCACCACGACAGCCAGGAGCTGCCCCAGCCCCCTTACAGTTCTCCTATCAGACTTG
TGAGCTGCCAAGCGCTGCTTCCCCCTGCGCCAGACTATCCCACTCCCTGTCAGTATCCTGT
GGATGGAGCCCAGCAGAGCGACCTAACGGGGCCAGACTGTCCAGAAGCCCAGGACTGCA
AGAGGCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTTTGATTG
TGAAATGCTAGACGCTGTGGATCCACAACACAACGGGTATGTCTGGTGAATTAGTCTCA
GCACAGGAATTGAGGTGGGTCAAGTGAAGGAAGAGTGTATGTTCTATTTTTTATTCCAGC
CTTTTAAATTTAAAGCTTATTTTCTTGCCCTCTCCCTAACGGGGAGAAATCGAGCCACCC
AACTGGAATCAGAGGGTCTGGCTGGGGTGGATGTTGCTTCTCCTGGTTCTGCCCCACCA
CAAAGTTTTCTGTGGCAAGTGTGGAACATAGTTGTAGGCTGAGGCAGGAGAATGGCGTG
AACCCGGGAGGCGGAGCTTGCACTGAGCAAGATCGTGCCACTGCACTCCAGCCTGGGCG
ACTGAGCAAGACTCCACCTCAAAAAAAAAAAAAAAAAAGGACAAGAGCAGTATCATCTGCCTC
TGTTTCTAAACTGGACAAAGAGATTTTCTTAAAGTTTCTATCATCTCCCTTCTGACAGGT
TCTACAGTGTGGTCTGAAGCACCTGTAATGTGAGAGCCCTTGTCTGGCCCTTGGTGGCAG
GTGAACGAAAGCAGTGGAGCCTCTCACCTTCCAGTAGCCTCTCACATTCTTATTTTACCA
TTTTTGTCTTAATTAAGGTAGCCTAGCTGATTCTAGAAGACAGCCATCCTACGTGCACCC
CCACCTTGTGTCCACATCTTCTCCAGGCAGGTTTCAACCTATCAGCAGACTCAGGCACAC
ACTGGGGCACAGATAGAGAACCAGGCGGCAGCAGTGCTCGCAGACCCACCCAGGGAGAGC
TGTGATGGGTTCTGCCCAGATACTCTGCTCGCCACCCACAAGGGAGCAATAGCTTATAT
TTGTACATTAGTTTTTACCAAGCACTTTCTCTTCTAACCCTCACAACAATTCTATGAAATT
AGCTGGGGAGATACTGTCCTTATTTTTTACAGCTGAAGAAACCAAAGCTTTGGGAAGTTT
GTGACTTCTCTGAGATCACAGCTGGTGATAGAAGGAGCTGGGACACGCGCTTGGGTGAC
TGGCTTCTGGTTTTTGGTTCTCTGGCTTCTAGTGCTGGAAGAAGCCCTCTCTTTCCCTTCT
CTTTCTCAGTAGCATCTGACTCTTTTCATAAGCAAACAGCTGTATAAAACAAAGCCCCCA
TTTTGGTCAAGCACAGGTGAATGTGATATTGTTCCCAACCTTATTCTCCACTCAACA
GCCGCCTGGCTTTGGGGAAGAGGCCGCTTCCAGGTGACAGTGCAGCTGTCCAGGTGGCCG
TGCAGTGAACCAGGCTGAGGGAGACAAAAACCCCGCAGACCCGCTGCCTTTCCAGCGTCC
AGTTAACTGCAGAAGTTTAGGCTCACCTCAAAGATGTCTAGTTTTTCCAAGTTACAATAC
AGCAGTTTCTTACAGAACACCCCTTCTCAATTGCCAAGGGGCCGATCGCACGGCATC
AGGCCACCACTGCAGGCCAGCAGATTCCACCCAGGAACGGTCATGAACTCAGCCTTTGT
CTCAACGAGGGGCGTAACATTTCTTACAGTCAAGCCCCATCACTAGAAGTGCTTATTA
CTTTTAGGATTAAAAAGTAATAACAGACTTTGACTTAATACTCTGTCTTTTTCAGAGGCA
AAGTGGGTGGGTAGAGGGGAGCTTTAAAAATAGAAGTACAAAACAACATCCTGGAAACAT
ATGACCCAGATGGAATAATGTACATTCCCCAGTGCAGATAATGGGCTGCTGCTGGCTC
TGTGGTGTCTGTCTGCAGAAGATTTGCTCAGTCAAGGAAATTCAAGTGGTGAGACCTTTC
CACCATGGGTGGTAAGAGAAACCTGCCTTACCACAAATCTCTGAAGGGGAAAGAAGTGGGA
GAGAAAGGTTTGCCTTCACTTCGGGGACTGCAGTTTGAAGAAATAAAAGGGATACAGAGATA
TCTGCACTTTGTAGAAAGGGCAAGATTATTTGCTTATATCTGAAGGGAGGTGGGTGGTTT
TGCTGGATGTTTGGTCTGAAAGAGTTACTTTTTGATAAAGTTAATCTAATTGTAGTTATAT
TTTCTGTGTGCTTTTTTTTTAATTACTAAGAAAAAAATTGGTGAGTTCAGTAGCTTTGGTA
TTATGAGTGCAAAATCATAATAGCTCCAATGTGAAAAAAAATCAAAGTATAAAGTGTGTC
ACTTAATGTTAGAAAATTGCCTAAATGCAGTGTAATAAATAATCTCTGTACCAAATAGT
AATTTAAATGGGGTAATTTTCTGCAAGGAAATGTACTGTTTTTATGTTTTCAACCCTCT
TGA

FIGURE 2DD

SEQ ID NO: 39_AA207220_H

GCTGTGGCTCCCCGTCTGGTGC GG GACCTGTGCCCCGCGCTTCAGCCCTCCCCGCAAGC
CTATTGATTCCCCTGCCGCCCTTGCTCCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTTC
GCGCGGCGCTCCGGCCCCACTCCCTCGGCCGAGAGCTAGCCCGCCGCTGGCGGAAGGG
CTGATCAAGTCGCCCCAAGCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAG
CACAACCTGCGGCACCGCTACGAGTTCTTGAGACCCTGGGCAAAGGCACCTACGGGAAG
GTGAAGAAGGCGGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAATCCGGAAGGAC
AAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTTCATCA
CTCAACCACCCTCACATCATTGCCATCCATGAAGTGTGAGAACAGCAGCAAGATCGTG
ATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAG
CTCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGC
CATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGATGCCAAT
GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG
CAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTAC
ACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGC
ACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCC
TACCGGGAGCCACCTAAACCTCTGATTGCCTGNNTGGCCTGATCCGGTGGCTGTTGATG
GTGAACCCCAACCGCGGGGCCACCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGG
GGCTACGCCACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCTGGCAGT
GACTCTGCCCGCGCCTCCATGGCTGACTGGCTCCGGCGTTCTTCCCGCCCCCTCTGGAG
AATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACC
CCTGGCCTGGAGCGCCAGCATTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCAG
TCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAG
CTGCCAAAGGGCATTCTCAAGAAGAAGGTGTGAGCCTCTGCAGAAGGGGTACAGGAGGAC
CCTCCGGAGCTCAGCCCAATCCCTGCGAGCCAGGGCAGGCTGCCCCCTGCTCCCCAAG
AAGGGCATTCTCAAGAAGCCCCGACAGCGGAGTCTGGCTACTACTCCTCTCCCGAGCCC
AGTGAATCTGGGGAGCTCTTGAGCGCAGGCGACGTGTTTGTGAGTGGGGATCCCAAGGAG
CAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACCTCAAT
GGCAAGTTCTCCAGACAGCCTTGAGGCTCGCGGCCCCCACCACCTTCGGCTCCCTGGAT
GAACTCGCCCCACCTCGCCCCCTGGCCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAG
GACAGCATCCTGTCTCTGAGTCTTTGACCAGCTGGACTTGCCTGAACGGCTCCAGAG
CCCCACTGCGGGGCTGTGTGTCTGTGGACAACCTCACGGGGCTTGAGGAGCCCCCTCA
GAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGTGCTTT
TCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCA
AAGCTCACCTGAGTGGAGTAGGCATTGCCCCAGCCGGTCAGGCTCTCAGATGCAGCTGG
TTGCACCCCGAGGGGAGATGCCTTCTCCCCACCTCCAGGACCTGCATCCCAGCTCAGA
AGGCTGAGAGGGTTTGCAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAGGCAAATG
AAATGCGCCAAGGGTTCAGTGTCTGTCTTCAGCCCTGCTGAACGAAGAGGATACTAAAGA
GAGGGGAACGGGAATGCCCGGACAGAGTCCACATTGCCTGTTTCTTGTGTACATGGAGG
GGCCACAGAGA

SEQ ID NO: 40_AA426580_H, MAK_V_H

ATGCCGGCGGCGGGGGGACGGGCTCCTGGGGGAGCCGGCGGCGCCTGGGGGCGGCGGC
GGCGCGGAGGACGCGGCCAGGCCCGCGGCGCCTGCGAGGGAAGTTTCTGCTGCCTGG
GTGAGCGGCGTGCCCCGCGAGCGGCTCCGCGACTTCCAGCACCACAAGCGCGTGGGCAAC
TACCTCATCGGCAGCAGGAAGCTGGGCGAGGGCTCCTTTGCCAAGGTGCGCGAGGGGCTG
CACGTGCTGACCGGGGAGAAGGTGGCCATAAAAGTCATTGATAAGAAGAGAGCCAAAAAG
GACACCTATGTACCAAAAACCTGCGGCGAGAGGGTCAGATCCAGCAGATGATCCGCCAC
CCCAATATCACTCAGCTCCTTGATATTTAGAAACGGAAAACAGCTACTACCTGGTCATG
GAGCTGTGCCCTGGGGGCAACCTGATGCACAAGATCTATGAGAAGAAGCGGCTGGAGGAG

FIGURE 2EE

TCCGAAGCCCCGAGATACATCCGACAGCTCATCTCTGCCGTAGAGCACCTGCACCGGGCC
GGGGTGGTCCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC
AAGCTGATTGACTTTGGTTTGAGCAACTGCGCAGGGATCCTGGGTTACTCGGATCCGTTT
AGCACACAGTGTGGCAGCCCTGCCTACGCTGCACCTGAACTGCTCGCCAGGAAGAAATAC
GGCCCCAAAATCGATGTCTGGTCCATAGGTGTGAACATGTATGCCATGTTGACCGGGACG
CTGCCTTTACGGTGGAGCCTTTCAGCCTGAGGGCTTTGTACCAGAAGATGGTAGACAAA
GAAATGAACCCCCCTCCCCACTCAGCTCTCCACAGGTGCCATCAGTTTCTGCGCTCTCTC
CTGGAACCGGATCCTGTGAAGAGGCCAAATATTGAGCAGGCACTGGCGAATCGCTGGCTT
AATGAGAATTACACGGGCAAAGTGCCCTGTAATGTCACCTATCCCAACAGGATTTCTCTG
GAAGATCTGAGCCCCGAGCGTCGTGCTGCACATGACCGAGAAGCTGGGTTACAAGAACAGC
GACGTGATCAACACTGTGCTCTCCAACCGCGCTGCCACATCCTGGCCATCTACTTCCTC
TTAAACAAGAACTGGAGCGCTATTTGTCAGGGAAATCTGACATCCAGGACAGCCTCTGC
TACAAGACCCGGCTCTACCAGATAGAAAAGTACAGGGCCCCCAAGGAGTCTATGAGGCC
TCTCTGGACACCTGGACACGAGATCTTGAATTCATGCCGTGCAGGATAAAAAGCCCCAA
GAACAAGAAAAAAGAGGGGATTTTCTTCATCGACCATTCTCCAAGAAGTTGGACAAGAAC
CTGCCCTCGCACAAACAGCCCTCAGGCTCGCTTATGACACAGATTGAGAACACCAAAGCC
CTCCTGAAGGACCGGAAGGCCTCCAAGTCCAGCTTCCCCGACAAAGATTCCTTTGGCTGC
CGCAATATTTTCCGCAAAACCTCAGATTCCAATTGTGTGGCTTCTTCTCCATGGAGTTC
ATCCCCGTGCCACCGCCAGGACCCCGAGGATTGTGAAGAAACCGGAGCCCCATCAGCCA
GGGCCCCGAAGCACTGGCATCCCCACAAGGAAGACCCCTGATGCTGGACATGGTGC GC
TCCTTCGAGTCTGTGGATCGCGACGACCACGTAGAAGTGCTGTCTCCCTCTCATCTACTAC
AGGATTCTGAACTCCCCGGTCAGCTTGGCTCGCAGAAATTCAGCGAGAGGACGCTGTCC
CCGGGTCTGCCATCCGGAAGCATGTGCGCTCTCCATACTCCTTTGCATCCAACCTCTGGTC
TCTTTTGCTCACGAAGATAAGAACAGCCCCCAAAAGAGGAGGGCCTGTGTTGCCACCT
CCGTTTCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAATTGTGTGAAAAGCCGA
GGCCGGTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCGCCATCAGAGTCTGCAG
CCATCTGCAGATAGGCCCTGGAGGCCAGCCTGCCCCACTGCAGCCCCTAGCCCCTGTG
AACCTTGCCTTTGACATGGCCGATGGGGTCAAGACCCAGTGCTAA

SEQ ID NO: 41_Z36720_H

ATGGACACAAAGCTGAACATGCTGAACGAGAAGGTGGACCAGCTCCTGCACTTCCAAGAA
GATGTCACAGAGAAGTTGCAGAGCATGTGCCGAGACATGGGCCACCTGGAGCGGGGCCTG
CACAGGCTGGAGGCCCTCCCGGGCACCGGGCCCCGGGCGGGCTGATGGGGTTCCCCACATT
GACACCCAGGCTGGGTGGCCCGAGGTCTTGAGCTGGTGAGGGCCATGCAGCAGGATGCG
GCCCAGCACGGTGCCAGGCTGGAGGCCCTCTTCAGGATGGTGGCTGCGGTGGACAGGGCC
ATCGCTTTGGTGGGGGCCACGTTCCAGAAATCAAAGGTGGCGGATTTCTCATGCAGGGG
CGTGTGCCCTGGAGGAGAGGCAGCCAGGTGACAGCCCTGAGGAGTGGGTAAAAGAGGAG
GAGGTCTGTTTCATGCCTCCAGTTCCCCCAGCTCCGGGGGCAGCAGGACAGAGCCTGCAG
AAGGATAAGGGGAGCTGTCTGCCGAGCAGGGGATCTGGGCCACATTGATGACGCTGGTG
ATCATGGTGACAGCGGCAAATAAAGAGCGAGTGGAAGAAGAGGGAGGAAAACCAAAGCAT
GTGCTGAGCACCAGTGGGGTGCACTGTATGCCAGGGAGCCTGGGGAAGAGAGCCAGAAG
GCGGACGTGCTGGAGGGGACAGCGGAGAGGCTGCCCCCATCAGAGCGTCAGGGCTGGGA
GCTGACCCCGCCAGGCAGTGGTCTCACCGGGCCAGGGAGATGGTGTTCCTGGCCAGCC
CAGGCATTCCCTGGCCACCTGCCCCCTGCCACAAAGGTGGAAGCCAAGGCTCCTGAGACA
CCCAGCGAGAACCTCAGGACTGGCCTGGAATTGGCTCCAGCACCCGGCAGGGTCAATGTG
GTCTCCCCGAGCCTGGAGGTTGCACCAGGTGCAGGACAAGGAGCATCGTCCAGCAGGCCT
GACCCTGAGCCCTTAGAGGAAGGCACGAGGCTGACTCCAGGGCCTGGCCCTCAGTGCCCA
GGGCCTCCAGGGCTGCCAGCCAGGCCAGGGCAACCCACAGTGGTGGAGAAACACCTCCA
AGGGCAGCCCTGCTGAAGGGCGCTGTGGCCCCGGGCTTCTCTCGGAGGGACCTGGTGT
CCTAGCATCTTCTGCGCCTGCCTAGGGATCTCCATCCACATACAAGAGATGGATACTCCT

FIGURE 2FF

GGGGAGATGCTGATGACAGGCAGGGGAGCCTTGGACCCACCCTCACCACAGAGGCTCCA
GCAGCTGCCCAGCCAGGCAAGCAGGGCCACCTGGGACCGGGCGCTGCCTCCAAGCCCCCT
GGGACTGAGCCCGGAGAACAGACCCCTGAAGGAGCCAGAGAGCTCTCCCCGCTGCAGGAG
AGCAGCAGCCCCGGGGGAGTGAAGGCAGAGGAGGAGCAAAGGGCTGGGGCCGAGCCTGGC
ACGAGACCAAGCTTGGCCAGGAGTGACGACAATGACCACGAGGTTGGGGCCCTGGGCCTG
CAGCAGGGCAAAGCCAGGGGCGGGAAACCCTGAGCCTGAGCAGGACTGTGCAGCCAGG
GCTCCGGTGAGAGCTGAAGCAGTAAGGAGGATGCCCCAGGCGCCGAGGCTGGCAGCGTG
GTTCTGGATGACAGTCCGGCCCCACCAGCTCCTTTTGAACACCGGGTAGTGAGCGTCAAG
GAGACCTCCATCTCTGCGGGTTACGAGGTGTGCCAGCACGAAGTCTTGGGAGGGGGTTCGG
TTTGGCCAGGTCCACAGGTGCACAGAGAAGTCCACAGGCCTCCCACTGGCTGCCAAGATC
ATCAAAGTGAAGAGCGCCAAGGACCGGGAGGACGTGAAGAACGAGATCAACATCATGAAC
CAGCTCAGCCACGTGAACCTGATCCAGCTCTATGACGCCCTTCGAGAGCAAGCACAGCTGC
ACCCTTGTTCATGGAGTACGTGGACGGGGGTGAGCTCTTCGACCGGATCACAGATGAGAAG
TACCACCTGACTGAGCTGGATGTGGTCTGTTCACCAGGCAGATCTGTGAGGGTGTGCAT
TACCTGCACCAGCACTACATCCTGCACCTGGACCTCAAGCCGGAGAACATATTGTGCGTC
AATCAGACAGGACATCAAATTAAGATCATTGACTTTGGGCTGGCCAGAAGGTACAAGCCT
CGAGAGAAGCTGAAGGTGAACCTTCGGCACTCCTGAGTTCTTGGCCCCAGAAAGTCGTCAAT
TATGAGTTTGTCTCATTCCCCACAGACATGTGGAGTGTGGGAGTCATCACCTACATGCTA
CTCAGTGGCTTGTCCCCATTTCTAGGGGAAACAGATGCAGAGACCATGAATTTTCATTGTA
AACTGTAGCTGGGATTTTGTGCTGACACCTTTGAAGGGCTCTCGGAGGAGGCCAAGGAC
TTTGTTCCTCGGTGCTGGTCAAAGAGAAGAGCTGCAGAATGAGTGCCACACAGTGCCTG
AAACACGAGTGGCTGAATAATTTGCCTGCCAAAGCTTCAAGATCCAAAACCTCGTCTCAA
TCCCAACTACTGCTGCAGAAATACATAGCTCAAAGAAAATGGAAGAAACATTTCTATGTG
GTGACTGCTGCCAACAGGTTAAGGAAATTTCCAACCTTCTCCCTAA

SEQ ID NO: 42_SGK088_H

GGGGAGATGGCGCTGTTTGAGTGCCTGGTGGCGGGGCCCACTGACGTGGAGGTGGATTGG
CTGTGCCGTGGCCGCTGCTGCAGCCTGCACTGCTCAAATGCAAGATGCATTTTCGATGGC
CGCAAATGCAAGCTGCTACTTACATCTGTACATGAGGACGACAGTGGCGTCTACACCTGC
AAGCTCAGCACGGCCAAAGATGAGCTGACCTGCAGTGCCCGGCTGACCGTGCGGCCCTCG
TTGGCACCCCTGTTTCACACGGCTGCTGGAAGATGTGGAGGTGTTGGAGGGCCGAGCTGCC
CGTTTCGACTGCAAGATCAGTGGCACCCCGCCCCCTGTTGTTACCTGGACTCATTTTGGC
TGCCCCATGGAGGAGAGTGAGAACTTGCGGCTGCGGCAGGACGGGGGTCTGCACTCACTG
CACATTGCCCCATGTGGGCAGCGAGGACGAGGGGCTCTATGCGGTCACTGCTGTTAACACC
CATGGCCAGGCCCACTGCTCAGCCAGCTGTATGTAGAAGAGCCCCGGACAGCCGCTCA
GGCCCCAGCTCGAAGCTGGAGAAGATGCCATCCATTCCCGAGGAGCCAGAGCAGGGTGAG
CTGGAGCGGTGTCCATTCCCGACTTCTGCGGCCACTGCAGGACCTGGAGGTGGGACTG
GCCAAGGAGGCCATGCTAGAGTGCCAGGTGACCGGCCTGCCCTACCCACCATCAGCTGG
TTCCACAATGGCCACCGCATCCAGAGCAGCGACGACCGGCGCATGACACAGTACAGGGAT
GTCCATCGCTTGGTGTTCCTGCCGTGGGGCTCAGCACGCCGGTGTCTACAAGAGCGTC
ATTGCCAACAAAGCTGGGCAAAGCTGCCTGCTATGCCACCTGTATGTACAGATGTGGTC
CCAGGCCCTCCAGATGGCGCCCCGAGGTGGTGGCTGTGACGGGGAGGATGGTCACACTC
ACATGGAACCCCCCAGGAGTCTGGACATGGCCATCGACCCGGAATCCCTGACGTACACA
GTGCAGCACCAAGTGTGGCTCGGACAGTGGACGGCACTGGTTCACAGGCCTGCGGGAG
CCAGGGTGGGCAGCCACAGGGCTGCGTAAGGGGGTCCAGCACATCTTCCGGGTCTCAGC
ACCACTGTCAAGAGCAGCAGCAAGCCCTCACCCCTTCTGAGCCTGTGCAGCTGCTGGAG
CACGGCCCAACCCTGGAGGAGGCCCTGCCATGCTGGACAAACCAGACATCGTGTATGTG
GTGGAGGGACAGCTGCCAGCGTCACCGTCACATTCAACCATGTGGAGGCCAGGTCTGTC
TGGAGGAGCTGCCGAGGGGCCCTCCTAGAGGCACGGGCCGGTGTGTACGAGCTGAGCCAG
CCAGATGATGACCAGTACTGTCTTCGGATCTGCCGGGTGAGCCGCCGGGACATGGGGGCC

FIGURE 2GG

CTCACCTGCACCGCCCCGAAACCGTCACGGCACACAGACCTGCTCGGTACACATTGGAGCTG
GCAGAGGCCCCCTCGGTTTGAGTCCATCATGGAGGACGTGGAGGTGGGGGCTGGGGAAACT
GCTCGCTTTGCGGTGGTGGTTCGAGGGAAAACCACTGCCGGACATCATGTGGTACAAGGAC
GAGGTGCTGCTGACCGAGAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGCTCC
CTGGTGGTGTCTCAGCACGGGGGGCCAGGATGGAGGCGTCTACACCTGCACCGCCCCAGAAC
CTGGCGGGTGAGGTCTCCTGCAAAGCAGAGTTGGCTGTGCATTACAGCTCAGACAGCTATG
GAGGTCGAGGGGGTGGGGAGGATGAGGACCATCGAGGAAGGAGACTCAGCGACTTTTAT
GACATCCACCAGGAGATCGGCAGGGGTGCTTTCTCCTACTTGCGGCGCATAGTGGAGCGT
AGCTCCGGCCTGGAGTTTGCGGCCAAGTTTCATCCCCAGCCAGGCCAAGCCAAAGGCATCA
GCGCGTCGGGAGGCCCCGGCTGCTGGCCAGGCTCCAGCACGACTGTGTCTCTACTTCCAT
GAGGCCCTTCGAGAGGCGCCGGGACTGGTCATTGTACCGAGCTCTGCACAGAGGAGCTG
CTGGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCCTATATGCGG
CAGGTGCTAGAGGGAATACACTACCTGCACCAGAGCCACGTGCTGCACCTCGATGTCAAG
CCTGAGAACCTGCTGGTGTGGGATGGTGTCTGCGGGCGAGCAGCAGGTGCGGATCTGTGAC
TTTGGAATGCCAGGAGCTGACTCCAGGAGAGCCCCAGTACTGCCAGTATGGCACACCT
GAGTTTGTAGACCCCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGACATCTGG
CCTGTGGGTGTTGTTGCCTTCTCTGTCTGACAGGAATCTCCCCGTTTGTGGGGAAAAT
GACCGGACAACATTGATGAACATCCGAAACTACAACGTGGCCTTCGAGGAGACCACATTC
CTGAGCCTGAGCAGGGAGGCCCGGGGCTTCTCATCAAAGTGTTGGTGCAGGACCGGCTG
AGACCTACCGCAGAAGAGACCCTAGAACATCCTTGTTTCAAACTCAGGCAAAGGGCGCA
GAGGTGAGCACGGATCACCTGAAGCTATTCTCTCCCGCGGAGGTGGCAGCGCTCCAG
ATCAGCTACAAATGCCACCTGGTGTCTGCGCCCCATCCCCGAGCTGCTGCGGGCCCCCCCCA
GAGCGGGTGTGGGTGACCATGCCAGAAGGCCACCCCCAGTGGGGGGCTCTCATCCTCC
TCGGATTCTGAAGAGGAAGAGCTGGAAGAGCTGCCCTCAGTGCCCCGCCACTGCAGCCC
GAGTTCTCTGGCTCCCGGGTGTCCCTCACAGACATTCCCACTGAGGATGAGGCCCTGGGG
ACCCAGAGACTGGGGCTGCCACCCCCATGGACTGGCAGGAGCAGGGAAGGGCTCCCTCT
CAGGACCAGGAGGCTCCAGCCCCAGAGGCCCTCCCCCTCCCCAGGCCAGGAGCCCCGAGCT
GGGGCTAGCCCCAGGCGGGGAGAGCTCCGCAGGGGCAGCTCGGCTGAGAGCGCCCTGCCC
CGGGCCGGGCCGCGGGAGCTGGGCGGGGGCTGCACAAGGCGGCGTCTGTGGAGCTGCCG
CAGCGCCGAGCCCCGGCCCCGGGAGCCACCCGCCTGGCCCGGGGAGGCCTGGGTGAGGGC
GAGTATGCCAGAGGCTGCAGGCCCTGCGCCAGCGGCTGCTGCGGGGAGGCCCCGAGGAT
GGCAAGGTGAGCGGCCTCAGGGGTCCCTGCTGGAGAGCCTGGGGGGCCGTGCTCGGGAC
CCCCGATGGCACGAGCTGCCTCCAGCGAGGCAGCGCCCCACCACCAGCCCCCACTCGAG
AACCAGGGCCTGCAAAAGAGCAGCAGCTTCTCCAGGGTGAGGCGGAGCCCCGGGGCCGG
CACCGCCGAGCGGGGGCGCCCTCGAGATCCCCGTGGCCAGGCTTGGGGCCCGTAGGCTA
CAGGAGTCTCCTTCCCTGTCTGCCCTCAGCGAGGCCAGCCATCCAGCCCTGCACGGCCC
AGCGCCCCAAACCCAGTACCCCTAAGTCTGCAGAACCTTCTGCCACCACACCTAGTGAT
GCTCCGAGCCCCCGCACCCAGCCTGCCCAAGACAAGGCTCCAGAGCCCAGGCCAGAA
CCAGTCCGAGCCTCCAAGCCTGCACCAACCCCCAGGCCCTGCAAACCTAGCGCTGCCC
CTCACACCTATGCTCAGATCATTCAGTCCCTCCAGCTGTGAGGCCACGCCAGGGCCCC
TCGAGGGCCCTGCCGCGCCGCTTCAGAGCCCAAGCCCCACGCTGCTGTCTTTGCCAGG
GTGGCTCCCCACCTCCGGGAGCCCCCGAGAAGCGCGTGCCTCAGCCGGGGGTCCCCCG
GTGCTAGCCGAGAAAGCCCCGAGTTCCACGGTGCCCCCAGGCCAGGCAGCAGTCTCAGT
AGCAGCATCGAAACTTGAGTTCGGAGGCCGTGTTTCGAGGCCAAGTTCAAGCGCAGCCGC
GAGTCGCCCCGTGCTGCTGGGGCTGCGGCTGCTGAGCCGTTTCGCGCTCGGAGGAGCGCGG
CCCTTCCGTGGGGCCGAGGAGGAGGATGGCATATACCGGCCAGCCCCGGCGGGGACCCCG
CTGGAGCTGGTGCACGGCCTGAGCGCTCACGCTCGGTGCAGGACCTCAGGGCTGTGGA
GAGCCTGGCCTCGTCCGCCGCTCTCGCTGTCACTGTCCCAGCGGCTGCGGCGGACCCCT
CCCGCGCAGCGCCACCCGGCCTGGGAGGCCCGCGGCGGGGACGGAGAGAGCTCGGAGGGC
GGGAGCTCGGCGGGGGCTCCCCGGTGTGGCGATGCGCAGGCGGCTGAGCTTACCCCTG

FIGURE 2HH

GAGCGGCTGTCCAGCCGATTGCAGCGCAGTGGCAGCAGCGAGGACTCGGGGGGCGCGTCG
GGCCGCGAGCAGCCGCTGTTTCGGACGGCTTCGACGGGCCACGTCCGAGGGCGAGAGTCTG
CGGCGCCTTGCCCTTCCGCAACAACAGTTGGCCGCCAGGCCGGCGCCACCACGCCTTCC
GCCGAGTCCCTGGGCTCCGAGGCCAGCGCCACGTCCGGCTCCTCAGCCCCAGGGGAAAGC
CGAAGCCGGCTCCGCTGGGGCTTCTCTCGGCCGCGGAAGGACAAGGGGTATCGCCACCA
AACCTCTCTGCCAGCGTCCAGGAGGAGTTGGGTACACGTACGTGCGCAGTGAGTCAGAC
TCCCCCCCAGTCTTCCACATCAAACCTCAAGGACCAGGTGCTGCTGGAGGGGGAGGCAGCC
ACCTTGCTCTGCCTGCCAGCGGCCCTGCCCTGCACCGCACATCTCCTGGATGAAAGACAAG
AAGTCCTTGAGGTCAGAGCCCTCAGTGATCATCGTGTCTTGCAAAGATGGGCGGCAGCTG
CTCAGCATCCCCCGGGCGGGCAAGCGGCACGCCGGTCTCTATGAGTGCTCGGCCACCAAC
GTACTGGGCAGCATCACCAGCTCCTGTACCGTGGCTGTGGCCCCGAGTCCAGGAAAGCTA
GCTCCTCCAGAGGTAACCCAGACCTACCAGGACACGGCGCTGGTGCTGTGGAAGCCGGGA
GACAGCCGGGCACCTTGCACGTATACGTGGAGCGGCAGTGAGTGGGAGTCTGTGTGG
CACCCTGTGAGCTCAGGCATCCCCGACTGTTACTACAACGTGACCCACCTGCCAGTTGGC
GTGACTGTGAGGTTCCGTGTGGCCTGTGCCAACCCTGCTGGGCAGGGGCCCTTCAGCAAC
TCTTCTGAGAAGGTCTTTGTGAGGGGTACTCAAGATTCTTCAGCTGTGCCATCTGCTGCC
CACCAAGAGGCCCTGTACCTCAAGGCCAGCCAGGGCCCGGCCTCCTGACTCTCCTACC
TCACTGGCCCCACCCCTAGCTCCTGCTGCCCCACACCCCGTCAGTCACTGTAGCCCC
TCATCTCCCCCACACCTCCTAGCCAGGCCCTGTCTCGCTCAAGGCTGTGGGTCCACCA
CCCCAAACCCCTCCACGAAGACACAGGGCCCTGCAGGCTGCCCCGCCAGCGGAGCCACC
CTACCCAGTACCCACGTACCCCCAAGTGAGCCCAAGCCTTTCGTCTTGACACTGGGACC
CCGATCCAGCCTCCACTCCTCAAGGGGTAAACCAGTGCTTCTCCTACTCCTGTGTAT
GTGGTGACTTCTTTGTGTCTGCACCACAGCCCTGAGCCCCAGCCCTGAGCCCCCT
CCTGAGCCTACCAAGGTGACTGTGCAGAGCCTCAGCCCGGCCAAGGAGGTGGTCAGCTCC
CCTGGGAGCAGTCCCCGAAGCTCTCCAGGCCCTGAGGGTACCACTCTTCGACAGGGTCCC
CCTCAGAAACCCCTACACCTTCTTGAGGAGAAAGCCAGGGGGCCGCTTTGGTGTTGTGCGA
GCGTGCCGGGAGAAATGCCACGGGGCGAACGTTTCGTGGCCAAGATCGTGCCCTATGCTGCC
GAGGGCAAGCCGCGGGTCTGCAGGAGTACGAGGTGCTGCGGACCCTGCACCACGAGCGG
ATCATGTCCCTGCACGAGGCCTACATCACCCCTCGGTACCTCGTGCTCATTGCTGAGAGC
TGTGGCAACCGGGAACCTCCTCTGTGGGCTCAGTGACAGGTTCCGGTATTCTGAGGATGAC
GTGGCCACTTACATGGTGCAGCTGCTACAAGGCCTGGACTACCTCCACGGCCACCACGTG
CTCCACCTAGACATCAAGCCAGACAACCTGCTGCTGGCCCCCTGACAATGCCCTCAAGATT
GTGGACTTTGGCAGTGCCAGCCCTACAACCCCCAGGCCCTTAGGCCCTTGGCCACCGC
ACGGGCACGCTGGAGTTCATGGCTCCGGAGATGGTGAAGGGAGAACCCATCGGCTCTGCC
ACGGACATCTGGGGAGCGGGTGTGCTCACTTACATTATGCTCAGTGGACGCTCCCCGTTT
TATGAGCCAGACCCCCAGGAAACGGAGGCTCGGATTGTGGGGGGCCGCTTTGATGCCTTC
CAGCTGTACCCCAATACATCCCAGAGCGCCACCTCTTCTTGCGAAAGGTTCTCTGTGA
CATCCCTGGAGCCGGCCCTCCCTGCAGGACTGCCTGGCCACCCATGGTTGCAGGACGCC
TACCTGATGAAGCTGCGCCGCCAGACGCTCACCTTCACCACCAACCGGCTCAAGGAGTTC
CTGGGCGAGCAGCGGCGGCGCCGGGCTGAGGCTGCCACCCGCCACAAGGTGCTGCTGCGC
TCCTACCTTGGCGGCCCTTAGAGGCACGGACCACAGCCAGGCCCTCGGGCTTCAACTGGGG
TTCCCACCAATGCCACGGGACATTCCAGGGCCACGCTGAGCCAGGCGGGCCTGGGGCTT
CGGTTACCACCAGCAGCAACATCTGGCTGGGCTCTTACCTCATAGACCTTCAAGGACAGA
GACCCAGGGCCTGGACCTGATGCCACCCACAGGCCAAAGCCAGAGTGGGAGACCCATTGG
TCAGGCTCAGCAGGGTGGGAACAGGCAGAGGGACAAGAGGGGAATGGAGAAGTGGAGAGG
AAAAGGAATCGAGGGACAGGAAGGGGGAGGCTCTAGGAAGGTTCTGGGTTGGGGGTGAGT
GCATCTCAGGGAGAACCAAGGAAGGTGGGCATGGCTGGAGAGGAGGAAAAGGAAGGAGCC
CCAGGTGTGAGGGCAGTAGGCTGGGAGTCAGTGTGGCAAAGCGGGGGCAGGACACAGATA
CAGTGGCAGGGGCCAGGGCTGGGACATGAGAGAAGGCAGCGAGCGGCAGAGGGAGAAG
AGAGGACTCAGGTGGAGGTGGGGTGGGTGAGCTGTGAGCATCCCTCAGAGGAGAAATGTG

FIGURE 2II

GAGAGCTGGAGGCCAGCAGTCACTCACACTCGCTCTGTCTCCTGTCCAGTGGATACAGC
CCTGGGCGCTCTGCTGGCCCAAGGATGTCCCCACTGCCCCTCCATGGCCTTTGGCCTTCT
TCCCATTCATATTTATTTATTTATTGACTTTTATGAAGTTTCCCCTTCCATCCGATCCCT
ACTGCCCATGTTGTCTGACCATCCCTCCCAGCCATCCAGCTGTCTGTCTGTCTGCCACA
AGGAAATAAAAATGGCAAGCAGCAAAAAA

SEQ ID NO: 43_AA542015_M SGK088_M

GCCACGGACATCTGGGGAGCGGGTGTGCTCACCTACATCATGCTTAGTGGGTACTCCCCA
TTCTATGAGCCAGACCCCCAGGAAACAGAGGCTCGGATTGTTGGGGGTGCTTTGATGCC
TTCCAGTTGTATCCTAACACATCCCAGAGTGCCACCCTCTTCTTGAGAAAGGTCTCTCA
GTACATCCCTGGAGCCGGCCCTCTCTGCAGGACTGCTTGGCCCACCCATGGCTGCAAGAT
GCCTACCTGATGAAGCTGCGCCGCCAGACACTCACCTTCACCACCAACCGGCTCAAGGAA
TTCCTGGGCGAGCAGCGGGCAGCTCGGGCTGAGGCTGCTACCCGTCACAAGGTGCTGCTC
CGCTCCTACCTGGCAGCCCCCTAGGTGGCACAGACCGCAGCCCGGCCACGGGCTTCAACT
TGGGTTCTCACTCGCGCTGCCAAGGGACATTCCAGAGCCCATGCTGAGCTGGACAGGCAG
GGGCTTCAGATACCAGCAGCAGCAGCAGCAGCAGCAGCAACATCTGGCTGGGCTATT
ACCTCATGGACCTAAGAGGACAAGGCCCTGGGGCTTCAGCCGAATGTCACCCCGGCCATA
ACCAGAGCAGGAGACCCACTGGCCAGGCTGGGCAAGGGTGAGAGCAGAAAGAGGCAAAGA
GGGAGTTGGGAAGTGAAGAATGAGACGGAGGATAGAGAGGGAGGAGTTTGAGGAAGGTTT
TAGGCTGGAGTGGAAATGCTATATCTCAGGGAGAAGCCAGAAGGGGACATGGCTGAAGAGG
AAGAAGGACCTGTGATGTGGGAATGTGGTGGAGAGGAGGACTGGACATAGAGAGTGTGC
CAGGAGCCAGAGCAGAGACATAAGGGAGGGCAGAAGGGTAGAAGGCAACAGGAGTGGGCT
CAGGGGTGGCAGGGCAGGCCAGCAGCTGCATCTTCAGAAAGAGAGAGGAGAAAGGCAAAG
AGACGAAAGGCCGCTCCAGCTGGTCTCCTGTCCCAGCCGATGCAGTTCTGGGCGTTCTCC
ACTGGCCCAGGGATGTCTCACTGCTCCTCCATGGCCTTTGCCCTCCTTCCCATTTGTAT
TTATTTATTTATTGCCTTTTGTGGAGTTTCTTTCTATCCAGTCCCTAGTGCCTATGTTG
TCCCGACCATCCCCCTTCAGTCACCCAGCTGTCTGTGCAGCTGTCTGTCTGTCTGTCTCACA
AGGAAATAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAGC

SEQ ID NO: 44_R19772_H

ATGAAGGGCGGCGACAGGGCTTACACCCGAGGTCCCTCTTTGGGGTGGCTCTTTGCTAAG
TGCTGCTGTTGCTTCCCGTGTAGAGATGCATACTCTCATTCCCTCAAGCGAGAATGGAGGC
AAGTCCGAGTCCGTAGCCAACCTGCAGGCCCAGCCCTCCCTGAACCTTCATCCACAGTTCC
CCGGGTCCCAAGCGCTCCACCAACACTCTTAAGAAAGTGGCTGACGAGTCTGTGCGTCGG
CTCAACAGCGGGAAGGCAGATGGAAACATCAAAAAGCAGAAGAAAGTTCGCGATGGTCGG
AAGAGCTTTGACCTGGGATCTCCCAAGCCTGGGGATGAAACAACCCCTCAGGGAGACAGC
GCTGATGAGAGCAAGAAAGGTTGGGGTGAAGATGAGCCGGATGAAGAGTCACACACACCC
CTCCCACCACCTATGAAGATTTTGAACAACGACCCTACACAGGATGAAATGTCCTCCTCT
TTGCTAGCAGCCCGGCAGGCTTCCACTGAAGTACCTACTGCTGCAGACCTTGTCAATGCA
ATAGAAAAGTTGGTCAAAAACAAGCTGAGTCTAGAAGGAAGCTCATAACGGGGGAGCTTG
AAAGACCCTGCAGGCTGCCTGAATGAGGGGATGGCCCCACCCACACCTCCTAAAAATCCA
GAAGAAGAACAGAAAGCCAAGGCCCTGAGAGGCAGGATGTTTGTCTGAATGAGCTGGTA
CAGACAGAGAAAGACTATGTCAAGGATCTGGGCATTGTGGTGGAGGGCTTCATGAAGAGA
ATAGAAGAAAAGGTTGTCCCTGAGGATATGCGAGGAAAGGACAAAATCGTGTTTGAAAT
ATTCATCAGATTTATGACTGGCATAAGGATTTTTTCTGGCGGAACTGGAAAAGTGTATC
CAGGAGCAAGACAGATTGGCACAGCTCTTTATTAAGCACGAGCGGAAGCTGCACATCTAC
GTGTGGTATTGTGAGAATAAGCCGCGCTCAGAGTACATCGTTGCTGAGTATGACGCTAC
TTTGAGGAGGTAAAACAGGAGATAAATCAGAGGCTGACACTGAGTGAAGTTCCTCATCAAG
CCCATTTCAGAGAATAACAAAATACCAAGTTGCTCCTCAAGGACTTCCTGAGATACAGTGAG
AAGGCTGGTTTGGAGTGTTTCAGATATCGAGAAAGCAGTGGAGTTAATGTGCCTTGTTCCC

FIGURE 2JJ

AAACGCTGCAATGACATGATGAATCTAGGACGTCTGCAGGGCTTTGAGGGCACTCTGACT
GCTCAGGGGAAGCTACTGCAGCAGGACACATTCTATGTGATCGAGCTGGATGCAGGCATG
CAGTCCCGGACCAAAGAGAGGGCGGTGTTCTCTTCGAGCAGATTGTCATCTTCAGTGAA
CTGCTCAGGAAGGGATCCCTCACCCCTGGCTACATGTTCAAAGGAGCATCAAGATGAAT
TACTTGGTCCTGGAGGAGAATGTGGACAATGATCCCTGCAAGTTTGCACTCATGAACAGA
GAGACTTCTGAGAGGGTTGTTCTGCAAGCCGCCAACGCTGACATCCAGCAGGCCTGGGTG
CAGGACATCAATCAAGTCTTAGAAACACAGCGAGACTTTTTGAATGCACTGCAATCGCCC
ATTGAGTATCAACGGAAAGAAAGGAGCACAGCTGTGATGAGGTCTCAACCTGCCAGGCTT
CCCCAAGCCAGCCCCAGGCCCTACTCCTCTGTTCTGCGGGCTCAGAGAAGCCCCCAAAG
GGCTCCAGCTATAACCCACCTCTGCCTCCCTGAAGATATCTACCTCCAATGGCAGTCCA
GGGTTTGAATACCACCAGCCTGGGGACAAGTTCGAAGCCAGCAAGAACGACCTGGGAGGC
TGCAATGGGACCTCGTCCATGGCCGTGATCAAAGATTACTATGCACTGAAGGAGAATGAA
ATCTGTGTGAGCCAAGGTGAGGTGGTCCAGGTCTCGCCGTCAACCAGCAGAACATGTGT
CTGGTGTACCAGCCTGCCAGCGACCATTCCCCCGCCGCGAGGGCTGGGTCCCAGGCAGC
ATCCTGGCGCCCCCTACCAAAGCCACAGCAGCAGAAAGTAGTGACGGGAGCATCAAGAAG
TCATGTTTATGGCATACTCTACGCATGAGAAAGCGGGCGGAAGTGGAGAACACGGGTAAA
AATGAAGCCACAGGGCCTCGTAAACCCAAGGATATTCTGGGCAACAAAGTCTCTGTAA
GAGACGAACAGTTCCGAGGAATCAGAGTGTGATGATCTTGACCCTAATACTAGCATGGAG
ATCTTAAATCCAAATTTTATCCAAGAAGTGGCCCCAGAATTCTTGTGCCCTTGGTGGAT
GTGACCTGCTTGCTTGGGGACACAGTGATACTGCAGTGCAAAGTCTGTGGGCGGCCAAAG
CCCACCATCACTTGGGAAGGGTCCAGACCAGAACATCCTTGACACTGATAACAGCTCAGCC
ACATACACGGTCTCCTCTTGTGATTCTGGAGAAATCACCTGAAGATCTGTAATCTGATG
CCCCAAGACAGTGGGATTTTATACCTGCATAGCAACAAATGACCACGGGACCACATCAACG
TCTGCAACAGTCAAAGTGCAAGGTGTTCCAGCAGCCCCCTAACCGCCCCATTGCCCAGGAG
AGAAGCTGCACCTCCGTGATTCTCCGCTGGCTGCCCCCTCCAGCACAGGAACTGCACT
ATTTCTGGTTTACACTGTGGAGTACAGAGAGGAAGGTTCTCAGATCTGGCAGCAGTCAGTG
GCTTCGACCTTGGACACTTACCTCGTCATCGAAGACCTTAGTCCCGGGTGTCCTTATCAG
TTCAGAGTCAGTGCCAGTAACCCCTGGGGAATCAGCCTTCCCAGCGAGCCCTCGGAGTTT
GTGCGACTTCCAGAATACGATGCTGCTGCTGATGGTGCCACCATTCTTGGAAGGAAAAAT
TTTGACTCAGCTTACACTGAGCTGAATGAAATTGGAAGAGGCCGTTTCTCTATAGTAAAG
AAATGCATTACAAAGCTACCCGCAAAGATGTGGCTGTGAAATTTGTAAACAAAAAATG
AAGAAGAAAGAACAGGCTGCCCACGAGGCTGCCCTGCTTCAGCACCTACAGCACCCCCAG
TACATCACTCTCCATGACACCTATGAGTCCCCCACATCCTACATCCTGATCTTGGAAGTG
ATGGATGATGGCCGGCTCTTAGACTACCTTATGAATCATGATGAACTGATGGAGGAAAAA
GTAGCTTTCTATATCCGAGACATCATGGAGGCTCTGCAGTACCTTCACAACTGCAGGGTT
GCACATTTGGACATAAAGCCTGAAAACTGCTCATTGACCTACGGATTCCAGTGCCTCGA
GTGAAGCTCATTGACTTGGAGGATGCTGTCCAGATCTCGGGTCACTTCCACATTACCAC
CTGCTGGGGAACCCCTGAGTTTGCTGCCCCAGAAGTCATTCAAGGCATCCCCGTCTCCCTG
GGGACAGACATCTGGAGCATCGGGGTTCTGACATATGTCATGCTGAGTGGGGTCTCCCC
TTCTTGATGAGAGCAAAGAGGAGACATGTATCAACGTATGCAGGGTGGATTTCAGCTTC
CCCCATGAATACTTCTGTGGTGTGAGCAATGCTGCCAGAGATTTTATCAATGTGATCTTA
CAGGAAGATTTTCGAGGCGGCCACAGCAGCCACATGCTTGAGCATCCATGGCTGCAG
CCCATAATGGCAGCTACTCTAAGATCCCCCTGGACACCTCCCGCTAGCATGCTTCATA
GAACGTCGCAAGCACCAGAATGATGTGCGGCCATCCCCAATGTCAAGAGCTACATTGTG
AACC GGTTGAACCAAGGGACGTAG

SEQ ID NO: 45_5R72_8_2_H

CGCCGCTGTTTGTCTCGCGCGGCCCCGTCCACTGCCCTGCGGTTGCTCTGCGGGCTGAA
AAGTTTCTCCCGGTGCAGAATTCGGGGCTCAGCGACAGCCTGCGCCGAGTGTGCGCACCT
GTCGGAGACCCGCCAGTCCGCGGCCCCGGCTTTGTTCTGTCGGAAGTGTAGTGGTGAGA

FIGURE 2KK

AAAACCTCCATGTCTGGGCACGCCTGGCTGATCTTCACCTCTTTCTTCTAGGACCTTCCTC
TGGGCTGTACGTGTGAATATGTGTCTAGTGCATCCTTAACCTGAGGACTTCACCAGTTC
GAAATTACAGTTTTTCACCATCAACTACCTTATCCTTTTGGCCTGGTTTTCTTCCTCAAA
CAGTGGAACATTTTTAAAGTTGCTTTTGTGTCAGAGTTAAACAAATGGCTGATAGTGGC
TTAGATAAAAAATCCACAAAATGCCCCGACTGTTTCATCTGCTTCTCAGAAAAGATGTACTT
TGTGTATGTTCCAGCAAAACAAGGGTTCCTCCAGTTTTGGTGGTGGAAATGTCACAGACA
TCAAGCATTGGTAGTGCAGAATCTTTAATTTCACTGGAGAGAAAAAAGAAAAAATATC
AACAGAGATATAACCTCCAGGAAAGATTTGCCCTCAAGAACCTCAAATGTAGAGAGAAAA
GCATCTCAGCAACAATGGGGTTCGGGGCACTTTTACAGAAGGAAAAGTTCCTCACATAAGG
ATTGAGAATGGAGCTGCTATTGAGGAAATCTATACCTTTGGAAGAATATTGGGAAAAGGG
AGCTTTGGAATAGTCATTGAAGCGACAGACAAGGAAACAGAAACGAAGTGGGCAATTAAA
AAAGTGAACAAAGAAAAGGCTGGAAGCTCTGCTGTGAAGTTACTTGAACGAGAGGTGAAC
ATTCTGAAAAGTGTAACCATGAACACATCATACATCTGGAACAAGTATTTGAAACGCCA
AAGAAAATGTACCTTGTGATGGAGCTTTGTGAGGATGGAGAACTCAAAGAAATCTGGAT
AGGAAAGGGCATTTCTCAGAGAATGAGACAAGGTGGATCATTCAAAGTCTCGCATCAGCT
ATAGCATATCTTCACAATAATGATATTGTACATAGAGATCTGAACTGGAAAAATATAATG
GTTAAAAGCAGTCTTATTGATGATAACAATGAAATAAACTTAAACATAAAGGTGACTGAT
TTTGGCTTAGCGGTGAAGAAGCAAAGTAGGAGTGAAGCCATGCTGCAGGCCACATGTGGG
ACTCCTATCTATATGGCCCCGTAAGTTATCAGTGCCACGACTATAGCCAGCAGTGTGAC
ATTTGGAGCATAGGAGTCGTAATGTACATGTTATTACGTGGAGAACCACCTTTTTGGCA
AGCTCAGAAGCGAAGCTTTTTGAGTTAATAAGAAAAGGAGAACTACATTTTGAAAATGCA
GTCTGGAATTCCATAAGTGACTGTGCTAAAAGTGTTTTGAAACAACCTTATGAAAGTAGAT
CCTGCTCACAGAATCACAGCTAAGGAACTACTAGATAACCAGTGGTTAACAGGCAATAAA
CTTTCTTCGGTGAGACCAACCAATGTATTAGAGATGATGAAGGAATGGAAAAATAACCCA
GAAAGTGTGAGGAAAAACAACAGAAGAGAAGAATAAGCCGTCCACTGAAGAAAAGTTG
AAAAGTTACCAACCTTGGGGAATGTCCCTGAGACCAATTACACTTCAGATGAAGAGGAG
GAAAAACAGTCTACTGCTTATGAAAAGCAATTTCTTGCAACCAGTAAGGACAACTTTGAT
ATGTGCAGTTCAAGTTTCACATCTAGCAAACTCCTTCCAGCTGAAATCAAGGGAGAAATG
GAGAAAACCCCTGTGACTCCAAGCCAAGGAACAGCAACCAAGTACCCTGCTAAATCCGGC
GCCCTGTCCAGAACCAAAAAGAACTCTAAGGTTCCCTCCAGTGTGAGACAGTACAAAAA
CAAAGCTGCTCTTGTAGCACTTTGATGAGGGGGTAGGAGGGGAAGAAGACAGCCCTATG
CTGAGCTTGTAGCCTTTTAGCTCCACAGAGCCCCGCCATGTGTTTGCACCAGCTTAAAT
TGAAGCTGCTTATCTCAAAGCAGCATAAGCTGCACATGGCATTAAGGACAGCCACCAG
TAGGCTTGGCAGTGGGCTGCAGTGGAAATCAACTCAAGATGTACACGAAGGTTTTTTAGG
GGGGCAGATACCTTCAATTTAAGGCTGTGGGCACACTTGCTCATTTTTACTTCAAATTCCT
TATGTTTAGGCACAGCTATTTATAGGGGAAAAACAAGAGGCCAAATATAGTAATGGAGGTG
CCAAATAATTATGTGCACTTTGCACTAGAAGACTTTGTTAGAAAATTACTAATAAACTTG
CCATACGTATTACAGCAGAAGTGCTTCAGTCATTCACATGTGTTTCGTGAGATTTTAGGTT
GCTATAGATTGTTTAAGACAGCTTATTTTAAATGTAGAAAAATAGGAGATTTTGTAAGTG
CTTGCCATTAACTTGCTGCTAAATTCCTAATGTATTGATTAAATCAATAAAAAACAGATG
TTACTC

SEQ ID NO: 46_SGK309_H

GGGTCCGCAGCCCCGCCCTCACAGGCCCTCCTCACTCCCCTAGGTAGATGGCCCCCTCAGG
GCAGGCCCGGCGGACACCCCTCCCTCTGGCTGGCGGATGCAGTGCCTAGCGGCCGCCCTT
AAGGACGAAACCAACATGAGTGGGGGAGGGGAGCAGGCCGACATCCTGCCGGCCAACTAC
GTGGTCAAGGATCGCTGGAAGGTGCTGAAAAAGATCGGGGGCGGGGCTTTGGTGAATC
TACGAGGCCATGGACCTGCTGACCAGGGAGAATGTGGCCCTCAAGGTGGAGTCAGCCAG
CAGCCCAAGCAGGTCTCAAGATGGAGGTGGCCGTGCTCAAGAAGTTGCAAGGTTCCGGC
CTCGGGCAGGGGGATGGGAAGGAAGAGATGATGAAGCCAGGGGCTAAGAGAGGGAAGGAC

FIGURE 2LL

CATGTGTGCAGGTTTCATTGGCTGTGGCAGGAACGAGAAAGTTTAACTATGTAGTGATGCAG
CTCCAGGGCCGGAACCTGGCCGACCTGCGCCGTAGCCAGCCGCGAGGCACCTTCACGCTG
AGCACCACATTGCGGCTGGGCAAGCAGATCTTGGAGTCCATCGAGGCCATCCACTCTGTG
GGCTTCCTGCACCGTGACATCAAGCCTTCAAACCTTTGCCATGGGCAGGCTGCCCTCCACC
TACAGGAAGTGCTATATGCTGGACTTCGGGCTGGCCCCGGCAGTACACCAACACCACGGGG
GATGTGCGGGCCCCCTCGGAATGTGGCCGGGTTTCGAGGAACGGTTCGCTATGCCTCAGTC
AATGCCCCACAAGAACCAGGAGATGGGCCGCCACGACGACCTGTGGTCCCTCTTCTACATG
CTGGTGGAGTTTGCAGTGGGCCAGCTGCCCTGGAGGAAGATCAAGGACAAGGAACAGGTA
GGGATGATCAAGGAGAAGTATGAGCACCAGGATGCTGCTGAAGCACATGCCGTCAGAGTTC
CACCTCTTCCTGGACCACATTGCCAGCCTCGACTACTTCACCAAGCCCCGACTACCAGTTG
ATCATGTGAGTGTGAGAACAGCATGAAGGAGAGGGGCATTGCCGAGAATGAGGCCTTT
GACTGGGAGAAGGCAGGCACCGATGCCCTCCTGTCCACGAGCACCTCTACCCCCGCCCCCA
GCAGAACACCCGGCAGACGGCAGCCATGTTTGGGGTGGTCAATGTGACGCCAGTGCCCTGG
GGACCTGCTCCGGGAGAACACCCGCGATGTGCTACAGGGAGAGCACCTGAGTGACCAGGA
GAATGCACCCCCAATTCTGCCCGGAGGGCCCTCTGAGGGGCTGGGCCACAGTCCCCACCT
TGTCCCCACCCCGGGGTCTGAGGCTGAAGTCTGGGAGGAGACAGATGTCAACCGGAA
CAAACCTCCGGATCAACATCGGCAAAGTAAGTCCCGCCAGGGCGAAGGGCGTGGGTGGCCT
TTTCTCTCACCCCCGATTCCAGCCTTGTGCCCTGCCCTGTTCTCTAAGCACCCCTGT
CCCCGCCAATCTCCCTGCTTGCCCGGCCTCTGTTTCCGGTCCCCTCCCCGGCACTAGCC
TCGCTGTGTCTTCATCATCATCATCCTCTGTCTCCTTCACACTGAGGAGACCATCCGCC

SEQ ID NO: 47_AA234451_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCGGCGGCGGCGGCAGGAGGGG
GAGCAGGTGCTGGCACAAGAGCAGCGGCTTGGGGGAGCCGGCAGCAGCAGTAACAGCAGC
AGCAGCCGCCGCCGCCGCCAGTAAACGCGGACCGTACCCAGGGGACTACCCAGCCG
GCCGGCCCTGGAAGCCGCGCTCGGGTCCCGCCGAGTCCGGCGGTGGGGGATGGGCAGGCA
GTGGCGGTCCCGCCTGCCGAGGGTTAACCCCGCCGGTCCCGGTCTGAGCTGGACCAGA
GCCCTCCTCCAGAAACCCCTGCGTCCGCCACGGCCAGGTAAATGGAAACCACCCTTGG
GAACTGGATGCCTGTGTAGCTGTTCTACCATATCAGTGTATTGCAATGAGTGGGGGAGGA
GAGCAGCTGGATATCCTGAGTGTGGAATCCTAGTGAAAGAAAGATGGAAAGTGTGAGA
AAGATTGGGGGTGGGGGCTTTGGAGAAATTTACGATGCCTTGGACATGCTCACCAGGGAA
AATGTTGCACTGAAGGTGGAATCAGCTCAACAACCAAAACAAGTTCTGAAAATGGAAGTT
GCTGTTTTGAAAAGCTGCAAGGGAAAGACCATGTTTGTAGATTTATTGGCTGTGGGAGG
AATGATCGATTCAACTATGTGGTCATGCAGTTGCAGGGTCGGAATCTGGCAGATCTTCGC
CGTAGCCAGTCCCGAGGCACATTACCATTAGTACCACTCTCCGGCTGGGTAGACAGATT
TTGGAGTCTATTGAAAGCATTCAATTCTGTGGGATCTTGNATCGAGACATCAAACCGTCG
AACTTCGCTATGGGTCGCTTTCTAGTACATGTAGGAAATGTTACATGCTTGATTTTGGC
TTGGCTCGACAATTTACCAATTCCTGTGGTGACGTGAGACCACCTCGAGCTGTGGCAGGT
TTTCGAGGGACAGTTCGTTATGCATCAATCAACGCACATCGGAACAGGGAAATGGGAAGA
CATGATGACCTTTGGTCCTTATTCTACATGTTGGTGGAGTTTGTGGTTGGTCAGCTGCCC
TGGAGAAAAATAAAGGACAAGGAGCAAGTAGGCTCTATTAAGGAGAGATATGACCACAGG
CTCATGTTGAAACATCTCCCTCCAGAATTCAGCATCTTTCTAGACCATATCTCTTCTTG
GATTATTTTACAAAACCAGACTACCAGCTTCTTACATCCGTGTTTGACAATAGCATCAAG
ACTTTTGGAGTAATTGAGAGTGACCTTTTGACTGGGAGAAGACTGGAAATGATGGCTCC
CTAACAACCACCACTACTTCTACCACCCCTCAGTTGCACACTCGCTTGACCCCTGCTGCA
ATTGGAATTGCCAATGCTACTCCCATCCCTGGAGACTTGCTTCGAGAAAATACAGATGAG
GTATTTCCAGATGAACAGCTTAGCGATGGAGAAAATGGCATCCCTGTTGGTGTGTACCA
GATAAATTGCCTGGATCTCTGGGACACCCCCGTCCCAGGAGAAGGATGTTTGGGAAGAG
ATGGATGCCAACAAAAACAAGATAAAGCTTGGAAATTTGTAAGGCTGCTACTGAAGAGGAG
AACAGCCATGGCCAGGCAAATGGTCTTCTCAATGCTCCAAGCCTTGGGTACCAATTCGT

FIGURE 2MM

GTCCGCTCAGAGATTACTCAGCCAGACAGAGATATTCCACTGGTGCGAAAGTTACGTTCC
ATTCACAGCTTTGAGCTGGAAAAACGTCTGACCCTGGAGCCAAAGCCAGACACTGACAAG
TTCCTTGAGACCTGGTATAAAATAGTGATTTTTCTTTTAAAGCTTCTAAGGTACCATT
ATTATTGTTGTCATTGTTGTTATTATTATTGTATATTTCTGTTACATAAAGTCTTTCAAA
TAAGAAATCCTTGCATTTTTGTAACTGAGTCTATTGAGCTCCAATTTTCATCCATGTT
TTTAATTATTATTATCCTGATTCTTAATTATTATAAATTCTATAGCATATCCTTTGGCTT
TGGAAGCTGAGCAGTAAGAGCTGATGACTTCCTAACACTAGGTACAAGTTAAATGAACAT
TTTTACAGTAACTTTGTGTTAGAAAGTAATCTCTTCCACACAACAGTGTAGTGCTGGAGAG
GGCATGATAAAGATGGCATTAGGCAGAGATGAGGGGAATACATAAAGGAGGGGAAAAAGT
AATTCATACACAAGGGACGGTGAGTTCATTCACCTTTAGTGAAGACCCTCTAGGAGTAAG
ATACTGTGGGAAAACAGATACCAATAAGTATATCATGCTTGCCCTAGAGAGTTTGCAATC
TACCTAGAGAGAAAGGAAGGTGAACTTGAGAGATCTATATACATAGGTAAAGATTGTAG
TGCATGGTTTTGAGGCACATTATCCCTACAACAATTTTGATAACAGAAGAC

SEQ ID NO: 48_AA435956_H

ACTTTTACTATATCTTTGAGATGACTGTTTTTGATTAGAGGCGAAATCAGCACGTGGT
GGCTCAAATCTCCTTATGGATAGTGTTCCTCCTCCAGCTTTTCATGTTTCAACTTTTG
CGGGGCTGGCGTACATCCACCACCAACACGTTCTTACAGGGACCTGAAACCTCAGAAC
TTACTCATCAGTCACCTGGGAGAGCTCAAACCTGGCTGATTTTGGTCTTGCCCGGGCCAAG
TCCATTCCCAGCCAGACATACTCTTCAAGAGTCGTGACCCTCTGGTACCGGCCCCCTGAT
GCTTTGCTGGGAGCCACTGAATATTCCTCTGAGCTGGACATATGGGGTGCAGGCTGCATC
TTTATTGAAATGTTCCAGGGTCAACCTTTGTTTCTGGGGTTTCCAACATCCTTGAACAG
CTGGAGAAAATCTGGGAGGTGCTGGGAGTCCCTACAGAGGATACTTGGCCGGGAGTCTCC
AAGCTACCTAACTACAATCCAGAATGGTTCCCACTGCCTACGCCTCGAAGCCTTCATGTT
GTCTGGAACAGGCTGGGCAGGGTTCCTGAAGCTGAAGACCTGGCCTCCCAGATGCTAAAA
GGCTTTCCCAGAGACCGCGTCTCCGCCCAGGAAGCACTTGTTTCATGATTATTTTCAGCGCC
CTGCCATCTCAGCTGTACCAGCTTCCTGATGAGGAGTCTTTGTTTACAGTTTTCAGGAGTG
AGGCTAAAGCCAGAAATGTGTGACCTTTTGGCCTCCTACCAGAAAGGTCAACCCAGCC
CAGTTTACGAAATGCTGGTGAAAAGAAAGGGCGAGATCACCAGGTTCTTCCAGGGCTGT
ATTTCTGCAGTTTCGGTTTTTCATTTGCTTCAGCTTACTAAGAAGCTTCAAATCTAACTCC
ATACTGAACAAGGGGCTTTATGTCCTCACCTATGACCTGGAATAGTTTAAATATGGTGTT
CAAGGCAATAGTACATAATAGTGGAAGAAAATTCAGTGGAAGGTTATTGCTATTGTGATT
TGCATAGAATTTAAGTGATTGATTTAAAAAACTGGACATAAACTAAGTCTAAGAAG

SEQ ID NO: 49_AA626859_H

AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA
TTTCTGTATATACATAACTGTATTACAGAGATATAAAACCTGAAAATATTCTAATAAC
TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGA
TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACCTCTGTGGGAGA
TACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCT
GACAGGCCAGCCACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAG
AACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCA
TGGCATCAGTATACCTGAGCCAGAAGACATGGAACTCTTGAGGAAAAGTTCTCAGATGT
TCATCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT
AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTGTATTCTTTCAAGAGGCCCAAATTA
AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAGAATCAACTGTTGCCTCT
CATACCAGGAAGCCACATCTCCCCACACCTGATGGAAGAAAACAAGTCCTCCAGTTAAA
ATTTGATCACCTTCCAAACATTTAGGAAAATGTTCTTTCAAGTGCAAAGTAATTTAATAT
GTACACATTTTGTACAAGTGAGATAGGAATTCAGTGTTTTCAAATGCAAATGAGCCATA

FIGURE 2NN

TGAAAATTAAGATGCCTTCTAGAATTGGTTTGCTCTGATCATTGCTGATTCTTTCCCCA
TGCTTTTACAT

SEQ ID NO: 50_AA061797 M

GAAAATAGCCCTGCGGAAATCCGTATGCTGAAGTTGAAACACCCAAACCTCGTGAACCT
CATCGAGGTGTTTCAAGAAAAGAGAAAGATGCATCTAGTTTTTTGAGTACTGTGATCACAC
ACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTAAAAAGTGT
GCTATGGCAAACCTTCAAGCCCTTAACCTTCTGTCACAAGCACAATTGTATTTCATCGGGA
TGTAAAACCTGAAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTTTGG
ATTTGCACGAATTCTAATTCCAGGAGACGCCTACACAGACTATGTTGCCACCAGGTGGTA
CCGAGCCCCGAACTTCTCGTGGGAGACACGAAGTACGGTTCCTCTGTAGACGTGTGGGC
CGTCGGCTGTGTTTTTGCAGAGCTCCTGACGGGTGAGCCACTCTGGCCGGGAAATCCGA
CGTGGACCAGCTTTACCTGATCATCAGGACGTTGGGGAAGCTGATTCCAAGACACCAGTC
TATCTTTAGGAGTAACCAGTTTTTCCGCGGCATCAGCATACCTGAACCAGAGGACATGGA
GACTCTTGAAAGAAAAATTCTCAAAATGTTTCAAGCTGTGGCTTTAAGTTTCATGAAGGGATG
CCTGAAGATGAATCCTGATGAGAGGCTGACCTGTGCCAGCTGCTGGACAGTGCCTACTT
TGAGTCTTTTCAAGAGGATCAAATGAAAAGAAAAGCCCGCAGTGAGGGGAGAAGCCGAAG
GCGCCAGCAGAATCAACTGCTGCCTCTTATTCTGGAAGCCACATCTCCCCACACCTGA
TGGAAGGAAACAAGTCGTCCAGTTAAAGTTTCGATCATCTTCCAAACATTTAGGGGACTCA
TCCTTCCCAGCACATCCTTTTAATATTGTCTACATAGGAATAAGACGGGAATCCTCAGCA
TCTCAAATACAGTGAGCGACGTGAACACCAGGGCACCTCTAATCACCACGGGCTCCTCCC
CTGTGCTTTTTTCCACGCCAGCTCCATCTCCTTAAACATTTCTCTTTAAATGTTGCAGTATC
AAAATGGCACATCCGAAAGAGATGCTTCCAGTTTCACCAGAGCCGGGCTTCTCAGGCAA
TCGGTACTGTGCATCTGTGGACTTATGCTCCGACCTAGGGAAAGATTTCCACGTAGCCGT
CTCACTTCAGCCGACCAGTGGTGTCTCTGAAGCAGACCCAGATCTGCTGGCTGCTGTTTGT
GGAGGGGATGGCCCTGAGCCCTCTCACTGGAGTTTCTTCTCCGTGCAGCCAGGTCTTACT
TTAGACTACATTTGTGTTATTGTGGCATGGCAATCGTGAAAGGTGGTCTAGGTTTACCCT
TGACTCCACAGCAGATGCTAGTCTCCTTCTCGTGAGGAGCTGACAAGTCTGCTTCTAAAA
CGAACTAGAGAAAAATTCCAAACGTGACCAGTTAGTGGACAGACTACAAGGAATCGACCAC
CATACCACAGTAACGCCCCCTGGATCCCTGGCTGCCACCCACTCTAAGGCTATCCTGGTT
CACCATGGTTTTCTCTTTCTTTCTTTTAAATCTATTGTACATATGAGAAAGAGGC
AGAGGGGCGAGAGAAACCTCGTGTGTGAAAATCAAAGACAAGCAGGAGGCCAGCCTAAG
CTACATAGCAAGGCCTTTTCTCTACACCCATTCTCTAAGGTTGCTTAAACCAAGTCCCT
GCTGCTGATTGTATAAACTATGAATAAGTCTACATATGTAGGACATATTGTTGTCATTG
TTGAAATATCTAAGGATCTTGGTAGAAGCAGAAGTGTTCTAAATATTCTCCACACTGGTG
AGTATCTTGGCATTTCATTTCTGACCTCATCACAGATGAACACATCAAAGGATGAGTATG
TATCACTTTGCATCTTAGAATTCTACCTGTTTGTAGCTGCGTTAAACCTTGTGAAAGGGCG
GGGCCATAACTGAACCTGTGGAGTTCTTGCTGTGTGCAGGAAACCTCTGGTTTTGTCT
CCAGCATGGAAGAAAACAGCTATAGTCACACCTACCTGAAAGTAGAAATTCAAAGTCACT
GTCCTTGACTACATATGCAGTCCAAGGCCACGCTGGGCTACACTTCTCCAGGCATGAAGG
TCCGTGTTTGTATCAAGGGGCAGGAAAGGAGAGTCCAAGGTCAAGGCCAGCCGAGGCTGC
ATAGTGAGTTGAGGCTCTTCAGCAAAAGAAAAGCAAACCTAATAGGAGTCGTTGAAGGTAG
CCACCGGCCATTTCTCTAAATATCATTCTGCTGAAAAGGGGGCTTAGTTTAGTTTGAAT
GCATTAATGTATGTAGAAGCTGGGCTATTTTCAGATTATTTGAAATTGTAGCTATTGTTAA
TTAGCACTTAATAACTAACTAGCATTATGGTAGTCTAAACTATTAGAGTTTACTACAAAG
AGGTTTTGATTGAATTATATTAACATATAATATGGATTTTAAAAATTTAAGATGTTTAA
GAAAGCTATATAAAGATTAAACATTTTTTGTGGCTGTATATTTGTGTATATACCTTGGTTG
TTCTTTAAATTATTTTAAATAAAAGCCAGAAACATT

FIGURE 200

SEQ ID NO: 51_AA397553_H

ATGCCCAATTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGAAC
TTGCAGCCGTCATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCG
AAGCACAAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTTGGTGACCCCCGAAGCA
GCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATATCAGCTCTGATTCC
GACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGAACGTCGT
GGATCAGATCGGAGCGACCGCCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGG
GACTTACTAAAAGCTAAACAGACCGAAAAAGAAAAAGCCAAGAAGTCTCCAGCAAGTCG
GGATCGATGAAGGACCGGATATCGGGAAAGTTCAAAGCGTTCGAATGAGGAGACTGATGAC
TATGGGAAGGCGCAGGTAGCCAAAAGCAGCAGCAAGGAATCCAGGTCATCCAAGCTCCAC
AAGGAGAAGACCAGGAAAGAACGGGAGCTGAAGTCTGGGCACAAAGACCGGAGTAAAAAGT
CATCGAAAAAGGGAAACACCCAAAAGTTACAAAACAGTGGACAGCCAAAACGGAGATCC
AGGAGCCCCCACAGGAAGTGGTCTGACAGCTCCAAACAAGATGATAGCCCCCTCGGGAGCT
TCTTATGGCCAAGATTATGACCTTAGTCCCTCACGATCTCATACCTCGAGCAATTATGAC
TCCTACAAGAAAAGTCCCTGGAAGTACCTCGAGAAGGCAGTCGGTCAGTCCCCCTTACAAG
GAGCCTTCGGCCTACCAGTCCAGCACCCGGTCACCGAGCCCCCTACAGTAGGCGACAGAGA
TCTGTGAGTCCCTATAGCAGGAGACGGTTCGTCCAGCTACGAAAGAAGTGGCTCTTACAGC
GGGCGATCGCCAGTCCCTATGGTCGAAGGCGGTCCAGCAGCCCTTTCTTGAGCAAGCGG
TCTCTGAGTCGGAGTCCACTCCCCAGTAGGAAATCCATGAAGTCCAGAAGTAGAAGTCCCT
GCATATTCAAGACATTTCATCTTCTCATAGTAAAAAGAAGAGATCCAGTTCACGCAGTCGT
CATTCCAGTATCTCACCTGTGAGCTTCCACTTAATTCCAGTCTGGGAGCTGAACTCAGT
AGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGCAGCAAAGATGGATGGAAAGGAGTCC
AAGGGTTCACCTGTATTTTTGCCTAGAAAAAGAGAACAGTTCAGTAGAGGCTAAGGATTCA
GGTTTGGAGTCTAAAAAGTTACCCAGAAGTGTAATAATTGGAAAAATCTGCCCCAGATACT
GAACTGGTGAATGTAAACATCTAAACACAGAGGTAAAAAATTCTTCAGATACAGGGAAA
GTAAAGTTGGATGAGAACTCCGAGAAGCATCTTGTTAAAGATTTGAAAGCACAGGGAAACA
AGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGTTACTCCAAGGAGACAGAAACA
TCAGAAAAGGAGACCCCTCCACCTCTTCCCACAATTGCTTCTCCCCACCCCTCTACCA
ACTACTACCCCTCCACCTCAGACACCCCTTTGCCACCTTTGCCTCCAATACCAGCTCTT
CCACAGCAACCACCTCTGCCTCCTTCTCAGCCAGCATTTAGTCAGGTTCCCTGCTTCCAGT
ACTTCAACTTTGCCCCCTTCTACTCACTCAAAGACATCTGCTGTGTCTCTCAGGCAAT
TCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGTAACAGCTGCTATTCCA
CACCTGAAAACTTCAACGTTGCCTCCTTTGCCCTCCCACCTTATTACCTGGAGGTGAT
GACATGGATAGTCCAAAAGAACTCTTCCTTCAAACCTGTGAAGAAAGAGAAGGAACAG
AGGACACGTCACTTACTCACAGACCTTCCTCTCCCTCCAGAGCTCCCTGGTGGAGATCTG
TCTCCCCAGACTCTCCAGAACCAAAGGCAATCACACCACCTCAGCAACCATATAAAAAG
AGACCAAAAATTTGTTGTCCTCGTTATGGAGAAAGAAGACAAACAGAAAGCGACTGGGGG
AAACGCTGTGTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCAA
GTATATAAAGCCAGGGACAAAGACACAGGAGAACTAGTGGCTCTGAAGAAGGTGAGACTA
GACAATGAGAAAGAGGGCTTCCCAATCACAGCCATTTCGTGAAATCAAATCCTTTCGTGAG
TTAATCCACCGAAGTGTGTTAATCATGAAGGAAATTGTGACAGATAAAACAAGATGCACTG
GATTTCAAGAAGGACAAAGGTGCCTTTTACCTTGTATTGAGTATATGGACCATGACTTA
ATGGGACTGCTAGAATCTGGTTTGGTGCATTTTCTGAGGACCATATCAAGTCGTTTCATG
AAACAGCTAATGGAAGGATTGGAATACTGTACAAAAAGAAATTTCTGCATCGGGATATT
AAGTGTCTTAACATTTTGCTGAATAACAGTGGGCAAATCAAACCTAGCAGATTTTGGACTT
GCTCGGCTCTATAACTCTGAAGAGAGTCGCCCTTACACAAACAAAGTCATTACTTTGTGG
TACCGACCTCCAGAACTACTGCTAGGAGAGGAACGTTACACACCAGCCATAGATGTTTGG
AGCTGTGGATGTATTCTTGGGGAATATTACAAAGAAGCCTATTTTCAAGCCAATCTG
GAACTGGCTCAGCTAGAATGATCAGCCGACTTTGTGGTAGCCCTTGTCCAGCTGTGTGG
CCTGATGTTATCAAACCTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGG

FIGURE 2PP

CGTCTACGAGAAGAATTCTCTTTTCATTCCTTCTGCAGCACTTGATTTATTGGACCACATG
CTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCTACAGAGCGACTTCCTT
AAAGATGTGGAACCTCAGCAAAATGGCTCCTCCAGACCTCCCCCACTGGCAGGATTGCCAT
GAGTTGTGGAGTAAGAAACGGCGACGTCAGCGACAAAGTGGTGTGTAGTCGAAGAGCCA
CCTCCATCCAAAACCTTCTCGAAAAGAACTACCTCAGGGACAAGTACTGAGCCTGTGAAG
AACAGCAGCCCAGCACCACCTCAGCCTGCTCCTGGCAAGGTGGAGTCTGGGGCTGGGGAT
GCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGAATTGGCAGTGTTATTA
AACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACATC
CACTCCAACCCAGAGATGCAGCAGCAGCTGGAAGCCCTGAACCAATCCATCAGTGCCCTG
ACGGAAGCTACTTCCCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAG
GAAGCACCCCTCTGCCCCAGTGATCCTGCCCTTCAGCAGAACAGATGACCCTTGAAGCTTCA
AGCACACCAGCTGACATGCAGAATATATTGGCAGTTCTCTTGAGTCAGCTGATGAAAACC
CAAGAGCCAGCAGGCAGTCTGGAGGAAAACAACAGTGACAAGAACAGTGGGCCACAGGGG
CCCCGAAGAACTCCCACAATGCCACAGGAGGAGGCAGCAGCATGTCCTCCTCACATTCTT
CCACCAGAGAAGAGGCCCCCTGAGCCCCCGGACCTCCACCGCCGCCACCTCCACCCCTT
CTGGTTGAAGGCGATCTTTCCAGCGCCCCCAGGAGTTGAACCCAGCCGTGACAGCCGCC
TTGCTGCAACTTTTATCCCAGCCTGAAGCAGAGCCTCCTGGCCACCTGCCACATGAGCAC
CAGGCCTTGAGACCAATGGAGTACTCCACCCGACCCCGTCCAAACAGGACTTATGGAAAC
ACTGATGGGCCTGAAACAGGGTTTCAGTGCCATTGACACTGATGAACGAAACTCTGGTCCA
GCCTTGACAGAATCCTTGGTCCAGACCTGGTGAAGAACAGGACCTTCTCAGGCTCTCTG
AGCCACCTTGGGGAGTCCAGCAGTTACCAGGGCACAGGGTCAGTGCAGTTTCCAGGGGAC
CAGGACCTCCGTTTGGCCAGGGTCCCCCTAGCGTTACACCCGGTGGTGGGCAACCATTCT
CTGAAGGCTGAGGGAAGCAGCAATTCTGTGGTACATGCAGAGACCAAATTGCAAAACTAT
GGGGAGCTGGGGCCAGGAACCACTGGGGCCAGCAGCTCAGGAGCAGGCCTTCACTGGGGG
GGCCCAACTCAGTCTTCTGCTTATGGAACCTCTATCGGGGGCCTACAAGAGTCCCACCA
AGAGGGGGAAGAGGGAGAGGAGTTCTTACTAA

SEQ ID NO: 52_AA789239_H

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TGAAATGTAAACATAAGAATACTGGGCAGATAGTGGCCATTAAGATATTTTATGAGAGAC
CAGAACAATCTGTCAACAAAATTGCGATGAGAGAAATAAAGTTTCTAAAGCAATTTTCATC
ACGAAAACCTGGTCAATCTGATTGAAGTTTTTAGACAGAAAAAGAAAATTCAATTTGGTAT
TTGAATTTATTGACCACACAGTATTAGATGAGTTACAACATTATTGTTCATGGACTAGAGA
GTAAGCGACTTAGAAAAATACCTCTTCCAGATCCTTCGAGCAATTGACTATCTTCACAGTA
ATAATGTAATCATTTCGAGATATAAAACCTGAGAATATTTTAGTATCCAGTCAGGAA
TTACTAAGCTCTGTGATTTTGGTTTTGCACGAACACTAGCAGCTCCTGGGGACATTTATA
CGGACTATGTGGCCACACGCTGGTATAGAGCTCCCGAATTAGTATTAAGATACTTCTT
ATGGAAAGTATGTGCCTGTGGATATCTGGGCTTTGGGCTGTATGATCATTGAGATGGCCA
CTGGAAATCCCTATCTTCTAGTAGTTCTGATTTGGATTTACTCCATAAAATTGTTTTGA
AAGTNGGATTTCATGCCAGAACTGAAAGCTAAATTACTGCAGGAAGCAAAGTCAATTCAT
TAATAAAGCCAAAAGAGAGTTCTAAAGAAAATGAACTCAGGAAAGATGAAAGAAAACAG
TTTATACCAATACACTGCTAAGTAGTTTCAGTTTGGGAAAGGAAATAGAAAAAGAGAAAA
AGCCCAAGGAGATCAAAGTCAGAGTTATTAAGTCAAAGGAGGAAGAGGAGATATCTCAG
AACCAAAAAAGAAAGAGTATGAAGGTGGACTTGGTCAACAGGATGCAAATGAAAATGTTC
ATCCTATGTCTCCAGATACAAAACCTTGTAACCATTTGAACCACCAAACCTATCAATCCCA
GCACTAATGTAATGGCTTGAAAGAAAATCCCAATTGCGGAGGTCTGTGACAATGCCAC
CCATCAATCTAATAACAGTAATTTGATGGCTGCAAATCTCAGTTCAAATCTCTTTTACC
CCAGTGTGAGGTTAACTGAAAGAGCAAAAAAGAGACGCACTTCTTCACAATCTATTGGAC
AAGTTATGCCTAATAGCAGGCAAGAGGATCCAGTCTTATTCAAAGCCAAATGGAGAAGG
GTATATTTAATGAGCGAACAGGTACAGTGACCAAATGGCAAATGAGAACAAAAGGAAGC

FIGURE 2QQ

TGAATTTTTCCAGATCTGACAGGAAAGAATTCATTTTTCCAGAATTGCCTGTCACAATAC
AGTCAAAAGATACAAAAGGAATGGAAGTTAAACAGATAAAAATGCTGAAGAGGGAGTCAA
AGAAAACAGAGTCATCTAAGATACCAACTTTACTTAACGTGGATCAAAATCAAGAAAAAC
AAGAGTTTATTCCCTTATCTCTGCTGTCTGCCTGCTGTCTTATTTTTCAAAATATTTGCT
CTCAGCTAACTATCAGGGTGGAGATGGCCATTGCGAGGGGAAGAATTTGAAGAGAAACAG
GTTTTTTTTCTGGTAGTGTCTTTTTCTTTTACATAGTCCAAAAAATACAAGATGACAACCTC
TTCCCGTTTTTATTTATCTACAATAGAAAGTGTGATGTGAGTTGTTGTTAAGACAGCCATCC
ATGTGCATGAGCATCATCCAGCTTTTTTTTGTAGCAAAACATTTACTGTTTTCTTTTCCC
TTTTAAGACTCTGTTGATGTGATAATTTGATTTGGAATTATAAAGTCATCTCTTCTCTGC
CTTGAA

SEQ ID NO: 53_AA124976_M

CTGGCAGATATAGTTTCATGCTTGTTTACAAATTGATCCTGCTGAGAGGACATCATCTACT
GATCTTTTTCGCTCACGATTACTTTACTAGAGATGGATTTATTGAGAAATTCATACCAGAG
CTGAGAGCTAAATTATTACAGGAAGCAAAGGTTAATTCATTTATAAAGCCAAAAGAGAAT
TTTAAAGAAAATGAACCTGTGAGAGATGAGAAGAAATCAGTTTTTACCAACACCCTGCTC
TATGGAAATCCATCCTTTATGGCAAGGAAGTGGACAGAGACAAAAGGGCCAAGGAGCTC
AAAGTCAGAGTCATTAAGGCCAAAGGGGGCAAAGGAGATGTCCAGACCAGAAGAAGCCA
GAGTATGAAGCGCACCACCGCCAGCAGGCGACAGCTGATGACACACAGCCCTCATCACTG
GACAAGAAGCCTTCTGTCTTGGAACTGACAAACCCTCTCAATCCAGTGAGAATTCTGAC
GGTGTCAAAGAAGACCCACACGCTGGGGGTTGTATGATAATGCCACCTATCAACCTGACA
AGCAGTAATTTGTTGGCCGCAAATCTCAGTTTCAAACCTTTCCACCCCAATTCACGGTTA
ACTGAAAGAACAAAAAGAGACGCACTTCTTCACAACTATTGGACAGACTTTGTCTAAT
AGCAGACAAGAGGACACAGGTCCACACAAAGTCCAAACAGAGAAAGGTGCATTTAATGAG
CGAACAGGTGAGAAATGACCAATATCGAGTGGGAACAAAAGAAAGCTGAATTTTCCCAA
TGCGACAGGAAAGAATTCATTTCCCTGAACCTGCCATTACAGTGCGAGCGAAGGAGATG
AAAGGGATGGAAGTTAAACAGATAAAAGTGCTGAAGAGAGAATCAAAGAAAACAGATTCA
TCTAAAATACCAACTTTACTTAGTATGGACCCAAATCAAGAAAAACAAGAGGGTGGAGAT
GGCGATTGTGAGGGGAAGAATTTGAAGAGGAACAGATTTTTTTTTTCCCGATAGTGCTTT
GTCTTTTAAGTAATCTTAAAAATACAAGCTTGACAATTCCTTCCTTTTTATTTTATATAC
ACTAGAATGTACATAGGTTGCTGCTAAGATAGCCACCCATCCCATCTGCATCAACATCAT
CTATTTTTTTGGTTTTGCTAGCAAAATTTTCAAAATTTTCTCTATCTTCCAAAACTGT
TATTTTGATGCTGTGATTTGAAATTATAAAGTCACCTCCTCTGTCTGCTTCCTTCCTTGC
CATGATTACTGAGTGGGTAGTCACATGATGTGCCCTGCTCGCACTGCTCTCAGACTGCTG
AGACTCAAACCTCATAAGCCAGGGGTCTCCTGGGAAGCACTGGCCTCTTCAAGTGGATGC
TCGATGAACCTTCTTATCTGTTGTCTTAGTAACCACTCGTTGCCATCACATGATGAAAGA
CATTCATTGTCCCCAGTGAAGCATTTATAGTACTTACATAACATGTTACAGTGATATGA
TGTTCTAGGTTAAACTCCTTGAGATGAAACTATTTCTGCACTCTCTGACTCCCCTAGT
CTAATAGTTCTCTTCATTTAGCCAGAAGAATTTCTGGAAGCGATGCACAACCTGGGA
AAGGTTTACTTTCTATCCTGGGCTGTTTTCTGTTGCTAAATAATATAGACTGGGTAGTTA
GTTAACAT

SEQ ID NO: 54_AA575635_M CCRK_M

AGCGCCTCAGGCCAGCTCAAGATAGCTGACTTTGGCCTGGCCCCGGTCTTCTCTCCGGAT
GGTGGTGCCTCTACACACATCAGGTGGCCACCAGGTGGTACCGAGCTCCTGAACTCCTG
TATGGCGCTCGGCAGTATGACCAGGGCGTTGACCTATGGGCTGTGGGCTGCATCATGGGA
GAGCTGTTGAATGGGTCCCCCTGTTCCCGGGCGAAAACGACATTGAACAACTGTGCTGT
GTGCTTCGCATCCTGGGTACCCCGAGTCTCGAGTCTGGCCGGAGATCACAGAGCTGCCT
GACTACAACAAGATCTCCTTCGAGGAGCAGGCACCAGTGCCCTGGAGGAGGTGCTGCCT
GATGCCTCTCCCCAGGCCTTGACCTGCTGGGCCAGTTCTCTCTACCTCCACGACAG

7/113

FIGURE 2RR

CGTATTGCAGCCTCCCAGGCCCTTCTGCATCAGTACTTCTTCACAGCGCCTCTGCCTGCC
CATCCATCCGAGCTGCCAATTCCCTCAGCGCCCAGGGGGACCTGCACCCAAGGCTCACCCA
GGGCCCCCCCCATGTCCACGACTTCCATGTGGATCGACCTATTGAGGAGTCACTGTTGAAC
CCAGAACTGATTTCGGCCCTTCATCCCAGAGGGGTGAGATGCTGGTCCAGGCCTTCCTGCT
CGCCCTAGGAGCACCTCTTTCTGATTTGCCCTCCATGGCCTCCCCACGGCTATATATACCA
CACCTGGTCTGCTCCTGAGTGTGCTTGAGGGCTGGGCTCTGGGAGGCAGAACCGTGAGA
TGTTTCATCCCAGCAGAGAAAGAGACTCACGTCCACAGACAAAGCCTCCAGAACTGCTA
GCTGTGTCTTCTCCAGGGCCACCCCTCAGTGGTGCCACCCGGCCTTAGAGATGATTGTC
AGGCTCTGTCCCTCTTCAAGGACATTGGTACTACAGCACCACTGGTGGAAGCACAGAG
TATAAGCTGTCTTCATACTGGGGACACAGCTGGGAAGTCAGACATGTTTTAGTTTTGGTT
CCACTGGGTGAGGATTTGAGGTTTCATATAAAAGCCCTGGGTGTTTCTGTCTAATTGCACC
TTGTCTGTTGCTGTTAGGGAAAGGACAATGGTGGGCCTTGATTACAGGGGTGAGGTACT
CAGAAGGGGCTCCTGTGAAGGCCATTTGGGTCTCAGGCTTCCCATGCTATTACGGGA
CTTGAGTGCTCATTTGGGAGCGAGGGTCCAGAAGCTGAGGCCAGGGATGGACAGTCCAG
TTCCCGAAGCCCACTTCCACATGTGGGTGGGTGAGTCACTGAGCCTGAGGCTGCCTTG
CAGATGCGGAAGCAGGCATTCCTGGAATCCACTCAGTAAATAAATTCCAGTGTGACTCAG

SEQ ID NO: 55_AA631990_H

GAACAACAATAACAGAATAAGGAAGAAAATCTCATGATTACCTCAATAAGTACAGAGAAA
TCTGGTCACACTCACTATCCATTTCATGATTACAACCTTTCAATACTATCGCGGCCGAGGA
GGGAAGACGGCAGTTTGGCGACATTTCTCGGCCGAAGGGCCATTTGCTTTTGCGGAGATG
CGGCATTCCAAAAGAACTCACTGTCTGATTGGGATAGCAGAGAAAGCTGGGGACATGAA
AGCTATCGTGGAAGTCACAAGCGGAAGAGGAGATCTCATAGTAGCACACAAGAGAACAGG
CATTGTAAACCACATCACCACTTTAAAGAATCTGATTGTCTATTATTTAGAAGCAAGGTCC
TTGAATGAGCGAGATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGT
GAAGGATATGTTTCTAGACATTATCACAGAGACATTGAAAGCGGGTATCGAATCCACTGC
AGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCTTAAAGGAAGCGCAATAGACACTGT
TCAAGTCATCAGTCACGTTTCGNATGAAATCGTGACACTTTGGGTGAAGGAGCCTTTGGC
AAAGTTGTAGAGTGCAATTGATCATGGCATGGATGGCATGCATGTAGCAGTGAAAATCGTA
AAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTTCAAAAATCCAAGTATTAGAGCACTTA
AATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCAT
CATGGTCATGTTTGTATTGTGTTTGAACACTGAGGACTTAGTACTTACGATTTTCATTAAA
GAAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGC
CAGTCAATAAATTTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAAT
ATTTTGTGTTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGTGATGAA
CGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAT
GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCT
TTAGGTTGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTAC
CTTGGTTTTCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA
ATATTAGGACCCATACCACAACACATGATTACAGAAAACAAGAAAACGCAAGTATTTTCAC
CATAACCAGCTAGATTGGGATGAACACAGTTCCTGCTGGTAGATATGTTAGGAGACGCTGC
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GTTTGAAGAATGTTAGAATATGATCCAACCTCAAAGAATTACCTTGGATGAAGCATTGCAG
CATCCTTTCTTTGACTTATTAATAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATA
CTTCTCTAGAAGAGATTACTTAAGACTGTGTCACTCAACTAAACATTCTAATATTTTGT
AAACATTAAATTATTTGTACAGTTAAGTGTAATATTGTATGTTTTGTATCAATAGCAT
AATTAACCTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAATAATTTT
TCTTTTGAATTACCATTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAAT
GTGATTGATCTTGCCCTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTTGTAGTAA
AGGAAATCTTGACTACTTTATATTCTTAAAGGAATATTCTTATATACTTCAAATTTAGA

FIGURE 2SS

ACTTAACTTTAAAAGTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAACTCTAG
ATAAGCAGGTACTAGAAAACCAAACCTCAGAAAATGTTTACTGTTAGAATTCTATTAAATT
TTAAGTGTGTGATTCTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAA
AGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAACCACATACACACTTTATTT
AAGATTAAAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGT
GAGTCACAGATATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCC
TTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTAT
AAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAG
GATTTGATTGGAAAGCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAATTTAATTGA
TTGGTTACATAAACTTTTGGACTTCAAT

SEQ ID NO: 56_AA557536_H

AGTAAGGCCCCGCGGGCGTCCTGGCCGCCATGTGCACCGTAGTGGACCCTCGCATTTGTCC
GGAGATACCTACTCAGGCGGCAGCTCGGGCAGGGGAGAACATTCCGGGAAATCACGCTCC
TCCAGGTGAGTGGCCTGGGCCCTCCAGTCCAATCCCCTTGCCCAGGTACAGATCTCTCCA
GACAGGAGAGAACTGGCCTTCTTGGGCCCCAGAGCACAGCCCCCTCCTGGCCTTCCAGCC
GCCTCCGACTCTCTCCCCAGGAGTTTGGGGACCATCCCAACATCATCAGCCTCCTTGACG
TGATCCGGGCAGAGAACGACAGGGACATTTACCTGGTGTGTTGAGTTTATGGACACTGACC
TGAACGCAGTCATCCGGAAGGGCGGCCTGCTGCAGGACGTCCACGTGCGCTCCATCTTCT
ACCAGCTCCTGCGGGCCACCCGGTTCCTCCACTCGGGGCACGTTGTGCACCGGGACCAGA
AGCCGTCCAATGTGCTCCTGGATGCCAACTGCACAGTGAAGCTGTGTGACTTTGGCCTGG
CCCGCTCCCTGGGCGACCTCCCTGAGGGGCCTGAGGACCAGGCCGTGACAGAGTACGTGG
CCACACGCTGGTACCGAGCACCGGAGGTGCTGCTCTCTTCGCACCGCTACACCGCTTCCT
GCCCCAGATACACCTTGGGGTGGACATGTGGAGTCTGGGCTGTATCCTGGGGGAGATGC
TGCGGGGGAGACCCCTGTTCCCCGGCACGTCCACCCTCCACCAGCTGGAGCTGATCCTGG
AGACCATCCACCGCCATCTGAGGAGXXXAGGCCACGACAGACGCTGGATGCCCTCCTAC
CGCCAGACACCTCCCCAGAGGCCTTGGACCTCCTTAGGCGACTCCTGGTGTTCGCCCCGG
ACAAGCGGTTAAGCGCGACCCAGGCACCTGCAGCACCCCTACGTGCAGAGGTTCCACTGCC
CCAGCGACGAGTGGGCACGAGAGGCAGATGTGCGGCCCCGGGCACACGAAGGGGTCCAGC
TCTCTGTGCCTGAGTACCGCAGCCGCGTCTATCAGATGATCCTGGAGTGTGGAGGCAGCA
GCGGCACCTCGAGAGAGAAGGGCCCGAGGGTGTCTCCCCAAGCCAGGCACACCTGCACA
AACCCAGAGCCGACCTCAGCTGCCTTCTAGGACACCTGTGCAGGGTCCCAGACCCAGGC
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CCCCTGGGGCGAAGGAAGCGCCCCCTTGACACTCTCGCTGGTGAAGCCAAGCGGGAGGG
GAGCTGCGCCCTCCCTGACCTCCCAGGCTGCGGCTCAGGTGGCCAACCAGGCCCTGATCC
GGGGTGACTGGAACCGGGGCGGTGGGGTGAGGGTGGCCAGCGTACAACAGGTCCCTCCCC
GGCTTCCTCCGGAGGCCCCGGCCCGGCGGAGGATGTTTCAGCACCTCTGCCTTGAGGGTG
CCCAGGGGGGTGCCAGGGCTTTGCTTGGAGGCTACTCCCAAGCCTACGGGACTGTCTGCC
ACTCGGCACTGGGCCACCTGCCCCTGCTGGAGGGGCACCATGTGTGAGCCGCCCTACTCC
CTTCACCTGGCCCTCTGTTCCCTGCCCCAGCNCCTTCCCCAGACCCCTCTCCAGTCTCCTG
CACCCCTTAGCCCTCCCTGCTTTGCCTGGCCCCGTTGAAGTTCAGGGAGCTTGCCCCGGGT
CTCCTCGGGGAGCAGATGAGGGCCCTGCCC

SEQ ID NO: 57_N28606_H, MOK_H

ATGAAGAACTATAAAGCAATTGGCAAAATAGGAGAGGGAACGTTTTCTGAAGTTATGAAG
ATGCAAAGCCTGAGAGATGGAACTACTATGCATGTAAACAAATGAAGCAGCGCTTTGAA
AGTATTGAGCAAGTCAACAACCTACGAGAGATCCAAGCACTGAGGCGCCTGAATCCGCAC
CCAAACATTCTTATGTTGCATGAAGTGGTTTTTGACAGAAAATCTGGTTCTCTTGCACTA
ATATGTGAACCTTATGGACATGAATATTTATGAGCTAATACGAGGGAGAAGATACCCATTA

FIGURE 2TT

TCAGAAAAAAAAATTATGCACTATATGTACCAGTTATGTAAGTCCCTGGATCATATTTCAC
AGAAATGGAATATTTACAGAGATGTAAAACAGAAAATATACTAATAAAGCAGGATGTC
CTGAAATTAGGGGACTTTGGCTCCTGCCGGAGTGTCTATTCCAAGCAGCCGTACACGGAA
TACATCTCCACCCGCTGGTACCGGGCCCCGGAGTGTCTCCTCACTGATGGGTTCTACACG
TACAAGATGGACCTGTGGAGCGCCGGCTGTGTGTTCTACGAGATCGCCAGTCTGCAGCCC
CTCTTTTCTGGAGTAAATGAACTGGACCAAATCTCAAAAATCCACGATGTTCATCGGCACA
CCCGCTCAGAAGATCCTCACCAAGTTCAAACAGTCGAGAGCTATGAATTTTGATTTTCTCT
TTTAAAAAGGGATCAGGAATACCTCTACTAACAACCAATTTGTCCCCACAATGCCTCTCC
CTCCTGCACGCAATGGTGGCCTATGATCCCGATGAGAGAATCGCCGCCCCACCAGGCCCTG
CAGCACCCCTACTTCCAAGAACAGAGGAAAACAGAGAAGCGGGCTCTGGGCAGCCACAGA
AAAGCTGGCTTTTCCGGAGCACCTGTGGCACCAGGAACTCAGTAACAGCTGCCAGATT
TCCAAGGAGGGCAGAAAGCAGAAACAGTCCCTAAAGCAAGAGGAGGACCGTCCCAAGAGA
CGAGGACCGGCTATGTCATGGAAGTCCCAAACTAAAGCTTTCGGGAGTGGTCAGACTG
TCGTCTTACTCCAGCCCCACGCTGCAGTCCGTGCTTGGATCTGGAACAAATGGAAGAGTG
CCGGTGTGAGACCTTGAAGTGCATCCCTGCGAGCAAGAAGACAGATCCGCAGAAGGAC
CTTAAGCCTGCCCCGAGCAGTGTGCCTGCCACCATAGTGCGGAAAGGCGGAAGATAA

SEQ ID NO: 58_AB023153_H, ICK_H

ATGAATAGATACACAACAATCAGGCAGCTCGGGGATGGAACCTACGGTTCCGTCTGCTG
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TCCTGGGAGGAATGCATGAACCAACGGGAGGTTAAGTCTTTAAAGAAGCTCAACCATGCC
AATGTAGTCAAATTTAAAGAAGTTATCAGGGAAAATGATCATCTTTATTTTATCTTCGAG
TACATGAAGGAAAATCTTTACCAGCTCATTAAGAGAGAAATAAGTTGTTTCTGAGTCT
GCTATAAGGAATATCATGTATCAGATATTACAAGGACTCGCATTTATTACAAACTCGGC
TTCTTTTCATCGAGACTTAAAGCCTGAGAACCTCCTCTGCATGGGACCAGAACTTGTGAAA
ATTGCAGACTTTGGTTTGGCCCCGAGAAATACGATCAAAACCTCCATATACAGATTATGTA
TCTACCAGATGGTACAGGGCTCCAGAAGTACTCCTGAGGTCTACCAACTACAGCTCCCCC
ATTGACGTCTGGGCGGTGGGCTGCATCATGGCAGAAGTTTACACCCTCAGGCCACTCTTC
CCTGGAGCCAGTGAAATTGACACAATATTCAAAATTTGCCAAGTGCTGGGGACACCAAAA
AAGACTGACTGGCCTGAAGGCTATCAACTTTCAAGTGCAATGAACCTCCGTTGGCCACAG
TGTGTACCCAATAACTTTAAAGACCTTGATTCCCAATGCTAGCAGTGAAGCAGTCCAGCTC
CTGAGAGACATGCTTCAGTGGGATCCCAAGAAACGACCAACAGCTAGTCAGGCACTTCGA
TATCCTTACTTCCAAGTTGGACACCCACTAGGCAGCACCACACAAAACCTTCAGGATTCA
GAAAAACCACAGAAAGGCATCCTGGAAAGGGCAGGCCACCTCCTTATATTAAGCCAGTC
CCACCTGCCCAGCCACCAGCCAAGCCACACACGAATTTCTTCAGCAGCATCAAGCC
AGCCAGCCCCCTCTGCATCTCAGTACCCCTACAAAGCAGAGGTCTCCAGGACAGATCAC
CCAAGCCATCTCCAGGAGGACAAGCCAAGCCCCGTTGCTTTTCCCATCCCTCCACAACAAG
CATCCACAGTCGAAAATCACAGCTGGCCTGGAGCACAAAATGGTGAGATAAAGCCAAAG
AGTAGGAGAAGGTGGGTCTTATTTCCAGGTCAACAAAGGATTGAGATGATTGGGCTGAC
TTGGATGACTTGGATTTTCAGTCCATCCCTCAGCAGGATTGACCTGAAAAACAAGAAAAGA
CAGAGTGATGACACTCTCTGCAGGTTTGGAGTGTGTTTGGACCTGAAGCCCTCTGAGCCT
GTGGGCACAGGAAACAGTGCCCCCACCAGACGTCATATCAGCGGCGAGACACGCCCACC
CTGAGATCTGCAGCCAAGCAGCACTATTTGAAGCACTCTCGATACTTGCCTGGGATCAGT
ATAAGAAATGGCATACTCTCGAATCCAGGCAAGGAATTTATTCACCTAATCCATGGTCT
AGTTCTGGCTTGTCTGGAATCTTCAGGGACAATGTGAGTAATCAGCAAAGTAAATTCA
GTTGGTTCCAGCTCTACAAGTTCTAGTGGACTGACTGGAACTATGTCCCTTCCTTTCTG
AAAAAAGAAATCGGTTCTGCTATGCAGAGGGTACACCTAGCACCTATTCCAGACCCTTCC
CCTGGTTATTCCTCCCTGAAGGCCATGAGACCTCATCCTGGGCGACCATTCTTGGACACC
CAGCCTAGAAGCACTCCTGGGTTGATACCACGGCCTCCAGCCGCCAGCCAGTGCATGGC
CGGACAGACTGGGCTTCCAAGTACCCATCCCGGCGGTGA

FIGURE 2UU

SEQ ID NO: 59_AA839940_M

AGCAGCAACAATGGTGGCATGAGTGCAGAGGAGGAGATAGGGCCTGGGGCTGAGCCTATG
AGAGGACCAAGCTTGGCTACAAGGGACTGGAGAGATGAGACTGTTGGGACCACAGACCTG
CAGCAAGGCATAGACCCAGGAGCAGTGAGCCCTGAGCCTGGGAAGGACCACGCAGCCCAG
GGCCCAGGAAGAACTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT
CTAGATGACAGCGCAGCACCCCCAGCCCCCTTTTGAACACCCGGGTAGTGAGCATCAAAGAT
ACCCTGATCTCAGCAGGCTACACGGTATCCCAACATGAAGTCTTAGGAGGGGGTCGGTTT
GGCCAGGTGCACAGGTGTACAGAGAGGTCTACAGGCCTTGCACTGGCAGCCAAGATCATC
AAAGTGAAGAACGTAAAGGACCGGGAGGATGTGAAGAATGAGGTCAACATCATGAACCAG
CTCAGCCACGTAAACTTGATCCAACCTTTATGATGCGTTTGAGAGCAAGAACAGCTTCACT
CTGATCATGGAGTATGTGGATGGAGGCGAACTCTTGACCGGATCACGGATGAGAAGTAC
CACCTCACTGAGTTGGATGTGGTCTTGTTACGAGGCAGATCTGTGAGGGTGTGCATTAC
CTGCATCAGCACTATATCCTGCACCTGGACCTCAAGCCTGAGAACAATTTGTGTGTCAGC
CAGACAGGGCATCAAATTAAGATCATTGACTTTGGGCTGGCTAGAAGATACAAGCCTCGG
GAGAAGCTAAAGGTGAACCTTTGGTACTCCGGAGTTTCTGGCCCCAGAGTTGTTAACTAT
GAGTTTGTGTCAATTTCCAACAGACATGTGGAGTGTGGGAGTTATCACCTACATGCTACTC
AGTGGTTTGTCCCCATTTCTAGGGGAGACAGATGCAGAGACCATGAATTTTATTGTGAAC
TGCAGCTGGGATTTTCGATGCTGATACCTTCAAAGGGCTGTCGGAGGAAGCCAAGGACTTT
GTTTCCCGGTTACTGGTCAAAGAGAAGAGCTGTAGGATGAGCGCCACACAGTGCCTGAAA
CACGAGTGGTTAAATCACCTGCCTGCCAAAGCCTCGGGCTCCAACGTTCCGCTCAGATCC
CAACAACCTGCTGCAGAAATATATGGCTCAGAGTAAATGGAAGAAACATTTCCACGTGGTG
GCTGCAGTCAACAGGCTACGGAAATTTCCAACGTGTCCCTAATCTTCAACTCTGGTGTTC
CACTGGGCCTGGGAATTCTTGAGGCAACACGAAGTGGTAATATGAAGAGATTACTCAAGA
TTTTATGTAGATTGGCGCTTTGCTATTATTGATTTTTCTTATTTTGCAAAGAAATGATGGA
AGGAAGCAAGAAAGAAAGAAAGAAAGAGGGGAAAGAAAGGAAAGGCAAGAAAGCAA
GGAAACAGGCTACGTTGTTGCTCTTCTTGTTAGGTGAAAGTGTTTTTATTAAAGCCCTAG
GAATGTTTTTCTGCCTCGTAAGGTGAGCAGGTCTCATATGCTGCTTGCTACCCCGCACCC
TTCCTTTTGGTAATAAGAGCAGGCACGCTCAGGATGGGCAGGGAAATCCTACTTGGCTTT
TGGTCAAATTTGAATTTCTAACTTGTCTATGATTAAAGAAGCCAGTAGGGAGGGAGGTATG
GAAGAGGGAGGAATTAGGTCCAACAGTGGGGGATGAATTTGACCGAAACATTGTATAAAA
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SEQ ID NO: 60_AA460132_H

GGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAACCACTTACAGGCCGGAAAG
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GGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAGAGACAGCTGATCGGTTGGAG
CTGTTGCGCCGAGCAGTCAATGGCGGCGGCCAGAGCTACTACGCCGCGCGATGGCGAGGAG
CCCGCCCCGGAGGCTGAGGCTCTGGCCGCAGCCCGGGAGCGGAGCAGCCGCTTCTTGAGC
GGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGTTCGTGGCCGCTTCCAGGGC
CGCGCGGCGGTGATCAAGCACCGCTTCCCAAGGGCTACCGGCACCCGGCGCTGGAGGCG
CGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCGGCGCTCCTCCGCTGTGCGCGCGCT
GGAATATCTGCCCCAGTTGTCTTTTTTTGTGGACTATGCTTCCAACCTGCTTATATATGGA
GAAATGAAGGCTCAGTGACTGTTTCGAGATTATATTAGTCCACTATGGAGACTGAAAAA
ACTCCCCAGGCTCTCTCAACTTAGCCAAGACAATTGGGCAGGTTTTGGCTCGAATGCAC
GATGAAGACCTCATTGATGTTGATCTCACCACCTCCAACATGCTCCTGAAACCCCCCTG
GAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTCATTTAGCACTTCCAGAG
GATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCTCAGTACCCATCCCAACACT
GAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCCTCCAAAAAGGCCAGGCCA
GTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAAAGAGGTCCATGGTTGGGTAG
AAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTTTCAAAGTAAATTTGAAGAAA

FIGURE 2VV

TGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGATATTTTAAAGTGGTATGTG
ATCGTGTCTATTATCATCTGCACTTCACTCAAGAGCTTACTATGTGTCTAAGTCATGTTCT
AGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTTCTCCAGATTGTGACATGTA
TATCTCAGATACATGGGTGTGGCATTGAACCACATAATGAGAACATTATTCTCTTTTATG
TCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTCGCTGAGCTTACTGGCCCTCT
AACCCAGTGTTTTTTTTTTGTGTGTGTGTGTGTACATGTTATATTTATTTTGAAACCAGTTT
AATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATACAGCATGG

SEQ ID NO: 61 SGK034_H

CAGAGAGAGAAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATG
GACACGGAGGAGGGGGTAGAGGTGGTGTGGAACGAGCTCCACTTCGGAGACAGGAAGGCC
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CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACTCTGAGGCCTGCGCGAGGGTCT
ATCTTCATCACAGAGTACGTGTCTCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAG
AAGAACCACAAGGCCATGAACGCCCCGGGCCTGGAAGCGCTGGTGCACGCAGATCCTGTCT
GCGCTCAGCTTCCTGCACGCCTGCAGCCCCCAATCATCCACGGGAACCTGACCAGCGAC
ACCATCTTCATTTCAGCACACCGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTC
TCCAATGCACTTCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACTTCGG
AACCTGCACTTCTTCCCCCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATC
TTCTCCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATCCAGACCAATGGGGAC
ACCCGGGTACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCAACATG
CGGGAGTTCATCCTTTGCTGCCTGGCCCCGGGACCTGCCCGCCGGCCCTCTGCCACAGC
CTCCTCTTCCACCGCGTGTCTTTCGAGGTGCACTCGCTGAAGCTCCTGGCAGCCCACTGC
TTCATCCAGCACCAAGTACCTCATGCCTGAGAATGTGGTGGAGGAGAAGACCAAGGCCATG
GACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGAGGCCCCCGCTGCAGTGGCGG
TACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCTTGAGGATGTGAGGAATGGAATC
TACCCACTGATGAACCTTTCAGCCACTCGACCCCTGGGGCTGCCCCGTGTGCTGGCCCCA
CCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGAGCCCTTTGACTCTGAGACC
AGAAAGGTTCATCCAGATGCAGTGCAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCAT
CTCACTCTGCTTCTGGTGTCTGGAAGACCGGCTGCACCGGCAGCTGACCTACGACCTGCTC
CCAACGGACAGCGCCAGGACCTCGCCTCGGAGCTCGTGCACTATGGCTTCCTCCACGAG
GACGACCGGATGAAGCTGGCCGCCTTCTTGAGAGCAGCTTCCTCAAGTACCGTGGGACC
CAGGCCTGACCCGGAGCCCCAGCCCCAGGGGACCATGCCGGGGTGTGCCCCGGGCAGGCC
ATGTTGGGGAGACTCCAGCACCGTGGGGCTGCCCTCCTCCATGCGCCTGGGAGCACAAAG
GCCCCGGTAGTGAAGGAACCCCCGTCTCCTGAGAGTGGGGCTGACCTGCCCTTGGGCGC
CGAGGGGTGGGGGTGGGTGTGGGGGAGCCGTTAGGCCTCCAGGTCTTATAGGATCAGG
GTTGCCCCCAGAACCCCTTCCATATCCTCCATTCTCCGCCCTGAGTTCTTACCCAGGCT
GCCTGGCTGGGGCCACTGCCTCCTCAGCATGCAGGAGGCTGCCCTGTAGGGAACCCAGC
TCTGGGGCTTGGGGGTGAGGGTCAGCCCTGGACAGACCTCTGCCCAGGGAACCTGCTCCAT
GGGGTCTGGGAGAGCAGCCATCCCCTGCTGGCACCATAGACCCACACAAGGAGCCTGCAC
AGCAAGCCAGCGGTGACACACCTGCAGGTGTCAGGCATGGCACTGGGCACAACAGGGACC
TGGCAGGAGAAACAGACCACAGAGAGGTCTGGAGTTGAGGCTGTTGTGAGCAAAGCCCCCT
GGTCCACACAGCTCTGCCCTAGAGCCACCTCTTTGACCTTTTACCCACCTGAGACCAG
AACTTGACGCCCCCTCTGCAGATCTCCTCTGGCCACTGCAGCCCCCTCCAATGGGCTTTTTC
TCTCATGCATTCCCTGGCCTGGAGGCGTCAGGGACCCACATCCTCCCTGCTCCTCAGAC
TCACAGCCCCCTCCATGTTACCTCCCGACCTCCTCCCTGGGGCAGCTGCTCCTGGGCCT
CTGAGGATGTGAGCTCCTGGCTCCTGCCTCTCTCCCACTCCACTCCTGGCTCAGTCTTA
GAGATTTCTATGCCCTCATGGATTCTACCCCTGCCTTCTGGCCTCTTGATTCTTGGCTT
GCCTCTCCTCCAATTCCAACTTAGTGAAATGGCCTTAAGCATTTTAACTGTATGTATA
CATTAGCGCATTTCATGCCCTTCTAAACGCATTTCAAATGTCAACCAGGAAGGCACACCAC

FIGURE 2WW

TGTATTAGTTTTTATACTGCCGCTGTAAAATTTACCACAACTTAGTGACTTAACACAAAT
TTATTGCAATTCTGTAGGCTGGAAGTCTGACTATGGGTCTCACTGGACTAGAATCAAGGC
TGGCAGGCTGCCTTCCTTCCTGGAGGTTCTAGGGGAGACTCTGTCTCCTGCTCCTTCAGG
CTGCTGGCAGAATCCACATCCTTTCCGGTGGCAGGGCCAAGGTCCCCACTTTCTTGCTGAC
TGTAACCTAAGGCCACTTCCAGCTTGTAGAGGCTGCCTACATTCCCTGGCTCTTGCCCCC
CTCCTCCATCTTCAGAGCTAGCAGGTTTCACTGTGTGTACGAACCATTTCTCTGGTTCCC
TGCAGACAGGAAAGGTTGTCCCTAAGGACTCATGAGATTAGGTTGGGCCCAGCCAGATAA
TACATGATAATCTCCCTCCTCAAGGTTTTTAATATTAAACACATCTGCAGGACACATTTT
GCCATGTAACTAACATTCAGTGGTTCCAGGGATTAAGGAATGAACCTCTTTTGTGGGG
AAGGCTGGCATTCTGCTGACCACAGCACTCCAACCAAAGCCAAAAACCAAAGCAAGACT
TACTAACGCATATCAAAATAATTAAAGGTACAAAATCGTGAATCTCAGTTATCTTAAATA
TTCCAATACTATTTACAAAATTATTCAAATTTCTCAGCCTTCCAACCTCAAAATTAGCAAT
CTAAAGTAATTTCCATATCCTAGATGGAAACCCTCATGCTAACTGTCTGATTATGCATG
GTTCTAAATGGTTTCAGTGGCAAATACATAACATTGTACTACTGATTAACTGAACCTAA
AAGC

SEQ ID NO: 62_AA103218_M SGK034_M

CCACGCGTCCGCACCAGAGTATGGCGAAGTCAATGATGGGACTGGCTTTGTGGACATCTT
CTCCTTCGGGATGTGTGCACTGGAGATGGCTGTACTCGAGATCCAAGCCAACGGGGATAC
CAGAGTCACAGAAGAGGCCATCGCTCGAGCCAGGCACTCACTGAGTGACCCCAACATGCG
GGAATTCATCCTCTCCTGCCTGGCCCCGGGACCCTGCCCGCCGACCCTCAGCCCCAACCT
CCTCTTCCACCGAGTGCTCTTTGAGGTGCACTCGCTGAAGCTGCTGGCAGCTCACTGCTT
CATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTAGAGGAAAAGACCAAGGCCATGGA
CCTCCATGCAGTTTTTGGCTGAGATGCCGAGCCCCATGGACCCCCAATGCAGTGGCGSTA
CTCAGAGGTCTCCTTCTTGGAGCTGGACAAATTCCTAGAGGATGTCAGGAACGGGATCTA
TCCACTGATGAACTTTGGGCTGCTCGGCCCTTGGGGCTTCCCCGTGTGTTGGCCCCACC
CCCAGAGGAAGCCCCAAAAGGCCAAAACCTCCAACGCCAGAACCCCTTGACTCGGAGACCAG
GAAGGTGGTCCAGATGCAGTGCAACCTGGAAAGAAGCGAGGACAAGGCTCGGTGGCACCT
TACTCTGCTCTTGGTGCTTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCC
AACGGACAGTGGCCAGGACCTCGCTGCTGAAGTAGTGATTATGGCTTCCTGCACGAGGA
TGACAGGACAAAGCTAGCAGCCTTTCTGGAGACCACTTTTCTCAAGTACCGAGGGACGCA
AGCGTGACCTTCCAGTCTGACGGCCAGCAGAGATACAGGGGCTCAGGGTTGTCCACT
TGGCAAAGAGCCCCCACACTGCTCAAAGCTGCCTTCTGCCTGTGTTCCCTGGAACCTGAAC
ACAGGCCCTGCTAGTGAAGACACCCCCACCCCCAGCTTTCTGCAGCAGTGTGGGACCCT
GGGGTGGTGATGGAGCCCTGAGCCTGGACGAGAGTGGATACAGGTCAGTTAGGGGAACCG
CTCCATCTGGTACTAGACAACAGCCATGCCTTCAGGTGGCATAGAAACCTAGGGAAGGAG
CCTGAACTCAGGTGTCACAGTGCTGGGCATCAGGCAGACCAGACCTGACCTGATTGGAGA
ACTGTAGACTAGATAGCTTGGAGTTGAACCCATGGCCAGGGAATTCCTTGGTCCTGCTCA
GACCAGTCTGATCCCTTGACAGCTGCCTTGAGCCCTCTTTCTGATCTTCCACACTCTT
GAGACCAGGACCTGTGTCTCCCCAAAGCCCTTGGGAAGGATCTTTCTATTTCATCATCCC
TCTGGCCTAGGGGCTCAGGGGTCAGGCATCCTCCACATTCCTCCCTGGGGAAGTTGTGT
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TCTTACTGGTTTCAAAGTCCTGATGAACGCTTCCCCCTCAGAGCCACCCTGGTTTTCTTG
TTCTTGAAGTGCCTCTCTCCCAACTTCAAACCAGGTCTTAAACGTTTTTTTAAATGCATAT
ATAAATGTAATGCAGTCACGGTCCCTTTTTTAAACACTTTGTGTATGAAACCAGGAAAGCTC
ACTATTGTATTAGGAATAGTTCCACATTGCTGCTGTTAACAGATATCATAAACCCAGTGG
TTTGAGACGACACACACACACACACACACACACACAGAGAGAGAGAGAGATTCTGTA
CATCAAGTGTGATCCAGGCTCTCACTAGATTAATACCCAGGCTAAGTTCCTTTCTGGAAG
CTGGGACTTACCTCCTGCTCCTTCAAGCTATTGGCAGAACTCACTTCCCTGCAATGGTAA
GGCAGAAATCCCTATTTTCTCAACAGCTGCCAACTAAGAACCCTCTCAGCTTCTAGAGG

FIGURE 2XX

CCACCAACTTTTCTTAGTTCTTCTTTCTCCCCCTCAAGACCAGCAGCGTCAAGTTGAAT
CTTTGTCTGGGCTAGCTGACTGGCTTGCCACTGCTGGGAAGAGTTGGGGCCTTTTGTGA
GTAGGTTGGACCCACCAGGATAACCGAGGATGATCCCCTTCTCAGGGTCTATAGATGAAC
CACACCTGCGCAGTTCCTTCTGCTGTATCCTGGGCTTTGGTGCTTGGAGAACAGCCGTG
GGCGGTGGGTGTTGTTACTGTGGTACCTACCATGCCATCTTAACCGAAACCAAGACCTAA
AATAAACAGATTTGTCTATGGGACATCTAATAAATTAATGAAGTCTG

SEQ ID NO: 63_NEK7_H, N34132_H

CACGAATCCGAGCCCGCTCGCCTCTCTCCAGCGAACCAGCCATGTCTGGCGGCGCCGCAG
AGAAGCAGAGCAGCACTCCCGGTTCCCTGTTCTCTCGCCGCCGGCTCCTGCCCCAAGA
ACGGCTCCAGCTCCGATTCTCCGTGGGGGAGAACTGGGAGCCGCGGCCGCCGACGCTG
TGACCGGCAGGACCGAGGAGTACAGGCGCCGCCGCCACACTATGGACAAGGACAGCCGTG
GGGCGGCCGCGACCACTACCACCACTGAGCACCGCTTCTTCCGCCGGAGCGTCTCTGCG
ACTCCAATGCCACTGCACTGGAGCTTCCCGGCCCTTCTCTTTCCCTGCCCCAGCCAGCA
TCCCCGCGGCTGTCCCGCAGAGTGCTCCACCGGAGCCCCACCGGGAAGAGACCGTGACCG
CCACCGCCACTTCCAGGTAGCCAGCAGCCTCCAGCCGCTGCCGCCCTGGGGAACAGG
CCGTGCGGGGCCCTGCCCCCTCGACTGTCCCGAGCAGTACCAGCAAAGACCGCCAGTGT
CCCAGCCTAGCCTTGTGGGGAGCAAAGAGGAGCCGCCGCCGGCGAGAAGTGGCAGCGCG
GCGGCAGCGCCAAGGAGCCACAGGAGGAACGGAGCCAGCAGCAGGATGATATCGAAGAGC
TGGAGACCAAGGCCGTGGGAATGTCTAACGATGGCCGCTTTCTCAAGTTTGACATCGAAA
TCGGCAGAGGCTCCTTTAAGACGGTCTACAAAGGTCTGGACACTGAAACCACCGTGGAAG
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AAGAAGCTGAAATGTTAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCTT
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GAACACTTAAACGTATCTGAAAAGGTTTAAAGTGATGAAGATCAAAGTTCTAAGAAGCT
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ACCGCGATCTTAAATGTGACAACATCTTTATCACCGGCCCTACTGGCTCAGTCAAGATTG
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CAGAGTTTATGGCCCCGTGAGATGTATGAGGAGAAATATGATGAATCCGTTGACGTTTATG
CTTTTGGGATGTGCATGCTTGAGATGGCTACATCTGAATATCCTTACTCGGAGTGCCAAA
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TAGCAATTCCTGAAGTGAAGGAAATTATTGAAGGATGCATACGACAAAACAAAGATGAAA
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CTTCTGCTAGCACCGGCATACCTACTGCTTCTACCACTTCAGCTTCAGTTTCTACACAAG
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CTACAGGCACAGTCCCAGGGCATATACCTTCTACTGTCCAAGCACAGTCTCAGCCCCATG
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CAGTGCAAGTATTCACTTTACAGACATCAACCTCCAGTGAGGCCACTACTGCACAGCCAG
TGAGTCAGCCTCAAGCTCCACAAGTCTTGCCCTCAAGTATCAGCTGGAAAACAGAGTACTC
AGGGAGTCTCTCAGGTTGCTCCTGCAGAGCCAGTTGCAGTAGCACAGCCCCAAGCTACCC
AGCCGACCACTTTGGCTTCTCTGTAGACAGTGCACATTGAGATGTTGCTTCAGGTATGA
GTGATGGCAATGAGAACGTCCCATCTTCCAGTGGAAGGCATGAAGGAAGAACTACAAAAC

FIGURE 2YY

GGCATTACCGAAAATCTGTAAGGAGTCGCTCTCGACATGAAAAAACTTCACGCCCAAAAT
TAAGAATTTTGAATGTTTCAAATAAAGGAGACCGAGTAGTAGAATGTCAATTAGAGACTC
ATAATAGGAAAATGGTTACATTCAAATTTGACCTAGATGGTGACAACCCCGAGGAGATAG
CAACAATTATGGTGAACAATGACTTTATTCTAGCAATAGAGAGAGAGTCTGTTTGTGGATC
AAGTGCGAGAAAATTATTGAAAAAGCTGATGAAATGCTCAGTGAGGATGTCAGTGTGGAAC
CAGAGGGTGATCAGGGATTGGAGAGTCTACAAGGAAAGGATGACTATGGCTTTTCAGGTT
CTCAGAAATTGGAAGGAGAGTTCAAACAACCAATTCCTGCGTCTTCCATGCCACAGCAAA
TAGGCATTCTTACCAGTTCTTTAACTCAAGTTGTTTCAATCTGCGGGAAGGCGGTTTATAG
TGAGTCCTGTGCCAGAAAGCCGATTACGAGAATCAAAAAGTTTTCCCCAGTGAAATAACAG
ATACAGTTGCTGCCTCTACAGCTCAGAGCCCTGGAATGAACTTGTCTCACTCTGCATCAT
CCCTTAGTCTACAACAGGCCTTTTCTGAACCTTAGACGTGCCCAAATGACAGAAGGACCCA
ATACAGCACCTCCAACTTTAGTCATACAGGACCAACATTTCCAGTAGTACCTCCTTTCT
TAAGTAGCATTGCTGGAGTCCCAACCACAGCAGCAGCCACAGCACCAGTCCCTGCAACAA
GCAGCCCTCCTAATGACATTTCCACATCAGTAATTCAGTCTGAGGTTACAGTGCCCACTG
AAGAGGGGATTGCTGGAGTTGCCACCAGCACAGGTGTGGTAACCTTCAGGTGGTCTCCCA
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CAGTTGTCTCAATATCTACTACATCCCCGTCACTTCAAGTCCCCACATCCACATCTGAGA
TCGTTGTTTCTAGTACAGCACTGTATCCTTCAGTAACAGTTTCAGCAACTTCAGCCTCTG
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GCACAGCTTCACAGCTGTCCATTACAGCTTAGCAGCAGTACTTCTACTCCTACTTTAGCTG
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TGGCTTTCTCCCTCTCTGCACCATCTTCCTCTTCTCTCCTGGAGCAGGAGTGTCTAGTT
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TCCCACCCTTGGTACAGCCTGTTGCCAATGTGCCTGCTGTACAGCAGACACTAATTCTATA
GTCAGCCTCAACCAGCTTTGCTTCCCAACCAGCCCCATACTCATTGTCCTGAAGTAGATT
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GGTCTCTGTTTCACTGAACACAGCTCATCTGGAGCTCAGCATGCCTCTGTCTCACTGGAGA
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CTACTACATCAGGAGTGAAACCTGGAAGTCTCCTCCAAGCCACCTCTAACTAAGGCTC
CGGTGCTGCCAGTGGGTACTGAACTTCCAGCAGGTACTCTACCCAGCGAGCAGCTGCCAC
CTTTTCCAGGACCTTCTCTAACCAGTCCCAGCAACCTCTAGAGGATCTTGATGCTCAAT
TGAGAAGAACAACCTTAGTCCAGAGATGATCACAGTGAATCTGCGGTTGGTCTGTGTCCA
TGGCGGCTCCAACAGCAATCACAGAAGCAGGAACACAGCCTCAGAAGGGTGTCTCTCAAG
TCAAAGAAGGCCCTGTCTAGCAACTAGTTTCAAGAGCTGGTGTCTTTTAAGATGGGACGAT
TTCAGGTTTCTGTTGCAGCAGACGGTGCCAGAAAGAGGGTAAAAATAAGTCAGAAGATG
CAAAGTCTGTTTCAATTTGAATCCAGCACCTCAGAGTCTCAGTGCTATCAAGTAGTAGTC
CAGAGAGTACCTTGGTGAAACCAGAGCCGAATGGCATAACCATCCCTGGTATCTCTTCAG
ATGTGCCAGAGAGTGCCCAAAAATACTGCCTCAGAGGCAAAGTCAGACACTGGGCAGC
CTACCAAGGTTGGACGTTTTCAGGTGACAACTACAGCAAAACAAAGTGGGTCTGTTTCTCTG
TATCAAAAATACTGAGGACAAGATCACTGACACAAAGAAAGAGGACCAGTGGCATCTCCTC
CTTTTATGGATTTGGAACAAGCTGTTCTTCTGCTGTGATACCAAAGAAAGAGAAGCCTG
AACTGTCAGAGCCTTCACATCTAAATGGGCCGTCTTCTGACCCGAGGCGCTTTTTTAA
GTAGGGATGTGGATGATGGTTCCGGTAGTCCACACTCGCCCCATCAGCTGAGCTCAAAGA
GCCTTCTAGCCAGAATCTAAGTCAAAGCCTTAGTAATTCATTAACTCCTCTTACATGA
GTAGCGACAATGAGTCAGATATCGAAGATGAAGACTTAAAGTTAGAGCTGCGACGACTAC
GAGATAAACATCTCAAAGAGATTGAGGACCTGCAGAGTCGCCAGAAGCATGAAATTGAAT

FIGURE 2ZZ

CTTTGTATACCAAACCTGGGCAAGGTGCCCCCTGCTGTTATTATTCCCCCAGCTGCTCCCC
TTTCAGGGAGAAGACGACGACCCACTAAAAGCAAAGGCAGCAAATCTAGTCGAAGCAGTT
CCTTGGGGAATAAAAGCCCCCAGCTTTTCAGGTAACCTGTCTGGTCAGAGTGCAGCTTCAG
TCTTGACCCCCCAGCAGACCCCTCCACCCTCCTGGCAACATCCCAGAGTCCGGGCAGAATC
AGCTGTTACAGCCCCCTTAAGCCATCTCCCTCCAGTGACAACCTCTATTTCAGCCTTCACCA
GTGATGGTGGCATTTCAGTACCAAGCCTTTCTGCTCCAGGTCAAGGTAATAAAGCAACCA
TCATCGTCCAAAACAATAAAATGGAGATGTTGCCATACCTGGGACAAAAGCCTGTAAAG
GCGGGTTGGGAGACTAGCTGACCAGAACACAGCCTGTGTGTTGTACACTGAAGAATCTGG
GTGAAAAGGGAAGTGGAGTGATAATGAGAATCGGTGGGCTCACTGCTCCCATTAGGTGAA
ATTACTTTTTTTCAAGGAATTACAGTGAAAAGTTACATCTGTGTGGCCTATATGACTTGC
TCATTTGGGATTTGGAACCTTAGGCTTTAATATTAGGCTGAGATTTCTGGATGAAAATCT
AAGGTGTTTTAGCAGTTTCTGAAGCTAATACATTTTCTTAGCCATTGTAGAATTTTGTTA
CTTTTAAGTATGGGAGTGGCATACTAAAATGAATAACCTTACAATTACGTTTTTTATCCA
TAATCTACTTTCCAAATATAGCTCTGTTTATTAGTGATTGCTGAAAAAATTCCCACAGAG
GAAAGAGCTTTTAGTCATATTAGAACAAGAATTGAAAAGACTTGGGCATCTGGGTGAGAA
GAATGAAAAAATATAGGTACTGGCTTATGTGCCTTTGCCACAGTTTCACAGAAATTAGA
GATCAGTCTCTTCACAGGAAGAATGCACTTGATTGGTAAGGAGGGCAAACCTAGCTAGCAT
TATTCGAACTAAGAAAAGCTTCCGCATTTTGCAGATGGGTAGAATTAAGACCTAATATTT
CATCTCTTACATATCTGACCTTCCCCCAGAAGCTTGTTCTTCTGTGTGCCATCTTAGTG
CATTTACCACTCCAGCCTCAAGTTTCTAACATCTTGTAGTTGTGTTCTGTCTCTTCTCC
TCTCTGTCTTACCCTGTTTTTCCCTCTCACAGGCTGTGCGAAGTTTAACTGTGCATC
TGAACAGGTGACATTCAAACCTGGTGGCAGGAGGACCCGATTTCTGAGTACGCCCTGCTT
GGCTCTTTGTGTGTAACACCTTTACTCCTTCTTGTCTTGTGTTTCTGCTGCTTGGATC
TGATGTTTCACGCAGTCCATTTTCATTTGTCTCTTTTGTATATCATCTACTCAGTGGCT
TGGCTGAATTACTGTTACCCTCAGAAGTTTGGGCCCCCACATTAATTATGATAAAAAATG
TCAAAATAACAAGTTATCTACAAATTTCAATGTAACTTTCTGGTAGAAGTGCTTCTTCAT
GGATCTGTGACAGAGAGTGGATATGGTATCTAGGCAATAGATTGCTGGGTCATTTAGAAT
AATGAAGACTGAACTCCACAGTCGTAGTCAGTGCTGTCTGTCTGCCCTAGCATTAGAAAT
GAGAGAAATCAGCCAGACACGGTGGCGTACACCTGTAATCCCAGCACTTTGGGAGGCCGA
GGCGGGAAGATTGCTTGAGGCCAGGAGCTCGAGACCAACCCTGGGCAACATGGTGATACC
CCATCTCT

SEQ ID NO: 64_BCON3_H

GCGGAGCGCAGCTGTGAGGGAGTCGCTGTGATCCGGGGCCCCGGAACCCGAGCTGGAGCT
GAAGCGCAGGCTGCGGGGCGGGAGTCGGGAGGCCTGAGTGTTCTTCCAGCATGTCCGA
GGGGGAGTCCCAGACAGTACTTAGCAGTGGCTCAGACCCAAAGGTAGAATCCTCATCTTC
AGCTCCTGGCCTGACATCAGTGTCACCTCCTGTGACCTCCACAACCTCAGCTGCTTCCCC
AGAGGAAGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTGGAAGAGTCGCCCTGTGGGCG
CTGGCAGAAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATA
CCTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGTGGAATGAGGTACAGTTCTCTGA
ACGCAAGAACTACAAGCTGCAGGAGGAAAAGGTTCTGTGCTGTGTTTGATAATCTGATTCA
ATTGGAGCATCTTAACATTGTAAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACAA
GGCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAA
GAAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACACA
AATCCTCTCTGCCCTAAGCTACCTGCACCTCCTGTGACCCCCCATCATCCATGGGAACCT
GACCTGTGACACCATCTTCATCCAGCACACCGGACTCATCAAGATTGGCTCTGTGGCTCC
TGACACTATCAACAATCATGTGAAGACTTGTGAGAAGAGCAGAAGAATCTACACTTCTT
TGCACCAGAGTATGGAGAAGTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGG
CATGTGTGCACTGGAGATGGCAGTGCTGGAGATTTCAGGGCAATGGAGAGTCCTCATATGT
GCCACAGGAAGCCATCAGCAGTGCCATCCAGCTTCTAGAAGACCATTACAGAGGGAGTT

FIGURE 2AAA

CATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTT
CCACCCAGCATTGTTTGAAGTGCCCTCGCTCAAACCTCCTTGCGGCCCACTGCATTGTGGG
ACACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACCAAAAACATGGATACTAG
TGCCGTACTGGCTGAAATCCCTGCAGGACCAGGAAGAGAACCAGTTCAGACTTTGTACTC
TCAGTCACCAGCTCTGGAATTAGATAAAATTCCTTGAAGATGTCAGGAATGGGATCTATCC
TCTGACAGCCTTTGGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACC
TGTCGTGCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAA
GGTGGTGTCTGATGCAGTGCACATTGAGTCGGTGGAGGAGGGAGTCAAACACCACCTGAC
ACTTCTGTGAAGTTGGAGGACAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAA
TGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGA
CCAGAGCCGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTGCCAGGAA
CAGTACCCCTCAACTCAGCCGCTGTACCGTCTCCTCTTAGAGCTCACTCGGGCCAGGCCC
TGATCTGCGCTGTGGCTGTCCCTGGACGTGCTGCAGCCCTCCTGTCCCTTCCCCCAGTC
AGTATTACCCCTGTGAAGCCCCCTCCCTCCTTTATTATTACAGGAGGGCTGGGGGGGCTCCC
TGGTTCTGAGCATCATCCTTTCCCTCCCTCTCTCCTCCCTCTGCACTTTGTTTACT
TGTTTTGCACAGACGTGGGCTGGGCTTCTCAGCAGCCGCTTCTAGTTGGGGGCTAGT
CGCTGATCTGCCGCTCCCGCCAGCCTGTGTGGAAAGGAGGCCACGGGCACTAGGGGA
GCCGAATTCTACAATCCCGCTGGGGCGGCCGGGGCGGGAGAGAAAGGTGGTGTCTGCAGTG
GTGGCCCTGGGGGGCCATTCGATTGCTCAGTTGCTGCTGTAATAAAAGTCTACTTTTT
GCT

SEQ ID NO: 65_AA711829_M

CTTAAGCAGTTTCTGAAGAAGACCAAAAAGAACCACAAGACTATGAATGAAAAGGCTTGG
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ATCATCCATGGGAACCTGACCTGTGACACCATCTTCATCCAGCACACGGACTCATCAAG
ATTGGCTCTGTGGCTCCTGACACTATCAACAATCACGTGAAGACTTGCCGGGAAGAACAG
AAGAACCTACACTTTTTTGCACCAGAGTATGGAGAAGTCACAAACGTGACAACAGCAGTG
GACATCTACTCCTTTGGCATGTGTGCACTGGAGATGGCAGTGCTGGAGATTACGGGCAAT
GGCGAGTCCTCATATGTGCCACAGGAAGCCATCAGCAGTGCCATCCAGCTACTAGAAGAC
TCATTACAGAGGGAGTTTATTCAAAGTGCCTGCAGTCTGAGCCTGCTCGGAGACCAACA
GCCAGAGAACTTCTGTTCCACCCAGCACTGTTTGAAGTGCCCTCACTCAAGCTTCTTGCT
GCTCACTGTATCGTGGGGCACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACC
AAGAACATGGATACCAGTGCTGTACTAGCTGAAATTCCTGCAGGGCCAGGACGAGAACCA
GTTACAGACTTTGTACTCTCAGTCACCAGCCCTAGAATTAGACAAATTCCTTGAAGATGTC
AGGAATGGGATCTACCCTCTGACAGCCTTTGGGCTACCTCGGCCTCAGCAGCCACAGCAG
GAGGAGGTGACATCACCTGTTGTGCCCCCTCTGTCAAGACTCCAACCTCCTGAGCCAGCT
GAAGTGGAGACACGAAAGGTGGTGTCTGATGCAGTGCAACATCGAATCTGTGGAGGAGGGA
GTCAAACACCATCTAACACTTCTGCTGAAGCTGGAGGACAAATTGAACCGGCACCTGAGC
TGTGACCTGATGCCAAATGAGAGCATCCCGGACTTGGCAGCTGAGCTGGTGCAGCTGGGC
TTCATTAGTGAGGCTGATCAGAGCCGCTGACTTCTCTGCTGGAGGAGACGCTCAACAAG
TTCAACTTCACCAGGAACAGTACACTCAACACAGCCACTGTACCGTCTCCTCGTAGAGC
TCACTTGAGCCAGGCCCCCTAGCCAGGCTGTGGCTGTCCCTGGGCATGCTGCAGTCTCCT
GTCCCTTCTCCCCAGTCAGTATTACCCTTCGCGCCCATATTATTTAGGAGGGCTTTAGGG
GCTCCCTGTTGAGTATCACCTGCCCCCTCCCTCTCTTCCCTCCCTCTGCACTTTGTT
TACTTGTTTTGACAGACGTGGGCCTGGGCCTTCTCAGCAGCCACCTTCTAGCTGGGGGC
TAGTAGCTGACCTGCTGCCTCCTACTTGTGTGGACAGGAGGCCACGGGCACTGG
GGAAGCTGAGTTCTACAATCCCGCTGGGGCGCATGGGCAGGAGAGAAAGGTGGTGTCTGCA
GGGGTGGCCCCCGGGGGGGGCATTCGAATCACCTCAGTTGCTGCTGTAATAAAGTCTAC
TTTTTGCT

FIGURE 2BBB

SEQ ID NO: 66_AA099102_H

ATGTCATCATGTGTCTCTAGCCAGCCAGCAGCAACCGGGCCGCCCCCAGGATGAGCTG
GGGGGCAGGGGCAGCAGCAGCAGCGAAAGCCAGAAGCCCTGTGAGGCCCTGCGGGGCCTC
TCATCCTTGAGCATCCACCTGGGCATGGAGTCCTTCATTGTGGTCACCGAGTGTGAGCCG
GGCTGTGCTGTGGACCTCGGCTTGGCGCGGGACCGGCCCTGGAGGCCGATGGCCAAGAG
GTCCCCCTTGACACCTCCGGGTCCCAGGCCCGGCCCCACCTCTCCGGTCGCAAGCTGTCT
CTGCAAGAGCGGTCCCAGGGTGGGCTGGCAGCCGGTGGCAGCCTGGACATGAACGAGCGC
TGCATCTGCCCGTCCCTGCCCTACTCACCCGTCAGCTCCCCGAGTCCTCGCCTCGGCTG
CCCCGGCGGGCCGACAGTGGAGTCTCACCACGTCTCCATCACGGGTATGCAGGACTGTGTG
CAGCTGAATCAGTATACCTGAAGGATGAAATTGGAAAGGGCTCCTATGGTGTCTGCAAG
TTGGCCTACAATGAAAATGACAATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAAG
CTGATCCGGCAGGCCGCTTTTCCACGTGCCCCCTCACCCGAGGCACCCGGCCAGCTCCT
GGAGGCTGCATCCAGCCCAGGGGCCCATTTAGCAGGTGTACCAGGAAATTGCCATCCTC
AAGAAGCTGGACCACCCCAATGTGGTGAAGCTGGTGGAGGTCTTGATGACCCCAATGAG
GACCATCTGTACATGGTGTTCGAACTGGTCAACCAAGGGCCCGTGATGGAAGTGCCACC
CTCAAAACCTCTCTGAAGACCAGGCCCGTTTCTACTTCCAGGATCTGATCAAAGGCATC
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GGAGAAGATGGGCACATCAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAAGGGCAGT
GACGCGCTCCTCTCAACTACGTGGGCACGCCCGCCTTCATGGCTCCCGAGTCGCTCTCT
GAGACCCGCAAGATCTTCTCTGGGAAGGCCAAGGATGTTTGGGCCATGGGTGTGACACTA
TACTGCTTTGTCTTTGGCCAGTGCCCATTCATGGACGAGCGGATCATGTGTTTACACAGT
AAGATCAAGAGTCAGGCCCTGGAATTTCCAGACCAGCCCGACATAGCTGAGGACTTGAAG
GACCTGATCACCCGTATGCTGGACAAGAACCCCGAGTCGAGGATCGTGGTGCCGGAATC
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TGCACGCTGGTCAAGTGACTGAAGAGGAGGTGAGAACTCAGTCAAACACATTCCCAGC
TTGGCAACCGTGATCCTGGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTC
GAGGGCAGCCGGCGGGAGGAACGCTCACTGTCAGCGCCTGGAACTTGCTACCAAAAAA
CCAACCAGGGAATGTGAGTCCCTGTCTGAGCTCAAGGAAGCAAGGCAGCGAAGACAACCT
CCAGGGCACCGACCCGCCCCCGTGGGGGAGGAGGAAGTGCTCTTGTGAGAGGCAGTCCC
TGCGTGGAAAGTTGCTGGGGCCCCCGCCCCGGCTCCCCCGCACGCATGCATCCACTGCGG
CCGGAGGAGGCCATGGAGCCCGAGTAG

SEQ ID NO: 67_5R69_17_2_H

CCGGGATGTGAGCCTGGTGGTTGGCAGCTGGAGCCACGTCCGAGGGGGAAGTGTGCGCAGC
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GCCATCCAAGTGGCTGAGTGGAGGGACCTGCTCAAGTGCAGCTGCAGTGGCCGGGGTTT
CCCTCAGGTAGGATCGGGGCGCCTTGTCGCCGCCAGCCACGTGTGGCGTCCGGTACAGT
CAGCAGAGTGCAGGGTGCGGGCACCAAGGAAAGGGGGCGCAGGGGAACCTCCCGCGGGCCTC
GCGTTTGCAAACCTTCTCGCCTGGGCAGGAGGCGGTGCTGGGAAAGAAGGTGGAAGAGCGA
GCTTTTGGAACTGTGCACGGGACAGATTGGACGCACACCCCTCGGGAGGCGCGAAGGCA
TGAAAAATTTGAAGCATATTATCACCCCTTGCCAGGTATCCACAAACGGTGTGAAGAGA
TGAAATACTGCAAGAAACAGTGCCGGCGCCTGGGCCACCGCGTCTCGGCCTGATCAAGC
CTCTGGAGATGCTCCAGGACCAAGGAAAGAGGAGCGTGCCCTCTGAGAAGTTAACCACAG
CCATGAACCGCTTCAAGGCTGCCCTGGAGGAGGCTAATGGGGAGATAGAAAAGTTCAGCA
ATAGATCCAATATCTGCAGGTTTCTAACAGCAAGCCAGGACAAAATACTCTTCAAGGACG
TGAACAGGAAGCTGAGTGATGTCTGGAAGGAGCTCTCGCTGTACTTCAGGTTGAGCAAC
GCATGCCGTGTTTACCCATAAGCCAAGGAGCGTCTGGGCACAGGAAGATCAGCAGGATG
CAGACGAAGACAGGCGAGCTTTCCAGATGCTAAGAAGAGATAATGAAAAAATAGAAGCTT
CACTGAGACGATTAGAAATCAACATGAAAGAAATCAAGGAACTTTGAGGCAGTGTAAAGT
TATCATGTGCCCTGCTGTTCTGATGGCCCCCAAAC TAGAAGTCATCAGTTTACTGGGAC

FIGURE 2CCC

CCCAGCCTCCCGCTACCCCTGCATTTGTCCATTTTCTGTGCTGGATGGCTGGAAGCAGCC
CACAGGTTTGGGGATCCATTCATGGCTAGCCAGGCTTCTGTCCATGGAATAACATGTGG
AGAGAGCTTCTTGACCAGTAAGATACCTTCTAGCAGCTGTCAAAGTACTTAAAAACCTCT
ATGAATAGAATCAAAGCTTCAGTTCAGTTGCTGAATTTCCAAGAAGAAATTCAAATCAAA
TTTAAATGCCCACTCATTCAATTCATTCAACAAAACCTGTGAGTATCTGGTTTATGCCAGA
GGCCATGCAAAGAGGTAACATAAGATGCAGAGAAGGACACTGCCTTCCAGGAGCTCACGGG
GTGGAGGAGGAAAGAGGAAAGACAGACAGTGAACACACAACAGCAAGGTTACTGAGCTTG
AACTATGTCCCTAACTACTAGATCTGAAATGACTACGCCAGATGCCAGATGCTCAAGTGC
CAAGCTCTGGGTAACAGGAATAGACATCCTTCCAGGATGAGAGAGATGAGTCTGGATGAG
GGTTAAGGCTGGAGGGACAGGCGGGATTGGAAGAGGAGGAAAGGAAGTGGATGACACAT
TCTGTTAACTGTCCAGCTGTGTCTCTACTGGTCACTCAGAGGCACGGGAGCCGCTCCCTT
GGGCTGAGTCCATCAGAAGCCCCAGCCACCACAGCTCTGGTTCATGTAGTAGAGCTTCC
CACTCACACATCACAATATGCCACCTCCCTTAGGACCCCTTCTCTGCTCATTGACTCT
TTTGTCTTCTTCTCTCGGGGGTGAGGTGAGATTTACCACCAAAATGCATGCAGGAGAT
CCCAGCAAGAGCAAATCAAGGAGATCAAGAAGGAGCAGCTTTCAGGATCCCCGTGGATTCT
GCTAAGGGAAAATGAAGTCAGCACACTTTATAAAGGAGAATACCACAGAGCTCCAGTGGC
CATAAAAGTATTCAAAAACTCCAGGCTGGCAGCATTGCAATAGTGAGGCAGACTTTCAA
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TTGCATTGATGAAACAGTGACTCCGCCTCAATTCTCCATTGTGATGGAGTACTGTGAACT
CGGGACCCCTGAGGGAGCTGTTGGATAGGGAAAAAGACCTCACACTTGGCAAGCGCATGGT
CCTAGTCCTGGGGGAGCCCGAGGCCCTATACCGGCTACACCATTAGAAGCACCTGAACT
CCACGGAAAAATCAGAAGCTCAAACTTCTGGTAACTCAAGGCTACCAAGTGAAGCTTGC
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AGATATCCCGTTTCAAGGTGAAGAATGTGAAGACTGGCTCAGCCAGTGGCTGTAATTCTG
AGAAGATCCGCAAGCTGGTGGCTGTGAAGCGGCAGCAGGAGCCACTGGGTGAAGACTGCC
CTTCAGAGCTGCGGGAGATCATTGATGAGTGCCGGGCCCATGATCCCTCTGTGCGGCCCT
CTGTGGATGAAATCTTAAAGAACTCTCCACCTTTTCTAAGTAGTGATCAAAATCTAAA
CCAAGGAGTCTCTGGACAAGAAGCTGGGAGAGGCACGAACTGGACATCTCTCTCTCAT
ATCCTTCGGCATTGGGTTATCTATGGGTGCAAGGAGTGGGCACGCTTCTCTGTTACAAAT
AGAAAACGATTCCAGTCATACAGACACATCCCACTCCAAATGATATTTCCAAAAACATA
CCTCTGACAGTAACCTTTGATAGATGGTTTGTCAAATGTATCTTTCTGGGTATCCACACCT
CTTGGCAATGAAATTTGCAGCTCCTCCCTTCCATAAATGAAGTCTCTTTCCCCACCATT
GAATCTGGGCTGGCACTGTGACTTGATTTGATCAATAGAATGTGGAAGAAGTGACTGTAT
GCCAGTTCCAAGCCTAGGTTTCAAGAGGCCTTATAAATGTCTGTTGGAACCTTACCCAGC
CATGGACATGTTGAGTGAGCATGCTGGAGAATGAGAGACCACATGAAGCAGAAACATGCT
TTCCTAGCTGAAGTCATACTAGCCCAACCAACATGGCAGCTAACACATGAATGAGGCCAA
TCAAGACCAGAAGAACCACTCAAGCAGATCCCAGCCCAAATTGCCCATTCACACAATCAG
GAGCTAAATAAATTACTGTTGTCTTTT

SEQ ID NO: 68_H85811_H

CGCCCCGGCCCCCTCCCCGGCGCCGGCCACGGGAGGCGGTGATGCGGGCGCGGGCGGCCCT
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CGATGGCCCCCGTGTACGAAGGTATGGCCTCACATGTGCAAGTTTCTCCCTCACACCC
TTCAATCAAGTGCCCTTCTGTAGTGTGAAGAACTGAAAATAGAGCCGAGTTCCAAGTGG
ACATGACTGGGTACGGCTCCACAGCAAAGTGTATAGCCAGAGCAAGAACATCCCCCTGT
CGCAGCCAGCCACCACAACCGTCAGCACCTCCTTGCCGGTCCCAAACCAAGCCTACCTT
ACGAGCAGACCATCGTCTTCCAGGAAGCACCGGGCACATCGTGGTCACCTCAGCAAGCA

FIGURE 2DDD

GCACCTTCTGTACACGGGCAAGTCCTCGGCGGACCACACAACCTAATGCGTTCGAAGCACTG
TGAGCCTCCTTGATACCTACCAAAATGTGGACTCAAGCGTAAGAGCGAGGAGATCGAGA
ACACAAGCAGCGTGCAGATCATCGAGGAGCATCCACCCATGATTGAGAATAATGCAAGCG
GGGCCACTGTGCGCACTGCCACCACGTCTACTGCCACCTCCAAAAACAGCGGCTCCAACA
GCGAGGGCGACTATCAGCTGGTGCAGCATGAGGTACTGTGCTCCATGACCAACACCTACG
AGGTCTTAGAGTTCTTGGGCGGAGGGACGTTTGGGCAAGTGGTCAAGTGCTGGAAACGGG
GCACCAATGAGATCGTAGCCATCAAGATCCTGAAGAACCACCCATCCTATGCCCCGACAAG
GTCAGATTGAAGTGAGCATCCTGGCCCGGTTGAGCACGGAGAGTGCCGATGACTATAACT
TCGTCCGGGCTACGAATGCTTCCAGCACAAGAACCACACGTGCTTGGTCTTCGAGATGT
TGGAGCAGAACCTCTATGACTTTCTGAAGCAAAACAAGTTTAGCCCCCTTGCCCCCTCAAT
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AGGCAATTGACATGTGGTCCCCTGGGCTGTGTTATTGCAGAATTGTTCTGGGTTGGCCGT
TATATCCAGGAGATTTCGGAGTATGATCAGATTTCGGTATATTTTCAAAACACAGGGTTTGC
CTGCTGAATATTTATTAAGCGCCGGGACAAAGACAACCTAGGTTTTTCAACCGTGACACGG
ACTCACCATATCCTTTGTGGAGACTGAAGACACCAGATGACCATGAAGCAGAGACAGGGA
TTAAGTCAAAAGAAGCAAGAAAGTACATTTTCAACTGTTTAGATGATATGGCCCAGGTGA
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TCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCACTCCAATCG
AAACCTGTAACCATCCCTTTGTACCATGACACACTTACTCGATTTTCCCCACAGCACAC
ACGTCAAATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACA
CGGTGAACCAGAGCAAAACCCCTTTCATCACGCACGTGGCCCCCAGCACGTCCACCAACC
TGACCATGACCTTTAACAACCAGCTGACCACTGTCCACAACCAGCCCTCAGCGGCATCCA
TGGCTGCAGTGGCCCAGCGGAGCATGCCCCCTGCAGACAGGAACAGCCCAGATTTGTGCCC
GGCCTGACCCGTTCCAGCAAGCTCTCATCGTGTGTCCCCCGGCTTCCAAGGCTTGCAAG
CCTCTCCCTCTAAGCACGCTGGCTACTCGGTGCGAATGGAAAATGCAGTTCCCATCGTCA
CTCAAGCCCCAGGAGCTCAGCCTCTTCAGATCCAACCAGGTCTGCTTGCCCAGCAGGCTT
GGCCAAGTGGGACCCAGCAGATCCTGCTTCCCCCAGCATGGCAGCAACTGACTGGAGTGG
CCACCCACACCTCAGTGACATGCCACCGTGATTCCCGAGACCATGGCAGGCACCCAGC
AGCTGGCGGACTGGAGAAATACGCATGCTCACGGAAGCCATTATAATCCCATCATGCAGC
AGCCTGCACTATTGACCGGTGATGTGACCTTCCAGCAGCACAGCCCTTAAATGTGGGTG
TGGCCACGCTGATGCGGCAGCAGCCAACCAGCACCACCTCCTCCCGGAAGAGTAAGCAGC
ACCAGTCATCTGTGAGAAATGTCTCCACCTGTGAGGTGTCTCCTCTCAGGCCATCAGCT
CCCCACAGCGATCCAAGCGTGTCAAGGAGAACACACCTCCCCGCTGTGCCATGGTGCACA
GTAGCCCGGCTGCAGCACCTCGGTACCTGTGGGTGGGGCGACGTGGCCTCCAGCACCA
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CTGTCTCCAAGCAAAGAAAAAACGTATCAGCTGTGTACAGTCCACGACTCCCCCTACT
CCGACTCCTCCAGCAACACCAGCCCCCTACTCCGTGCAGCAGCGTGCTGGGCACAACAATG
CCAATGCCTTTGACACCAAGGGGAGCCTGGAGAATCACTGCACGGGGAACCCCCGAACCA
TCATCGTGCCACCCCTGAAAACCCAGGCCAGCGAAGTATTGGTGGAGTGTGATAGCCTGG
TGCCAGTCAACACCAGTCAACACTCGTCTCTCTACAAGTCCAAGTCTCAGCAACGTGA
CCTCCACCAGCGGTCACTCTTCAGGGAGCTCATCTGGAGCCATCACCTACCGGCAGCAGC
GGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCAGGCTCAGCAGCACA
TCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCCTACATCACTCCCACCATGG
CCCAGGCTCCGTACTCCTTCCCGCACAAACAGCCCCAGCCACGGCACTGTGCACCCGCATC
TGGCTGCAGCCGCTGCGCTGCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTG
CGCCGGCGGCCCTGGGCTCCACCGGCACCGTGGCCACCTGGTGGCCTCGCAAGGCTCTG

FIGURE 2EEE

CGCGCCACACCGTGCAGCACACTGCCTACCCAGCCAGCATCGTCCACCAGGTCCCCGTGA
GCATGGGGCCCCCGGTCTGCCCCTCGCCACCATCCACCCGAGTCAGTATCCAGCCCAAT
TTGCCCACCAGACCTACATCAGCGCCTCGCCAGCCTCCACCGTCTACACTGGATACCCAC
TGAGCCCCGCCAAGGTCAACCAGTACCCCTTACATATAAACTGGAGGGGAGGGAGGGAG
GGAGGGAGGGAGAGAATGGCCCCGAGGGAGGAGGGAGAGAAGGAGGGAGGGCGCTCCTGGGA
CCGTGGGCGCTGGCCTTTTATACTGAAGATGCCGCACACAAACAATGCAAACGGGGCAGG
GGCGGGGGGGGGGGGGCAGAGGGCAGGGGGACGGGTCTGGGACACCAGTGAAACTTGAACC
GGGAAGTGGGAGGACGTAGAGCAGAGAAGAGAACATTTTTTAAAAGGAAGGGATTAAAGAG
GGTGGGAAATCTATGGTTTTTTATTTTAAAAAAG

SEQ ID NO: 69_DYRK3_H

CGGGAGCGAAAGTGCCTGAGCTGCAGTGTCTGGTCGAGAGTACCCGTGGGAGCGTCGCG
CCGCGGAGGCAGCCGTCCCGGCGTAGGTGGCGTGGCCGACCCGACCCCCAACTGGCGCCT
CTCCCCGAGCGGGGTCCCGAGCTAGGAGATGGGAGGCACAGCTCGTGGGCCTGGGCGGAA
GGATGCGGGGCCGCTGGGGCCGGGCTCCCGCCCCAGCAGCGGAGTTGGGGGATGGTGTCT
TATGACACCTTCATGATGATAGATGAAACCAAATGTCCCCCTGTTCAAATGTACTCTGC
AATCCTTCTGAACCACCTCCACCCAGAAGACTAAATATGACCGCTGAGCAGTTTACAGGA
GATCATACTCAGCACTTTTTGGATGGAGGTGAGATGAAGGTAGAACAGCTGTTTCAAGAA
TTTGGCAACAGAAAATCCAATACTATTCACTCAGATGGCATCAGTGAATCTGAAAAATGC
TCTCCTACTGTTTCTCAGGGTAAAAGTTCAGATTGCTTGAATACAGTAAAATCCAACAGT
TCATCCAAGGCACCCAAAGTGGTGCCTCTGACTCCAGAACAAGCCCTGAAGCAATATAAA
CACCACCTCACTGCCTATGAGAACTGGAAATAATTAATTATCCAGAAATTTACTTTGTA
GGTCCAAATGCCAAGAAAAGACATGGAGTTATTGGTGGTCCCAATAATGGAGGGTATGAT
GATGCAGATGGGGCTATATTTCATGTACCTCGAGACCATCTAGCTTATCGATATGAGGTG
CTGAAAATTATTGGCAAGGGGAGTTTTTGGGCAGGTGGCCAGGGTCTATGATCACAACTT
CGACAGTACGTGGCCCTAAAAATGGTGCCTCAATGAGAAGCGCTTTCATCGTCAAGCAGCT
GAGGAGATCCGGATTTTGGAGCATCTTAAGAAACAGGATAAACTGGTAGTATGAACGTT
ATCCACATGCTGGAAAGTTTCACATTCCGGAACCATGTTTGCATGGCCTTTGAATTGCTG
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GTACGCAAGTTTGGCCAGTCCATCTTGCAATCTTTGGATGCCCTCCACAAAAATAAGATT
ATTCATGCGATCTGAAGCCAGAAAACATTCTCCTGAAACACCACGGGCGCAGTTCAACC
AAGGTCATTGACTTTGGGTCCAGCTGTTTTCGAGTACCAGAAGCTCTACACATATATCCAG
TCTCGGTTCTACAGAGCTCCAGAAATCATCTTAGGAAGCCGCTACAGCACACCAATTGAC
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GAGGATGAAGGAGACCAGTTGGCCTGCATGATGGAGCTTCTAGGGATGCCACCACCAAAA
CTTCTGGAGCAATCCAAACGTGCCAAGTACTTTATTAATTCCAAGGGCATAACCCGCTAC
TGCTCTGTGACTACCCAGGCAGATGGGAGGGTTGTGCTTGTGGGGGTCTGCTCACGTAGG
GGTAAAAAGCGGGGTCCCCAGGCAGCAAAGACTGGGGGACAGCACTGAAAGGGTGTGAT
GACTACTTGTTTATAGAGTTCTTGAAAAGGTGTCTTCACTGGGACCCCTCTGCCCGCTTG
ACCCAGCTCAAGCATTAAGACACCCTTGGATTAGCAAGTCTGTCCCCAGACCTCTCACC
ACCATAGACAAGGTGTCAGGGAAACGGGTAGTTAATCCTGCAAGTGCTTTCCAGGGATTG
GGTTCTAAGCTGCCTCCAGTTGTTGGAATAGCCAATAAGCTTAAAGCTAACTTAATGTCA
GAAACCAATGGTAGTATAACCCCTATGCAGTGTATTGCCAAACTGATTAGCTAGTGGACA
GAGATATGCCAGAGATGCATATGTGTATATTTTTATGATCTTACAAACCTGCAATGGA
AAAAATGCAAGCCATTGGTGGATGTTTTTGTAGAGTAGACTTTTTTTTAAACAAGACAA
AACATTTTTTATATGATTATAAAAGAATTCTTCAAGGGCTAATTACCTAACCAGCTTGTAT
TGGCCATCTGGAATATGCATTAAATGACTTTTTTATAGGTCA

FIGURE 2FFF

SEQ ID NO: 70_AA589241_M DYRK3_M

CCACGCGTCCGGAGTTGCTAGGAATGCCACCGCAGAACTTCTGGAGCAATCCAAGCGTG
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ACGGGAGGGTGCTTCTCGGGGGTCTGCTCACGCAGGGGTAAAAAGCGAGGCCCGCCAG
GCAGCAAAGACTGGGCAACCGCACTGAAGGGCTGTGGTGACTACTTGTTTCATAGAGTTTC
TGAAACGATGCCTCCAGTGGGACCCCTCTGCCCGCCTCACCCCGGCTCAAGCATTAAAGAC
ATCCTTGGATTAGCAAGTCTACACCCAAACCTCTCACCATGGACAAGGTGCCAGGGAAGC
GGGTAGTTAACCCTACAAATGCTTTCCAGGGACTGGGTTCCAAGCTGCCTCCAGTCGTTG
GGATAGCCAGTAAGCTTAAAGCTAACCTAATGTCCGAAACCAGTGGTAGTATACCTCTGT
GCAGTGTATTGCCAAAGCTGATTAGCTAGTGGACCACTCAGAGACTGATACATATCATAT
GTATTTTAAATTACCTTGCAAACATGCAAATGGAAAACGGAATAATTGAAGCCCATTAC
TGATGGATATGTTTTTGTAGACTTTTTTTTTTAACAAGGCAGAACATTTTTATATGACTAT
AAAAGAACGCTTCAAGGGCTAATGTCAAACCAGCTTGTATTGGCCATCTGGAGTATACAT
TAAATGACTTTTTTCATAGGTC

SEQ ID NO: 71_5R72_16_2_H

GTCGAGGCGCAGCGCTGCCATGGCTGGGGGCGCGTGGGGCCCCCGGCGCGGCGGGGACGA
GCCTCCGGAGAGCTACCCGCAACGACAGGACCACGAGCTACAGGCCCTGGAGGCCATCTA
CGGCGCGGACTTCCAAGACCTGCGGCCGACGCTTGCGGACCGGTCAAAGAGCCCCCTGA
AATCAATTTAGTTTTGTACCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGA
TTTGAGGGTTAAATGCCACCTACCTATCCAGATGTAGTTCTGAAATAGAGTTAAAAAA
TGCCAAAGGTCTATCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAAGAACTGGC
CAAGAAACACTGTGGGGAGGTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCT
CAGCGAGCATAACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGC
TCAGGAGGAGCAGCAGAGGCTGTTGGAGGCCAAGCGGAAAGAAGAGCAGGAGCAACGTGA
AATCCTGCATGAGATTAGAGAAGGAAAGAAGAGATAAAAGAAGAGAAAAAAGGAAAGA
AATGGCTAAGCAGGAACGTTTGAAATTGCTAGTTTGTCAAACCAAGATCATACCTCTAA
GAAGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGT
AGGAAATGGTAAACATCGGGCAAACCTCTCAGGAAGGTCTAGGCGAGAACGTCAGTATTC
TGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATTCTGTATTTCAATATGGGGAG
TCCTGATCAGCTCATGGTGCAAAAGGGAAATGTATTGGCAGTGATGAACAACCTTGAAA
ATTAGTCTACAATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTGTATGAGTGGGT
CCTTCAGTGGCAGAAAAAATGGGTCCATTCTTACCAGTCAAGAAAAAGAGAAGATTGA
TAAGTGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAG
CCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATCGT
GGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGCACACCTGAGCCACTC
AGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTGAGGCCTTGA
TTATCTGCACAGCAATTCTGTGGTGCAAGGTCTGAGTGCATCTAATGTCTTGGTGGA
TGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTG
CAAGGAGGATGTGTTTGAAGCAAAACCGAGTTTCGTTTTAGTGACAATGCTCTGCCTTATAA
AACGGGGAAGAAAGGAGATGTTTGGCGTCTTGGCCTTCTGCTGCTGTCCCTCAGCCAAGG
ACAGGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGA
TTTTCTAAAGAAATGTGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTT
GAAACACAGCTTTATAAATCCCCAGCCAAAAATGCCTCTAGTGGAACAAAGTCCTGAAGA
TTCTGGAGGACAAGATTATGTTGAGACTGTTATTCTTAGCAACCGGCTACCCAGTGCTGC
CTTCTTTAGTGAGACACAGAGACAGTTTTTCCCGATACTTCATTGAGTTTGAAGAATTACA
ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCTCAAGGTGCAGAACAAAGTTGGACGGCTG
CTGCTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAA
GGGCGAAGTGACACTGCTGTACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC
CTGGATCGAGCGGCACGAGCGGCCGCGGGACCGGGACGCCGCCCCCGGACTCCGGGCC

FIGURE 2GGG

CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA
CAGCGTAGAGGCCGCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC
GGGCGAGCGCTCGGCCAGTGCCCGTTTTCCCGCCACCGGCCCGGGCTCCAGCGATGACGA
GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCCAGTCCTTCTGCCTGCTTCAGA
TTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAAGTCAGAATCAGGA
TGAAGATTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGC
TGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTTACGAGACACCAT
TGACCAGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTTCGAGAGATTCTGGA
TGGATTAGCTTATATCCATGAGAAAGGAATGATTCACCGGGATTTGAAGCCTGTCAACAT
TTTTTTGGATTCTGATGACCATGTGAAAATAGGTGATTTTGGTTTGGCGACAGACCATCT
AGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCC
TTCAGGTCACTTAAGTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGG
AAGCACCAAATCTGCATACAACCAGAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTT
TGAGATGTCTATCACCCCATGGTCACGGCTTCAGAAAGGATCTTTGTTCTCAACCAACT
CAGAGATCCCACTTCGCCTAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCA
GAAATCAGTCATCTCCTGGCTGTTGAACCACGATCCAGCAAACCGGCCACAGCCACAGA
GCTGCTCAAGAGTGAGCTGCTGCCCCACCCAGATGGAGGAGTCAGAGCTGCATGAAGT
GCTGCACCACACGCTGACCAACGTGGATGGGAAGGCCTACCGCACCATGATGGCCCAGAT
CTTCTCGCAGCGCATCTCCCTGCCATCGATTACACCTATGACAGCGACATACTGAAGGG
CAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGCAT
CTTTAAAGACATGGAGCTGTTCAAGTTGTGTACTCCACTACTGCTTCCCCGAAACAGACA
AATATATGAGCACAACGAAGCTGCCCTATTTCATGGACCACAGCGGGATGCTGGTGATGCT
TCCTTTTGACCTGCGGATCCCTTTTGCAAGATATGTGGCAAGAAATAATATATTGAATTT
AAAACGATACTGCATAGAACGTGTGTTCAAGCCGCGCAAGTTAGATCGATTTTCATCCCAA
AGAACTTCTGGAGTGTGCATTTGATATTGTCACTTCTACCACCAACAGCTTTCTGCCAC
TGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAG
AAATTACAGTATTTATTTGAACCATAACCATGTTATTGAAAGCAATACTCTTACACTGTGG
GATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGACAGAGAA
GCTGACGAGGAGAGAAGTGAAGCTAAATTTTGTAACTCTGTCTTTGTCTTCTAATAGTCT
GTGTGCACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAAAT
AAATTCATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAGA
CCTAGAGGAGGTTGTTGGACTGTTGAAGAACTCGGCATCAAGTTACAGGTCTTGATCAA
TTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTT
CATCAAACGAAGGCAAAGGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGATATGACCT
GCTGATTCCCCAGTTTGAAGGGCCACAAGCTCTGGGGCCAGTCCCACTGCCATTGGGGT
CAGCATAGCTATAGACAAGATATCTGCTGCTGTCTCAACATGGAGGAATCTGTTACAAT
AAGCTCTTGTGACCTCCTGGTTGTAAGTGTGGTCAGATGTCTATGTCCAGGGCCATCAA
CCTAACCCAGAACTCTGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACA
GTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGT
CTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTCGAGAAGGAAGGCAGACAGA
GAAGCGTGTGCTGGAGACTGAACTTGTGGACCATGTACTGCAGAACTGAGGACTAAAGT
CACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTGCAGTGCAAAATCTGAAGGG
GTCATTTTCTAATGCTTCAGGTTTGTGTTGAAATCCATGGAGCAACAGTGGTTCCCATGT
GAGTGTGCTAGCCCCGAGAAGCTGTGAGCCAGCAC'TAGGAGGCGCTATGAAACTCAGGT
ACAAACTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAAGCAGTGAAATTGAAAT
TCTGGCTGTGGATCTACCCAAAGAAACAATATTACAGTTTTTATCATTAGAGTGGGATGC
TGATGAACAGGCATTTAACACAACGTGTAAGCAGCTGCTGTACGCCCTGCCAAAGCAAAG
ATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAGGTGTCTGT
GCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAACCCTAAAGAAC
TGTGCTTAACCTCATTCAAACAGACAGAGGCTTACTGGAATAATGGAATGTTGTACAT

FIGURE 2HHH

TCATCATAATTTAAAATTAAATTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAA
TCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAG
CCT

SEQ ID NO: 73_R43524_H, HRI_H

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TTTGAGTGTGCAACCAACTCTTGCTGGTTTCTTTGCTGGAGCACTTGAGCCACGTGCAT
GAACCAAACCCACTTCGTTCAAGACAGGTGTTTAAAGCTACTTTGCCAGACGTTTATCAAA
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GAGGATATTTCTCGTATCCAGAAAATCAGATCAAGGGAAGTAGCCTTGGAAGCACAAACT
TCACGTTACTTAAATGAATTTGAAGAACTTGTGTCATCTTAGGAAAAGGTGGATACGGAAGA
GTATACAAGGTCAGGAATAAATTAGATGGTCAGTATTATGCAATAAAAAAATCCTGATT
AAGGGTGCAACTAAACAGTTTGCATGAAGGTCTACGGGAAGTGAAGGTGCTGGCAGGT
CTTCAGCACCCCAATATTGTTGGCTATCACACCGCGTGGATAGAACATGTTTCATGTGATT
CAGCCACGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTGGAAGTGCTCTCCGACCAG
GAAGAGGACAGAGAGCAATGTGGTGTAAAAATGATGAAAGTAGCAGCTCATCCATTATC
TTTGCTGAGCCACCCAGAAAAAGAAAAACGCTTTGGAGAATCTGACACTGAAAATCAG
AATAACAAGTCGGTGAAGTACACCACCAATTTAGTCATAAGAGAATCTGGTGAACCTTGAG
TCGACCCTGGAGCTCCAGGAAAATGGCTTGGCTGGTTTGTCTGCCAGTTCAATTGTGGAA
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TCTTCCGAAGAAAATGTCAACTTTTGGGTGAGACAGAGGCACAGTACCACCTGATGCTG
CACATCCAGATGCAGCTGTGTGAGCTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAAG
CGGGGCCGGGAGTATGTGGACGAGTCTGCCTGTCTTATGTTATGGCCAATGTTGCAACA
AAAATTTTTCAAGAATTGGTAGAAGGTGTGTTTTACATACATAACATGGGAATTGTGCAC
CGAGATCTGAAGCCAAGAAATATTTTTCTTCATGGCCCTGATCAGCAAGTAAAAATAGGA
GACTTTGGTCTGGCCTGCACAGACATCTACAGAAGAACACAGACTGGACCAACAGAAAC
GGGAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGCTTCACCCGAA
CAGTTGGAAGGATCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTGGTCCTG
CTAGAGCTCTTTCAGCCGTTTGGAAACAGAAATGGAGCGAGCAGAAGTTCTAACAGGTTTA
AGAACTGGTCAGTTGCCGGAATCCCTCCGTAAAAGGTGTCCAGTGCAAGCCAAGTATATC
CAGCACTTAACGAGAAGGAACCTCATCGCAGAGACCATCTGCCATTAGCTGCTGCAGAGT
GAACTTTTCAAATTTCTGGAATGTTAACCTCACCTACAGATGAAGATAATAGAGCAA
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AGGGATGACGGAAGGATGGGGCGTGGGATGA

SEQ ID NO: 74_17000057519457_H

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AGACAGCTGATCGGTTGGAGCTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTA
CGCCGGCCGATGGCGAGGAGCCCGCCCGGAGGCTGAGGCTCTGGCCGAGCCCGGGAGC
GGAGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGT
TCCGTGGCCGCTTCCAGGGCCGCGCGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACC
GGCACCCGGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGGTGAGGAGGCGCGGCGC
TCCTCCGCTGTGCGCCGCTGGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTT
CCAACCTGCTTATATATGGAAGAAATTGAAGGCTCAGTGAAGTGTTCGAGATTATATTCAGT
CCACTATGGAGACTGAAAAAATCCCCAGGGTCTCTCCAACCTAGCCAAGACAATTGGGC

FIGURE 2III

AGGTTTTGGCTCGAATGCACGATGAAGACCTCATTTCATGGTGATCTCACCACCTCCAACA
TGCTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTT
TCATTTTCAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCC
TCAGTACCCATCCCAACACTGAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCT
CCTCCAAAAAGGCCAGGCCAGTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAA
AGAGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTT
TCAAAGTAAATTTGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAG
ATATTTTTTAAGTGGTATGTGATCGTGTTCATTATCATCTGCACCTTCACTCAAGAGCTTACT
ATGTGTCTAAGTCATGTTCTAGGCAGAAATTGGGTATTTAAAGTAAATTGAGGACAGGCCTT
CTCCCAGATTGTGACATGTATATCTCAGATACATGGGTGTGGCATTGAACCACATAATGA
GAACATTATTCTCTTTTAGTCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTC
GCTGAGCTTACTGGCCCTCTAACCCAGTGTTTTTTTTTTGTTGTTGTTGTGTACATGTTAT
ATTTATTTTTGAAACCAGTTTAATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATA
CAGCATGGAAAATATCAGTGTATTGTTTTATGAAACTTTCACGTGTATATATAGACCAAG
GATATGTGCTGAGTTTGTATGTCAAATATATTTCTCTTCAGGGTCATGATCAAAAAATG
AAAAGTCTGCTTAACTCCAATTTCTCTTTTAAAAAAGCAGACTTACAGCTTTCAGGCAAC
TGAAATTCATGTTAACATGTTTTTATTTTATTGCTTTGTATTTTTGTGGTTACCTTCTA
AGACAAGTGATTGATCTAAAGTTCCTTTTAAAGTTTATACCGCTAAACAAACTGAGTTGAT
TTCTATCACAGGCAGTAAGTAGGTAGAGCAAAAATGGTGAAGTGACTTGTGAAGACTGAA
GTTTGATGAAGTCTGGTTTAAAGGCACAGGTAACTGAGTGTGGATGCAAAAGTACCAGGA
GCTAGCTTTTAACTTGCCAGCCTCAGTTTCTTTTCTTAGAAGAAGCTATGTTTGGGTG
GGAAGGGAAGAGAGGGATAAGAAAATACCTTTCTTCCTTGTAACCTCCAATCAACAAACA
TATTTTGAGTGCTTTTGTGTTCCCTTGGCACCTGTTGGGTATTGGGTACTTGGCACCTT
GTTGGGTATTGGGTACAATGGTGAGCCAGACAGACACAGCGCTGTCCTTTTGTAAGAAT
ATTTATTTTTTATAAAAAAGTATAAAGTATACAGTGGGATGTTTTGATATACATTATGAAA
TGATTGCTACAGCTGAGCTAATTAACACCCATCACCTCACATAGTTACTGTCTTGTCTTCT
TAATATGGACATTTGCAGCTATGAATTTCCCTCTGCACACTGTTGTCATCACACACTCTC
AGTTTGGTATTTTGTGTTTTTGTTCATTTCATCTCAAAGTATTTTCTAATTTCCCTTG
TGATTTCTTCTTTGACCCCTTGATTGTTTAGAAATCTGTTAATTTCCACACATTTGTAAA
TGTTCCAATTTTTCTTTTGTATTGCCAGCTTCATTCCATTGTGTTTCAAGATGATACAG
TCAGTGCCTGTTCTTATGAAGCAAACATTCTATAATAGTAGGACCAGTACCCTGTCTGTT
TCATTACACACAGTCAGCATGCCCCAAGTGCCAGCATGGGGCGGATGGCCAGGAATGAG
TGAAAACCTCCCTTCTGGGTAGTTGTGACTAGTAGAGAGGAAAAATAATATAATTGCCT
GCTTACTGCATGCCAGGCATTGGGCTGGGAATTTTTATATTGGATCTAAAATAACTCTTA
AGTTAGGCATTATCCCCATTTTATAGATGGAGAACTGGCCCCAAAAGGTGGGAACCTGT
CCAAGACGTCACAGGTAGCAAGAGGTACTTTTACCTGGCTCCAAATCTGTGTTCTTTCCA
CTGACAAATGAGATATGGGATATGGTGCATCTTACAGTACTATAATAAGTATTGGCGTA
TAACATTATTTTCAAGGAACTCCAAGGGCCACAGGAGCTGACAGGTTTTTCAATTAATAT
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SEQ ID NO: 75_AA013524 M

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CGTCGGCGGACGGTGCAGGAGGCGCGCGCTGCTCCGCTGCCGCCGTGCGGGGATAGCT
GCCCCAGTCGTCTTCTTTGTGGACTATGCGTCTAACTGCTTATATATGGAAGAAATCGAA
GACTCGGTGACTGTTTGGGATTATATCCAATCCACTATGGAGACTGAAAAGGACCCCCAG
TGCTCTTGGACCTGGCCAGGAGGATGGGGCAGGTTCTGGCCGGAATGCACGACCAAGAC
CTCATTACAGGGGACCTCACACCTCCAACATGCTCCTGAGGCGGCCCTGGCGCAGCTG
CACATCGTGTCTCATCGACTTTGGGCTGAGCTTTGTCTCAGGACTGCCGGAAGATAAAGGC

FIGURE 2JJJ

GTCGACCTCTATGTCCTGGAGAAGGCCTTCCTCAGCACGCACCCCCACACCGAGACCGCG
TTTGAAGCCTTTCTGAAGAGTTACGGGGCCTCGTCCAAGAAGTCCAGTCCAGTGCTGAAG
AAGTTAGATGAGGTGCGCCTGAGAGGGCGAAAGCGGTCCATGGTCGGGTAGTGGAGCTGT
GGTGAACCTGGCTCACGGTGAAGGATGATGTAGACGAGGCTGGACCCCTCAGCAAAGCATG
GGTTGTAAAGTGGTCTGTGATCGTGCTGGGCCACCACCATCCATGGCTCACTGTTCTCAG
GGGCTTCATGTACATGAGGTTTATTCTGGGCAGAACTGGGTAGGTAGCCCAGGCTAGCCT
TGAATTTATGGCAACATCCTACCTCAGCTTGCTTGAAGAGGTTATAAGCCACCATACT
GACTTTGCACTGATTCTGTCAGAAAC

SEQ ID NO: 76_17000139801197_H, IRAKM_H

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CCGCCCCGCTGCTCGGAGAGCTCTGCGCTGTTCTGGACAGCTGCGACGGCGCGCTGGGC
TGGCGCGGCCTGGCAGAGAGACTTTCAAGCAGCTGGCTGGATGTTTCGTATATTGAAAAG
TATGTAGACCAAGGTAAAAGTGAACAAGAGAATTACTTTGGTCTGGGCACAGAAAAAC
AAGACCATCGGTGACCTTTTACAGGTCTCCAGGAGATGGGACATCGTCGAGCTATTTCAT
TTAATTACAACTATGGAGCAGTGTTGAGTCCTTCAGAGAAGAGTTATCAGGAAGGTGGA
TTTCCAAATATATTATTCAGGAAACAGCCAATGTCACCGTGGATAATGTTCTTATTCCT
GAACATAATGAAAAAGGAGTACTGCTTAAATCTTCCATCAGCTTTCAAATATCATAGAA
GGAAGTAGAAATTTCCACAAAGACTTCTAATTGGAGAAGGAGAGATTTTGGAGGTATAC
AGAGTGGAGATTCAAACCTAACATATGCTGTCAAATTATTTAAACAGGAGAAAAAATG
CAGTGTAAAGAAGCATTGGAAGAGGTTTTATCTGAGCTTGAAGTTTTACTACTGTTTCAT
CACCCAAACATACTAGAGTTGGCTGCATATTTTACAGAGACTGAGAAGTTCTGTCTGATT
TATCCATACATGAGAAATGGAACACTTTTGGACAGATTGCAGTGTGTAGGTGACACGGCC
CCACTCCCTTGGCACATTCGAATCGGTATATTAATAGGAATATCCAAAGCCATTCACTAC
CTGCACAACGTTCAACCATGCTCGGTATCTGTGGCAGTATATCAAGTGCAAACATCCTT
TTGGATGATCAGTTTCAACCCAACTAACTGATTTTGCCATGGCACACTTCCGGTCCAC
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GGAATTGTAATAATGGAAGTTCTAACAGGATGTAGAGTAGTGTAGATGATCCAAACAT
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TTGGCAGGCCGGTGTGCTGCAACGCGGGCAAAGTTAAGACCATCAATGGATGAAGTTTAA
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GATGATGAAAGCCAGAATAACAATTTACTACCTTCTGATGAAGGCCTGAGGATAGACAGA
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AAAAAGCCAGAGAGCAAGAGAAATGAGGAAGCTTGCAACATGCCAGTTCTTCTGTGAA
GAAAGTTGGTTCCCAAAGTATATAGTTCCATCCCAGGACTTAAGGCCCTATAAGGTAAAT
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AGCAACGGGACGCTTTTCGACAGATTACAGTGCACAAATGGCACAACCCCGCTTTCTGG
CACGTTTGAATCAGCGTATTGATAGGAATAGCCAAAGCCATCCAATACTTGACAAACACT
CAGCCGTGCGCCGTATCTGTGGCAACGTTTCCAGTGCAACATACTCTTGGATGACCAG
CTCCAACCCAACTAACGGATTTTGTCTGCAGCGCACTTCCGACCCAATCTAGAGCAGCAG
AGTTCTACCATAAATATGACCGCGGTGGCAGGAAACATCTGTGGTACATGCCAGAAGAA

FIGURE 2KKK

TACATCAGACAGGGAAGACTTTCCGTTAAACTGATGTCTACAGCTTCGGAATCGTGATC
ATGGAGGTTCTAACGGGCTGCAAAGTGGTGTGGATGACCCGAAACACGTTTCAGCTGCGG
GACCTCCTCATGGAAGTGTGGAGAAAAGAGGCCTAGACTCCTGCCTGTCTTCTTAGAC
AGGAAGATAACCACCTGTCTCGGAACCTTCTCTGCAAAGCTCTTCTCTCTGGCGGGCCGG
TGTGTGGCAACGAAGGCCAAGTTAAGACCCACGATGGACGAAGTCCTGTCTCTCTGGAG
AGCACCCAGCCTAGCTTGTATTTTGCAGAAGACCTCCCACGTCCTTGAAGTCCTTCAGG
TGTCTTCTCCACTGTTCTTGGATAATGTCCCAAGTATTCCAGTAGAAGATGATGAAAAC
CAGAATAACCATTCAGTACCTCCCAAGGAAGTTTGGGGACAGATAGAGTGACTCAGAAA
ACCCCTTTGAATGCAGCCAGTCTGAGGTCACCTTTCTAGGCTTGGACCGAAACAGAGGG
AACAGGGGAAGTGAAGCGGATTGCAACGTGCCAGTCTTCTCATGAGGAATGCTGGTCC
CCAGAGCTTGTGGCGCCATCCCAGGACTTAAGTCCTACTGTGATCAGTTTGGGCTCGTCT
TGGGAAGTACCAGGCCATTCTTATGGGAGCAAGCCAATGGAGAAGAGGTGTTCTCTGGG
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AAAATAAAAGCAAACGTCACTGAAGGCACTGAGCAAATAGCATCCCCGTGAAAAGACACG
AGCTCTGAGCTCCGTGAGTACAGCCAAGGGACCAACTGATGGAGAATTTGAATGGTGCAG
ATTAGCAGCAAGGAAGTCTATTCTTCTCCAAACAGAATAATTTCAAGAGATGCTTTAT
TCAAGTGACCGCTCTCAGTCAAACCTGAGAAGCTAAACTGGAGCCAATCAGAATTATCC
AAGATTCCGGGTTCTGACAACCAAAACCTAGCAAAGAGTAGCAGGACAAGTCTCTCTCTT
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CCCACCTTCCAGAACCAGAACCACCTTCTCCCCAAGCCAGCAGTCAGTCACTCACCATCA
GCAGCCAGTAGTCACCAGCAGCCAATCATGATACAGTGTCACTCTCCCTCTGCGCATGCC
CTACGTCCTTTATAAAACCCAGGTCTTCAGGGCCCCACCCCTTTCTTTTTCCATCCTTGCT
CAGAGGCAGCCTTTTGTATACATTCCCTGACCCCAACCAATTATATCTCTCATATGATA
TCTGTTGCGTAGTGTGACTTTGTGGCATGACTTGGTTGTCAGATCATTTGCACAAGAACA
AGCGAATACACAACAACAAGCCCCACCATCATTACCACCGGCACCTTAATGCTAGTCTTTC
TGCTAGGGATACTGACAGTCTATTGTCTTCCCATGGTTCATAGGGAAGTTGCTCAAATGCA
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TTTTACAGCCAGTTGCTACTCTTGTATTATCGCTGGTTAACCGGTCTGTCCGGAAGTGAGC
CAAGTCATCCTTGCTAGGGCTTTTTCTGTGTAGAGAGGGAATTCCAGTCCAAAGTCTGCT
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SEQ ID NO: 78_AA088547_H

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GATGGGGTCTTCTACACAGGCCGGAAGCAGGATGCCTGGTTTGTGGTGGACCCTGAGTCA
GGGAGACCCAGATGACACTGACCACAGAGGGTCCCTCCACCCCCGCCTCTACATTGGC
CGAACACAGTATACGGTCACCATGCATGACCCAAGAGCCCCAGCCCTGCGCTGGAACACC
ACCTACCGCCGCTACTCAGCGCCCCCATGGATGGCTCACCTGGGAAATACATGAGCCAC
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GGCCACATCCGACTGCCCTGCCTCAGGCCCCCGGGACACAGCCACCCTCTTCTCTACCTTG
GACACCCAGCTGCTAATGACGCTGTATGTGGGGAAGGATGAACTGGCTTCTATGTCTCT
AAAGCACTGGTCCACACAGGAGTGGCCCCGGTGCCTCGTGGACTGACCCTGGCCCCCGCA
GATGGCCCCACCACAGATGAGGTGACACTCCAAGTCTCAGGAGAGCGAGAGGGCTCACCC

FIGURE 2LLL

AGCACTGCTGTTAGATACCCCTCAGGCAGTGTGGCCCTCCCAAGCCAGTGGCTGCTCATT
GGACACCACGAGCTACCCCCAGTCCTGCACACCACCATGCTGAGGGTCCATCCCACCCCTG
GGGAGTGGAAGTGCAGAGACAAGACCTCCAGAGAATACCCAGGCCCCAGCCTTCTTCTTG
GAGCTATTGAGCCTGAGCCGAGAGAAAACCTTGGGACTCCGAGCTGCATCCAGAAGAAAAA
ACTCCAGACTCTTACTTGGGGCTGGGACCCCAAGACCTGCTGGCAGCTAGCCTCACTGCT
GTCCTCCTGGGAGGGTGGATTCTCTTTGTGATGAGGCAGGTGGTGGAGAAGCAGCAGGAG
ACCCCCCTGGCACCTGCAGACTTTGCTCACATCTCCAGGATGCCAGTCCCTGCACTCG
GGGGCCAGCCGGAGGAGCCAGAAGAGGCTTCAGAGTCCCTCAAAGCAAGCCCAGCCACTC
GACGACCCTGAAGCTGAGCAACTACCGTAGTGGGGAAGATTTCTTCAATCCCAAGGAC
GTGCTGGGCCCGGGGAGGCGGGACTTTCGTTTTCCGGGGACAGTTTGAGGGACGGGCA
GTGGCTGTCAAGCGGCTCCTCCGCGAGTGCTTTGGCTGGTTCGGCGGGAAAGTTCAACTG
CTGCAGGAGTCTGACAGGCACCCCAACGTGCTCCGCTACTTCTGCACCGAGCGGGGACCC
CAGTTCCACTACATTGCCCTGGAGCTCTGCCGGGCTCCTTGCAGGAGTACGTAGAAAAAC
CCGGACCTGGATCGCGGGGTCTGGAGCCCCGAGGTCGTGCTGCAGCAGCTGATGTCTGGC
CTGGCCCCACCTGCACTCTTTACACATAGTGCACCGGGACCTGAAGCCAGGAAATATTCTC
ATCACCGGGCTGACAGCCAGGGCCTGGGCAGAGTGGTGTCTCTCAGACTTCGGCCTCTGC
AAGAAGCTGCCTGCTGGCCGCTGTAGCTTCAGCCTCCACTCCGGCATCCCCGGCACGGAA
GGCTGGATGGCGCCCGAGCTTCTGCAGCTCCTGCCACCAGACAGTCTTACCAGCGCTGTG
GACATCTTCTCTGCAGGCTGCGTGTCTACTACGTGCTTTCTGGTGGCAGCCACCCCTTT
GGAGACAGTCTTTATCGCCAGGCAAACATCCTCACAGGGGCTCCCTGTCTGGCTCACCTG
GAGGAAGAGGTCCACGACAAGGTGGTTGCCCGGGACCTGGTTGGAGCCATGTTGAGCCCA
CTGCCGCGAGCCACGCCCCCTCTGCCCCCAGGTGCTGGCCACCCCTTCTTTTGGAGCAGA
GCCAAGCAACTCCAGTTCTTCCAGGACGTGAGTACTGGCTGGAGAAGGAGTCCGAGCAG
GAGCCCCCTGGTGGAGGCACCTGGAGGCGGGAGGCTGCGCAGTGGTCCGGGACAACCTGGCAC
GAGCACATCTCCATGCCGCTGCAGACAGATCTGAGAAAGTTCCGGTCTATAAGGGGACA
TCAGTGCGAGACCTGCTCCGTGCTGTGAGGAACAAGAAGCACCCTACAGGGAGCTCCCA
GTTGAGGTGCGACAGGCACCTCGGCAAGTCCCTGATGGCTTCGTCCAGTACTTCACAAAC
CGCTTCCACGGCTGCTCCTCCACACGACCGAGCCATGAGGAGCTGCGCCTCTGAGAGC
CTCTTCTGCCCCTACTACCCGCCAGACTCAGAGGCCAGGAGGCCATGCCCTGGGGCCACA
GGGAGGTGA

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TTCACCTCCGACCTTTCTTCCAGGCGGTGAGACTCTGGACTGAGAGTGGCTTTCACAAT
GGAAGGGATCAGTAATTTCAAGACACCAAGCAAATTATCAGAAAAAAGAAATCTGTATT
ATGTTCAACTCCAATAATAATATCCCGGCTCTCCGTTTATGCAGAAGCTTGGCTTTGG
TACTGGGGTAAATGTGTACCTAATGAAAAGATCTCCAAGAGGTTTGTCTCATTCTCCTTG
GGCTGTAAAAAAGATTAATCCTATATGTAATGATCATTATCGAAGTGTGTATCAAAAGAG
ACTAATGGATGAAGCTAAGATTTTGAAGAGCCTTCATCATCCAAACATTGTTGGTTATCG
TGCTTTTACTGAAGCCAATGATGGCAGTCTGTGTTCTGCTATGGAATATGGAGGTGAAAA
GTCTCTAAATGACTTAATAGAAGAACGATATAAAGCCAGCCAAGATCCTTTTCCAGCAGC
CATAATTTTAAAGTTGCTTTGAATATGGCAAGAGGGTTAAAGTATCTGCACCAAGAAAA
GAAACTGCTTCATGGAGACATAAAGTCTTCAAATGTTGTAATTAAGGCGATTTTGAAC
AATTAATAATCTGTGATGTAGGAGTCTCTCTACCACTGGATGAAAATATGACTGTGACTGA
CCCTGAGGCTTGTTACATTGGCACAGAGCCATGGAAACCCAAAGAAGCTGTGGAGAGAA
TGGTGTATTACTGACAAGGCAGACATATTTGCCTTTGGCCTTACTTTGTGGGAAATGAT
GACTTTATCGATTCCACACATTAATCTTTCAAATGATGATGATGATGAAGATAAAACCTT
TGATGAAAGTGATTTTGATGATGAAGCATACTATGCAGCGTTGGGAACTAGGCCACCTAT
TAATATGGAAGAACTGGATGAATCATACCAGAAAGTAATTGAACTCTTCTCTGTATGCAC

FIGURE 2MMM

TAATGAAGACCCTAAAGATCGTCCTTCTGCTGCACACATTGTTGAAGCTCTGGAAACAGA
TGCTAGTGATCATCTCAGCTGAAGTGTGGCTTGCCTAAATAACTGTTTATTCCAAAATA
TTTACATAGTTACTATCAGTAGTTATTAGACTCTAAAATTGGCATATTTGAGGACCATAG
TTTCTTGTTAACATATGGATAACTATTTCTAATATGAAATATGCTTATATTGGCTATAAG
CACTTGGAAATTGTACTGGGTTTTCTGTAAAGTTTTAGAACTAGCTACATAAGTACTTTG
ATACTGCTCATGCTGACTTAAAACACTAGCAGTAAAACGCTGTAACTGTAACATTAAAT
TGAATGACCATTACTTTTTATTAATGATCTTTCCTTAAATATTCTATATTTTAATGGATCTA
CTGACATTAGCACTTTGTACAGTACAAAATAAAGTCTACATTTGTTTAAAACACTGAACC
TTTTGCTGATGTGTTTATCAAATGATAACTGGAAGCTGAGGAGAATATGCCTCAAAAAGA
GTAGCTCCTTGGATACTTCAGACTCTGGTTACAGATTGTCTTGATCTCTTGGATCTCCTC
AGATCTTTGGTTTTTGTCTTAATTTATTAAATGTATTTTCCATACTGAGTTTAAAATTTA
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SEQ ID NO: 80_AA449542_M

ATCTCCAAGAGGGTGTCTCATTCTCCTTGGGCCGTGAAAAAGATAAGTCTTTTATGCGA
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CCTTAATCACCCAAACATTATAGGATATCGTGCTTTTACTGAAGCCAGTGATGGTAGTCT
GTGCCTTGCTATGGAGTATGGAGGTGAAAAGTCTCTGAATGACTTAATAGAAGAGCGGAA
CAAAGACAGTGGAAGTCTTTTCCAGCAGCTGTAATTCTCAGAGTTGCTTTGCACATGGC
CAGAGGGCTAAAGTACCTGCACCAAGAAAAGAAGCTGCTTCATGGAGACATAAAGTCTTC
AAATGTTGTAATTAAAGGTGATTTTGAAACAATTAAAATCTGTGATGTAGGAGTCTCTCT
GCCATTGGATGAAAAATGACTGTGACTGATCCTGAGGCCTGTTATATTGGTACTGAGCC
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TGCTTTTGGCCTTACTCTGTGGGAAATGATGACTTTATGTATTCCACACGTCATCTTCC
AGATGATGATGTTGATGAAGATGCAACCTTTGATGAGAGTGACTTCGATGATGAAGCATA
TTATGCAGCTCTGGGGACAAGGCCATCCATCAACATGGAAGAGCTGGATGACTCCTACCA
GAAGGCCATTGAACTCTTCTGTGTGTGCCTAATGAGGATCCTAAAGATCGCCCGTCTGC
TGCACACATCGTTGAAGCTTTGGAAGTAGATGGCCAATGTTGTGGTCTAAGCTCAAAGCA
TTAACTTGTATGGGAAGTGTAACTAGATATATGTAGTTAATATAACTTATGGTAGCTAG
ATTCTAGAAGTAGCTTTAACTAGTAGTACCCTGTCTAAGATGACTTAAGAATCAAGGGA
CCATTGCTTTGTTACAGATCTTTTATAGATATTCTTGCTTCTTTAGTGGGTACTAAAAAT
TTCCTACGTACATGTGGTACAGATATCTGTCTGCTCATAGTGTGAGTCTTTCAGCTGGC
CTGTGAGCCCATGCGCCCTGGGACTTGAGAAGAGTTTCATAAACGTAGCTCCTAGGGTGTG
TTGCCCTCTCTACACTTAGCTTCTAATTTATTACTTTGTTTCTACTGATTGTGTCTTAAGT
CTTTTAAATAAATGTAAGAATAAACAATAAAAGACAGTTTGTAGTACCAG

SEQ ID NO: 81_5R57_10_2_M TESK2_M

GCTGCTGGACAGTGACTTGTATTTACCGTGGACTGTGAGAGTGAACTGGCCTATGGCAT
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GGTGTGAAGGCTTTGCTTTC

SEQ ID NO: 82_AA232253_H

ATGTCGTCTCTCGGTGCCTCCTTTGTGCAAATTAAATTTGATGACTTGCAGTTTTTTTGAA
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GAGGTGGCTGTAAAGAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTCTC
AGTCACAGAAACATCATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATT
GTCACAGAATATGCTTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAG
GAGATGGATATGGATCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTAT
TTACATATGGAGGCTCCTGTCAAGGTGATTACAGAGACCTCAAGTCAAGAAACGTTGTT

FIGURE 2NNN

ATAGCTGCTGATGGAGTATTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCAT
ACAACACACATGTCTTGGTTGGAACCTTCCCATGGATGGCTCCAGAAGTTATCCAGAGT
CTCCCTGTGTGAGAACTTGTGACACATATTCCTATGGTGTGGTTCTCTGGGAGATGCTA
ACAAGGGAGGTCCCTTTAAAGGTTTGAAGGATTACAAGTAGCTTGGCTTGTAGTGGAA
AAAAACGAGAGATTAACCATTCGAAGCAGTTGCCCCAGAAGTTTGTGCTGAACTGTTACAT
CAGTGTGGGAAGCTGATGCCAAGAAACGCCCATCATTCAAGCAAATCATTTCATCCTG
GAGTCCATGTCAAATGACACGAGCCTTCTGACAAGTGTAACCTCATTCTACACAACAAG
GCGGAGTGGAGGTGCGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGAT
CTCAGCTTTAAGGAGCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAA
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ATGAGTGTATATGCAAGCTTGTTTAAAGAAAACAACATTACAGGGAAGCGGCTGCTGCTG
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AAGTCAGCCATTGAGAAATTAACCCATGATTACATAAATTTGTTTCACTTCCCACCACTA
ATTAAGGACTCAGGAGGTGAACCTGAAGAAAATGAGGAAAAAATAGTGAACCTGGAACCTG
GTTTTTGGTTTTCACTTGAAACCAGGAACTGGCCACAGGATTGTAAGTGGAAAATGTAT
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GATGAAGTGAAAGCAGTCCAACCTTGCCATTGACACATTATTCACCAATTGAGATGGCAAC
CCTGGAAGCAGGTCCGACTCAAGTGCTGATTGCCAGTGGTTAGATACTCTGAGGATGCGG
CAGATTGCATCCAACACTTCTTTACAGCGTTCCTCAGAGCAATCCTATTCTGGGGTCACCG
TTCTTCTCACACTTTGATGGCCAGGATTCTACGCTGCTGCTGTGAGACGGCCCCAGGTG
CCCATTAAGTATCAACAGATTACACCTGTGAACCAGTCCAGAAGCTCGTCTCTACTCAG
TATGGACTGACCAAAAACCTTCTCTTCTTACATCTCAACTCTAGGGACAGTGGCTTTTCC
AGTGGCAATACTGACACCTCTTCAGAGAGGGGTCGATACTCAGACAGAAGCAGGAACAAA
TATGGACGTGGTAGTATATCACTCAATTCTTCTCTCTAGAGGAAGATACAGTGGAAAGAGT
CAGCATTCCTCATCAAGAGGAAGATACCTGGAAAGTTCTACAGGGTTTCTCAGTCA
GCACTCAATCCTCACCAGTCGCCTGACTTCAAGAGAAGCCCCAGGGACCTCCACCAACCC
AACACCATAACAGGGATGCCCTTTGCACCCTGAGACTGACTCAAGAGCCAGTGAAGAGGAC
AGCAAAGTCAGCGAAGGGGGCTGGACAAAAGTGGGAATACCGGAAAAAGCCCCACAGGCCA
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TGA

SEQ ID NO: 83_AI375137_H

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GAACTGACAGAACTAAGGAATATATTTGGCTCTGATGAAGCCTTCAGTAAAGTCAATTTA
AATTACCGCACTGAAAATGGGCTGTCTCTACTTCATTTATGTTGCATTTGTGGAGGCAAG
AAATCACATATTCGAACTCTTATGTTGAAAGGGCTCCGCCCATCTCGACTGACAAGAAAT
GGATTTACAGCCTTGCAATTTAGCAGTTTACAAGGATAATGCAGAATTGATCACTTCTCTG
CTTCACAGTGGAGCTGATATACAGCAGGTTGGATACGGTGGCCTCACTGCCCTCCATATT
GCTACAATAGCTGGCCACCTAGAGGCTGCTGATGTGCTGTTGCAACATGGAGCTAATGTC
AATATTCAAGATGCAGTTTTTTTTCACTCCATTGCATATTGCAGCGTACTATGGACATGAA
CAGGTAACCTCGCCTTCTTTTGAATTTGGTGTGATGTAAATGTAAAGTGGTGAAGTTGGA
GATAGACCCCTCCACCTAGCATCTGCAAAAGGATTCTTGAATATTGCAAACTCTTGATG
GAAGAAGGCAGCAAAGCAGATGTGAATGCTCAAGATAATGAAGACCATGTCCCACTCCAT
TTCTGTTCTCGATTTGGACACCATGATATAGTTAAGTATCTGCTGCAAAGTGATTTGGA
GTTCAACCTCATGTTGTTAATATCTATGGAGATACCCCTTACACCTGGCATGCTACAAT

FIGURE 2000

GGCAAATTTGAAGTTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAG
GAAACATCTTCAGTGAAACAGCTTTTCATAGTGCTTGACCTATGGCAAGAGCATTGAC
CTAGTCAAATTTCTTCTTGATCAGAATGTCATAAACATCAACCACCAAGGAAGGGATGGG
CACACTGGATTACACTCTGCTTGCTACACGGTCACATTGCGCTGGTTCAGTTCTTACTG
GATAATGGAGCTGATATGAATCTAGTGGCTTGATGCCAGCAGGTCTAGTGGTGAAAAA
GATGAGCAGACATGTTTGATGTGGGCTTATGAAAAAGGGCATGATGCCATTGTCACACTC
CTGAAGCATTATAAGAGACCACAAGATGAATTGCCCTGTAATGAATATTCTCAGCCTGGA
GGAGATGGCTCCTATGTGTCTGTTCCATCACCTTGCGGAAGATTAAAAGCATGACAAAA
GAGAAGGCAGATATTCTCCTCCTAAGAGCTGGATTGCCCTTCACATTCCATCTTCAGCTC
TCAGAAATTGAGTTCCATGAGATTATTGGCTCAGGTTCTTTTGGGAAAGTATATAAAGGA
CGATGCAGAAATAAAATAGTGGCTATAAAACGTTATCGAGCCAATACCTACTGCTCCAAG
TCAGATGTGGATATGTTTGGCCGAGAGGTGTCCATTCTCTGCCAGCTCAATCATCCCTGC
GTAATTCAGTTTGTGGGTGCTTGCTTGAATGATCCCAGCCAGTTTGCCATTGTCACTCAA
TACATATCAGGGGGTCTCTGTTCTCCCTCCTTCATGAGCAGAAGAGGATTCTTGATTG
CAGTCTAAATTAATTATTGCAGTAGATGTTGCCAAAGGCATGGAGTACCTTCACAACCTG
ACACAGCCAATTATACATCGTGACTTGAACAGTCACAATATTCTTCTCTATGAGGATGGG
CATGCTGTGGTGGCAGATTTTGGAGAATCAAGATTTCTACAGTCTCTGGATGAAGACAAC
ATGACAAAAACAACCTGGGAACCTCCGTTGGATGGCTCCTGAGGTGTTACGCAGTGCCT
CGGTACACCATCAAAGCAGATGTCTTCAGCTATGCTCTGTGTCTGTGGGAAATTCTCACT
GGCGAAATTCCATTGCTCATCTCAAGCCAGCGCTGCGGCAGCAGACATGGCTTACCAC
CACATCAGACCTCCCATTTGGCTATTCCATTCCCAAGCCCATATCATCTCTGCTGATACGA
GGGTGGAACGCATGTCTGAAGGAAGACCCGAATTTTCTGAAGTTGTCATGAAGTTAGAA
GAGTGTCTCTGCAACATTGAGCTGATGTCTCCTGCATCAAGTAACAGCAGTGGGTCTCTC
TCACCTTCTTCTTCTCTGATTGCCTGGTGAACCGGGGAGGACCTGGCCGGAGTCATGTG
GCAGCATTAAGAAGTCGTTTGAATTTGGAATATGCTCTAAATGCAAGGTCCTATGCTGCT
TTGTCCCAAAGTGCTGGACAATATTCCTCTCAAGGTCTGTCTTTGGAGGAGATGAAAAGA
AGTCTTCAATACACACCCATTGACAAATATGGCTATGTATCCGATCCCATGAGCTCAATG
CATTTTTCATTCTTGCCGAAATAGTAGCAGCTTTGAGGACAGCAGCTGA

SEQ ID NO: 84_H97685_H

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GAAACTGGGCTCGGAGATAATAGACTCCTCAACCAGGAGAATGGAGAGCGAAAGATCACC
GCTTTATCGCCAGCTAATTGACCTGGCTATCTGAGCAGCAGTCACTGGAAGTGTGGGGC
TCCTGGCCAGGATACTAAAGCTCAGAGCATGTTGGTGGAACAGAGTGAAAAGCTGAGACA
CTTGAGCACATTTCTCACCAGGTGTTACAGACTCGCCTGGTGGATGCAGCCAAGGCCCT
GAACCTGGTGCAGTGCCTTGACATCTTTATTAACCAGGCATTTGACATGCAGCG
GGACCTGCAGATCACTCCCAAACGTCTGGAATATACTCGAAAAAGGAGAATGAGTTGTA
TGAATCATTGATGAATATTGCCAACCAGGAGGAAATGAAGGATATGATTGTTGA
GACACTTAATACCATGAAGGAGGAACCTCTGGATGATGCTACTAACATGGAGTTTAAAGA
CGTCATTGTCCCTGAGAATGGAGAACCAGTAGGCACCAGAGAGATCAAATGCTGCATCCG
ACAGATCCAGGAACTCATCATCTCCGACTTAATCAGGCAGTGGCTAATAAGCTGATCAG
CTCAGTGGATTACCTGAGGGAAAGCTTCGTGCGGAACCTGGAACGATGTCTGCAGAGCCT
GGAGAAGTCTCAGGATGTCTCAGTTCACATCACCAGTAATTATCTCAAACAGATCTTAA
TGCTGCCTATCATGTTGAAGTCAGTTTCACTCAGGGTCGTGAGTTACAAGGATGCTATG
GGAGCAAATCAAACAGATCATCCAGCGCATCACATGGGTGAGCCACCTGCCATCACTCT
GGAATGGAAGAGGAAGGTGGCCCAAGGCAATTGAGAGCCTCAGCGCCTCCAAATTGGC
TAAGAGCATTGTCAGCCAATTCGGACTCGGCTCAATAGTTCCACGAGGCTTTTGCAGC
CTCCTTGCGGCAGCTGGAAGCTGGCCACTCAGGCCGGTTAGAGAAAACGGAAGATCTATG
GCTGAGGGTTGCGAAAGATCATGCTCCCCGCTGGCCCGCTTTCTCTGGAAGCCGTTCT

FIGURE 2PPP

TTTACAGGATGTCTTGCTTCATCGTAAACCTAAACTGGGACAGGAACTGGGCCGGGGCCA
GTATGGTGTGGTATACCTGTGTGACAACCTGGGGAGGACACTTCCCTTGTGCCCTCAAATC
AGTTGTCCCTCCAGATGAGAAGCACTGGAATGATCTGGCTTTGGAATTCACATATATGAG
GTCTCTGCCGAAGCATGAGCGATTGGTGGATCTCCATGGTTTCAGTCATTGACTACAACATA
TGGTGGTGGCTCCAGCATTGCTGTGCTCCTCATTATGGAGCGGCTACACCGGGATCTCTA
CACAGGGCTGAAGGCTGGGCTGACCCTGGAGACACGTTTGCAGATAGCACTAGATGTGGT
GGAGGGAATCCGCTTCCTGCACAGCCAGGGACTTGTCCATCGTGATATCAAACCTGAAAAA
TGTGCTGCTGGATAAGCAGAACCGTGCCAAGATCACTGACTTAGGATTCTGCAAGCCAGA
GGCCATGATGTCAGGCAGCATTGTGGGGACACCAATCCATATGGCCCCCTGAACCTTTTCAC
AGGGAAGTACGATAATTCCGTGGATGTCTACGCTTTTGAATTCCTTTCTGGTATATCTG
CTCAGGCTCTGTCAAGCTCCCTGAGGCATTTGAGAGGTGTGCTAGCAAAGACCATCTCTG
GAACAATGTGCGGAGGGGGGCTCGCCAGAACGTCTTCTGTGTTTGTATGAGGAGTGCTG
GCAGTTGATGGAAGCCTGTTGGGATGGCGACCCCTTGAAGAGGCCTCTCTGGGCATTGT
CCAGCCCATGCTCCAGGGCATCATGAATCGGCTCTGCAAGTCCAATTCTGAGCAGCCAAA
CAGAGGACTAGATGATTCTACTTGAAAGCAAAGACCTTTCTCTTTCACTCTCTAGTTATT
TCCTTCCCCCTCACCATTTGGCCATGGGGAGAATTTGACATTTATTCACTATAGGACACA
CTCCCAAGGGAACCTGGTGTCTGCTGGGAACTTGGAACTTCCCAGGCAGGGATGACTCC
TGGACAGTGAAGAGTTGAATGACTGAGCATATTCAGCAGCTCACTGAAGCGCCAAGCTAT
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SEQ ID NO: 85_W20810_M

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CTCCCGGCTTGGAAAACTGAAGGAGTTAATGATTCAATTGCTGGGGTTCCAGTCCGAAA
ACAGGCCATCCTTCCAGGACTGCGAACCAAAAAACCAATGAAGTTTACAATCTGGTAAAGG
ACAAGGTAGATGCTGTCTCTCCGAGGTAAAGCATTATCTGTCTCAGCACAGAAGCAGCG
GCAGAACTTGTCTGCCAGAGAGCCAAGCCAAAGAGGCACAGAAATGGATTGCCCGAGGG
AAACCATGGTTTTCTAAAATGCTGGACCGCCTGCATTTGGAGGAACCCCTCCGGACCAGTTC
CTGGAAAATGTCTGAGAGGCAAGCACAGGACACATCAGTTGGGCCTGCCACACCAGCAA
GGACATCTTCTGACCCCGTGGCTGGCACTCCTCAGATTCCACATACTTTACCCTTCAGAG
GCACAACACCTGGGCCAGTCTTTACTGAGACTCCCGGTCTCACCCTTCAAGGAATCAGG
GAGATGGAAGACACGGCACTCCTTGGTATCCTTGGACCCACCGAATCCAATGACAGGGC
CACCGGCTCTCGTCTTCAACAACCTGTTCTGAAGTGCAGATTGGGAACTACAACCTCCTTGG
TAGCACCACCAAGAACTACTGCCTCAAGTTCGGCCAAGTATGACCAAGCACAGTTCGGCA
GGGGTAGGGGCTGGCAGCCCTTCCACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGA
AGTGTGCCATTTCAGCGTGGCAATAAAAAGCACGTTTAAAGCAACCTGGACTGGCTAAGAC
AGTCCTTGCCACTTCTTGAAGCTCACAACTTCTGTGAGGACAGTTGGACCTACACCCAA
ACTGACTCTTGACCCATCTCCTTAAAGTCAATAAACATAGCATGTTAACTGTG

SEQ ID NO: 86_AA744236_H

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CGTCACCTTGCTTGCTAAGATTTTATCTTGTACTGTGGAAGCGGATGGCATTTCATCTT
GTCAGTGAAGAGTACAGCCCTTGAAGTGGCTTTGGAAACATTGTCTTCTGCAGAGGTC
TGTGCTGGGATCTATGACATATTGCTGGCTCTTATCTTCTTCATGACAGAGGACACCTA
ACACACAATAATGTCTGTTTATCATCTGTGTTTGTGAGTGAAGATGGACACTGGAAGCTA
GGAGGAATGGAACTGTTTGTAAAGTTTCTCAGGCCACACCAGAGTTTCTGAGGAGTATT

FIGURE 2QQQ

CAGTCAATAAGAGACCCAGCATCTATCCCTCCTGAAGAGATGTCTCCAGAATTCACAACT
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TTGCTCACAATCTTAAATGAACAGGTTTCAGCGGATGTTCTCTCCAGCTTTCAACAGACC
TTGCACTCAACTTTGCTGAATCCCATTCCAAAATGTGCGCCAGCGCTCTGCACCTTACTA
TCTCATGACTTCTTCAGAAATGATTTTCTGGAAGTTGTGAATTTCTTGAAAAGTTTAAACA
TTGAAGAGTGAAGAGGAGAAAACGGAATTCTTTAAATTTCTGCTGGACAGAGTCAGCTGC
TTGTCAGAGGAATTGATAGCTTCAAGGTTGGTGCCTCTTCTGCTTAATCAGTTGGTGT
GCAGAGCCAGTGGCTGTAAAGAGTTTTCTTCCTTATCTGCTTGGCCCCAAAAAGATCAT
GCGCAGGGAGAAACTCCTTGCTTGCTCTCACCAGCCCTGTTCCAGTCACGGGTGATCCCC
GTGCTTCTCCAGTTGTTTGAAGTTCATGAAGAGCATGTGCGGATGGTGTGCTGCTCTCAC
ATCGAGGCCTACGTGGAGCAC'TTCACTCAGGAGCAGCTGAAGAAAAGTCATCTTGCCACAG
GTTTTGCTGGGCCTGCGTGATACTAGCGATTCCATTGTGGCAATTACTCTGCATAGCCTA
GCAGTGCTGGTCTCTCTGCTTGGACCAGAGGTGGTTGTGGGAGGAGAACGAACCAAGATC
TTCAAACGCACTGCCCCAAGTTTTACTAAAAATACTGACCTTTCTCTAGAAGGCGATCCA
TTTTCTCAGCCTATTAAATTTCCCATAAATGGACTCTCAGATGTAAAAAATACTTCGGAG
GACAGTGAAAAC'TTCCCATCAAGTTCTAAAAAGTCTGAGGAGTGGCCTGACTGGAGTGAA
CCTGAGGAGCCTGAAAATCAAAC'TGTCAACATACAGATTTGGCCTAGAGAACCTTGTGAT
GATGTCAAGTCCCAGTGCAC'TACCTTGGATGTGGAAGAGTCATCTTGGGATGACTGCGAG
CCCAGCAGCTTAGATACTAAAGTAAACCCAGGAGGTGGAATCACTGCTACAAAACCTGTT
ACCTCAGGGGAGCAGAAGCCTATTCTGCTTTGCTTTCCTCACTCACTGAAGAGTCTATGCCT
TGGAATCAAGCTTACCCCCAAAAGATTAGCCTTGTACAAAGGGGGGATGACGCAGACCAA
ATCGAGCCGCCAAAAGTGTATCACAAGAAAGGCCCTTAAGGTTCCATCAGAACTTGGT
TTAGGAGAGGAATTCACCATTCAAGTAAAAAAGAAGCCAGTAAAGATCCTGAGATGGAT
TGTTTTGCTGATATGATCCAGAAATTAAGCCTTCTGCTGCTTTTCTTATATTACCTGAA
CTGAGGACAGAAATGGTCCCCAAAAGGATGATGTCTCCCAGTGATGCAGTTTTCTCA
AAATTTGCTGCAGCAGAAATTACTGAGGGAGAGGCTGAAGGCTGGGAAGAAGAAGGGGAG
CTGAAGTGGGAAGATAATAACTGGTGA

SEQ ID NO: 87_AI052250_H

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CCATGCTTAATAAATTGAAGAGTACTGTTACAAAAGTCACAGCTGATGTCACTAGTGCAG
TAATGGGAATTCCTGTCACTAGAGAATTTGATGTTGGTTCGACACATTGCCAGTGGTTGCA
ATGGGCTAGCTTGGAAAGATTTTAAATGGCACAAAAAAGTCAACAAAGCAGGAAGTGGCAG
TTTTTGCTTTGATAAAAAACTGATTGACAAGTATCAAAAATTTGAAAAGGATCAAATCA
TTGATTCTCTAAAACGAGGAGTCCAACAGTTAACTCGGCTTCGACACCCTCGACTTCTTA
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ATCAGTTGAGTCGTTTAGGATCTAGTTCACTTACAAATATACCTGAGGAAGTTCGTGAAC
ATGTAAAGCTACTGTTAAATGTAACCTCGACTGTAAGACCAGATGCAGATCAAATGACAA
AGATTCCCTTCTTTGATGATGTTGGTGCAGTAACACTGCAATATTTTGATACCTTATTCC
AAAGAGATAATCTTCAGAAATCACAGTTTTTCAAAGGACTGCCAAAGGTTCTACCAAAC

FIGURE 2RRR

TGCCCCAAGCGTGTCAATTGTGCAGAGAATTTTGCCTTGTTGACTTCAGAATTTGTAAACC
CTGACATGGTACCTTTTGTGTTTGTCCCAATGTTCTACTTATTGCTGAGGAATGCACCAAAG
AAGAATATGTCAAATTAATTCTTCCTGAACCTGGCCCTGTGTTTAAGCAGCAGGAGCCAA
TCCAGATTTTGTAAATTTTCTACAAAAAATGGATTTGCTACTAACCAAAACCCCTCCTG
ATGAGATAAAGAACAGTGTCTACCCATGGTTTACAGAGCACTAGAAGCTCCTTCCATTC
AGATCCAGGAGCTCTGTCTAAACATCATTCCAACCTTTGCAAATCTTATAGACTACCCAT
CCATGAAAAACGCTTTGATACCAAGAATTAAAAATGCTTGCTACAAACATCTTCCCTTGC
GGTTCGTGTAAATTCATTAAACAACATTGGAGCAGACCTTCTGACTGGCAGTGAGTCCG

SEQ ID NO: 88_AA278842_H

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GGGACCCGGTCCGGGACTTTCCGTTGAGCTCATCCCGAGCCCCAGAGGGCGGCCTGC
CCGGGCCCTGGGCCCTGCACCGCGGCCGCAAGAAGGCCACAGGCAGCCCCGTGTCCATCT
TCGTCTATGATGTGAAGCCTGGCGCGGAAGAGCAGACCCAGGTGGCCAAAGCTGCCTTCA
AGCGCTTCAAACTCTACGGCACCCCAACATCCTGGCTTACATCGATGGACTGGAGACAG
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GAGTGGAGGCTGGTGGCCTGAAGGAGCTGGAGATCTCCTGGGGGCTACACCAGATCGTGA
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CCGTGTTCTGTGGACCGAGCTGGCGAGTGGAAGCTTGGGGGCTGGACTACATGTATTCGG
CCCAGGGCAACGGTGGGGGACCTCCCCGCAAGGGGATCCCCGAGCTTGAGCAGTATGACC
CCCCGGAGTTGGCTGACAGCAGTGGCAGAGTGGTCAGAGAGAAGTGGTCAGCAGACATGT
GGCGCTTGGGCTGCCTCATTTGGGAAGTCTTCAATGGGGCCCTACCTCGGGCAGCAGCCC
TACGCAACCCTGGGAAGATCCCCAAAACGCTGGTGCCCCATTACTGTGAGCTGGTGGGAG
CAAACCCCAAGGTGCGTCCCAACCCAGCCCGCTTCTTGCAAGACTGCCGGGCACCTGGTG
GCTTCATGAGCAACCGCTTTGTAGAAACCAACCTCTTCTGGAGGAGATTGAGATCAAAG
AGCCAGCCGAGAAGCAAAAAATTTCTTCAGGAGCTGAGCAAGAGCCTGGACGCATTCCCTG
AGGATTTCTGTGCGCACAAGGTGCTGCCCCAGCTGCTGACCGCCTTCGAGTTCGGCAATG
CTGGGGCCGTGTCTCTACGCCCCCTTTCAAGGTGGGCAAGTTCCTGAGCGCTGAGGAGT
ATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTCATCCACTGACCGGGCCATGC
GCATCCGCCTCCTGCAGCAGATGGAGCAGTTTCATCCAGTACCTTGACGAGCCAACAGTCA
ACACCCAGATCTTCCCCACGTCGTACATGGCTTCTTGGACACCAACCCTGCCATCCGGG
AGCAGACGGTCAAGTCCATGCTGCTCCTGGCCCCAAAGCTGAACGAGGCCAACCTCAATG
TGGAGCTGATGAAGCACTTTGCACGGCTACAGGCCAAGGATGAACAGGGCCCCATCCGCT
GCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCAGACACA
GGGTCTTTACCTCTGCCTTCAGCCGAGCCACTAGGGACCCGTTTGCACCGTCCCGGGTTG
CGGGTGTCTGGGCTTTGCTGCCACCCACAACCTCTACTCAATGAACGACTGTGCCCAGA
AGATCCTGCCTGTGCTCTGCGGTCTCACTGTAGATCCTGAGAAATCCGTGCGAGACCAGG
CCTTCAAGGCCATTTCGAGCTTCTGTCCAAATTGGAGTCTGTGTGCGAGGACCCGACCC
AGCTGGAGGAAGTGGAGAAGGATGTCCATGCAGCCTCCAGCCCTGGCATGGGAGGAGCCG
CAGCTAGCTGGGCAGGCTGGGCCGTGACCGGGGTCTCCTCACTCACCTCCAAGCTGATCC
GTTGCGACCCCAACCACTGCCCCAACAGAAACCAACATTCCCCAAGACCCACGCCTGAAG
GAGTTCTTGGCCCCAGCCCCACCCCTGTTCTGCCCCCTACAACCTCAGGCCACTGGG
AGACGCAGGAGGAGGACAAGGACACAGCAGAGGACAGCAGCACTGCTGACAGATGGGACG
ACGAAGACTGGGGCAGCCTGGAGCAGGAGGCCGAGTCTGTGCTGGCCAGCAGGACGACT
GGAGCACCGGGGGCCAAGTGAGCCGTGCTAGTCAGGTCAGCAACTCCGACCACAAATCCT
CCAAATCCCCAGAGTCCGACTGGAGCAGCTGGGAAGCTGAGGGCTCCTGGGAACAGGGTT
GGCAGGAGCCAAGCTCCCAGGAGCCACCTCCTGACGGTACACGGCTGGCCAGCGAGTATA
ACTGGGGTGGCCAGAGTCCAGCGACAAGGGCGACCCCTTCGCTACCCTGTCTGCACGTC
CCAGCACCCAGCCGAGGCCAGACTCTTGGGGTGAGGACAACCTGGGAGGGCCTCGAGACTG

FIGURE 2SSS

ACAGTCGACAGGTCAAGGCTGAGCTGGCCCCGGAAGAAGCGCGAGGAGCGGCGGCGGGAGA
TGGAGGCCAAACGCGCCGAGAGGAAGGTGGCCAAGGGCCCCATGAAGCTGGGAGCCCCGA
AGCTGGACTGAACCGTGGCGGTGGCCCTTCCCGGCTGCGGAGAGCCCCGCCACAGATGT
ATTTATTGTACAAACCATGTGAGCCCCGCCGCCAGCCAGGCCATCTCACGTGTACATA
ATCAGAGCCACAATAAATTCTATTTAC

SEQ ID NO: 89_AA599286_H

ATGGCCTTCATGGAGAAGCCGCCAGCCGGCAAGGTGCTGCTGGACGACACGGTGCCGCTG
ACAGCAGCCATCGAGGCGAGCCAGAGCCTGCAGTCCCACACGGAATATATTATTTCGAGTG
CAAGGAGGAATTTCTGTGGAAAACAGCTGGCAGATTGTTAGAAGATACAGTGACTTTGAT
TTGCTTAACAACAGCTTACAGATTGCAGGCCTAAGTCTACCTCTTCCTCCAAAAAATTG
ATTGGTAACATGGATCGTGAATTCATAGCTGAAAGGCAGAAAGGTCTTCAGAACTATCTC
AACGTGATCACAACAAATCATATCTTGTCTAATTGTGAGCTGGTTAAGAAGTTTTTTAGAT
CCAAACAACATATCCGCAAACTATACTGAGATTGCCTTGCAACAGGTTTCATGTTCTTC
CGATCAGAGCCAAAGTGGGAGGTGGTGGAACTTTGAAAGACATAGGTTGGAGAATAAGG
AAGAAATATTTCTTGATGAAGATTAATAATCAGCCAAAGGAACGGCTAGTGTTAAGCTGG
GCTGACCTTGGCCCAGACAAGTATTTGTCAGATAAAGATTTTCAGTGTCTAATCAAACCTT
CTGCCTTCTTGTGTTGCACCTTACATCTATCGGGTTACCTTTGCCACAGCTAATGAATCC
TCAGCGTTGCTAATTAGGATGTTTAAACGAAAAGGGAACATTGAAGGATCTGATCTACAAG
GCAAAACCAAAGACCCATTTCTAAAGAAGTACTGCAACCCTAAGAAGATTCAGGGCCTG
GAACTCCAGCAAATAAAAACATATGGACGGCAAATATTAGAGGTACTGAAGTTTCTTCAT
GACAAGGGATTCCCTTATGGGCATCTTCACGCCTCCAATGTGATGCTCGATGGGGACACT
TGCCGGCTGCTGGACCTTGAGAATTCCTTATGGGCCTGCCTTCCTTCTACCGATCTTAT
TTTTACAAATTCAGGAAAATCAATACATTGGAAAGTGTGGATGTCCACTGCTTTGGCCAC
TTACTGTATGAAATGACTTATGGACGACCGCCAGACTCGGTGCCTGTGGACTCCTTCCCT
CCTGCCCGTCCATGGCTGTGGTGGCCGTGTTGGAGTCTACGCTGTCTTGTGAAGCCTGT
AAAAATGGCATGCCTACCATCTCCCGCTCTTACAGATGCCATTATTTCAGCGATGTTTTTA
CTAACCCTTCTGAAAAACCACAGTTTAAAGATCCCTACAAAGTTAAAAGAGGCATTGAGA
ATTGCCAAAGAATGTATAGAGAAGAGACTAATTGAGGAACAGAAACAGATTCACCAGCAT
CGAAGACTGACAAGAGCTCAGTCCACCATGGATCTGAGGAGGAAAGAAAAAAGAAAG
ATTTTAGCTCGAAAGAAGTCAAAACGATCTGCTCTTGAAAAATAGTGAAGAGCATTTCAGCG
AAGTACAGCAACTCCAATAATTCAGCAGGATCTGGGGCCAGCTCACCTCTCACGTCCCCG
TCATCGCCAACCTCCACCCTCTACATCAGGGATATCTGCATTACCTCCACCTCCTCCACCT
CCACCACCACCAGCAGCTCCCTTGCTCCTGCGAGCACCGAGGCACCTGCCCAGCTCTCG
TCTCAGGCTGTGAATGGCATGAGCCGAGGGGCCCTTGCTCAGCTCCATCCAGAATTTCAA
AAAGGAACTTTGAGGAAAGCCAAACCTGTGATCACAGTGCTCCGAAGATCGGCTGAAGCT
TCCTGTTTACACTTGGAGGGAAGTTCTTTTTTTATTCTACTCACCCCTACCCCCAAC
TACCCTCTTCTGGGAAAGTAATTGCTGAGCCAGTACAGCCACAAACAGTACTATTTTGC
AGATGCTCATGTAAGCAGCTTTTCGAGAGAAATAATTCTTTAAGCAGAATAAAGTTAGGC
TGGCATGCAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 90_AA425725_H

ATGAGCGCCAGCACGGGCGGTGGTGAGGACAGCGGCGGCAGCGGCGGCAGTAGCAGCAGC
TCACAGGCCTCCTGCGGGCCCCGAGTCTCGGGCTCCGAACTAGCCCTGGCCACACCGGTG
CCTCAGATGCTGCAGGGCCTTCTGGGCTCCGACGACGAGGAACAGGAAGACCCCAAAGAC
TACTGCAAGGGCGGCTACCACCCTGTGAAGATCGGCGACGTGTTCAATGGGCGGTACCAC
GTGGTGCGCAAACTGGGCTGGGGCCACTTCTCCACCGTCTGGCTCTGCTGGGACATCCAG
CGCAAGCGCTTTGTGGCCCTCAAAGTGGTGAAGAGTGCGGGGCATTACACGGAGACAGCT
GTGGATGAGATCAAGCTCCTGAAATGTGTCCGGGACAGCGACCCCAAGTGACCCCAAGA
GAGACCATTGTCCAGCTCATTGATGACTTCAGGATCTCAGGAGTCAATGGAGTCCATGTG

FIGURE 2TTT

TGCATGGTGTGCTGGAGGTGCTGGGCCACCAGCTCCTCAAATGGATCATCAAGTCCAACTAC
CAGGGCCTGCCCCTGCCCTGCGTGAAGAGCATCGTGAGGCAGGTGCTGCACGGCCTGGAC
TACCTCCACACCAAGTGCAAGATCATCCACACGGACATCAAGCCCCGAGAACATCTTGCTG
TGTGTGGGGGACGCTTACATCAGGCGCCTGGCTGCCGAGGCCACGGAGTGGCAACAGGCA
GGGGCGCCGCCCCCTCCCGCTCCATAGTCAGCACTGCCCCCAGGAGGTCTTGACCGGT
AAGCTGTCCAAAAACAAGAGGAAGAAGATGAGGCGCAAACGGAAACAGCAGAAGCGGCTG
CTGGAGGAGCGGCTGCGGGACCTGCAGAGGCTGGAGGCCATGGAGGCTGCCACCCAGGCT
GAGGACTCTGGCTTGAGACTAGACGGGGGACGCGGCTCCACATCCTCTTCAGGCTTCTCC
GGCTCCCTCTTCTCTCTCTGCTCCTGCTCCATCCTCTCCGGCTCGTCCAATCAGCGAGAG
ACCGGGGGCCTCCTGTGCGCTAGCACACCATTCGGTGCCTCGAACCTCCTGGTGAACCCC
CTGGAGCCCCAAAATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGGCAACGCCTGC
TGGGTGCACAAGCACTTCACGGAAGACATCCAGACTCGGCAGTACCGGGCCGTCGAGGTG
CTGATCGGCGCCGAATACGGCCCCCGGCAGACATCTGGAGCACAGCCTGCATGGCCTTC
GAGCTGGCCACTGGTGAATACCTGTTTCGAGCCGATTCTGGAGAAGACTACAGTCGTGAT
GAGGACCACATCGCTCACATAGTGGAGCTTCTGGGGGACATCCCCCAGCCTTCGCCCTC
TCAGGCCGCTATTCCCGGGAGTTCTTCAACCGGAGAGGAGAGCTGCGGCACATCCACAAT
CTCAAGCACTGGGGCCTGTACGAGGTACTCATGGAAAAGTACGAGTGGCCCCTAGAGCAG
GCCACACAGTTTCAGCGCCTTCTGCTGCCCATGATGGAGTACATCCCCGAAAAGCGGGCC
AGTGCCGCTGACTGCCTCCAGCACCCCTGGCTCAACCCCTAG

SEQ ID NO: 91_SGK022_H

TCTGGCCCTGTCCCTCCCCACCCCGCGCTGTGTCCAGACAGAGAATGTTCTAACGCT
GGGGGCGGCTGCGGATGAAGTCCTTGGGGAGAAAAGGAGCAGGCCAAGGGCGATGGTGA
GTAGAGCTGCCTCTCAGAGGCAGCATGAGCTGAGAGGGTGATAGGAAGGCGGCGCTAGAC
AGCATGGAGGACTTTCTGCTCTCCAATGGGTACCAGCTGGGCAAGACCATTGGGGAAGGG
ACCTACTCAAAAGTCAAAGAAGCATTTCACAAAAACACCAAAGAAAAGTGGCAATTAAA
GTTATAGACAAGATGGGAGGGCCATCAGAGTTTATCCAGAGATTCTCCCTCGGGAGCTC
CAAATCGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCT
GCCGACGGGAAAATCTGCCTGGTGTATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGC
GTGCTGAATGGGGGGGCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTGAGATGGTT
GAGGCCATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAAC
GCCTTGTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCC
AAGTCACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCGAG
GTGCTGCAGGGCATTCACACGATAGCAAAAAGGTGATGTCTGGAGCATGGGTGTGGTC
CTGTATGTGCTCTGTGCCAGCTACCTTTTGACGACACAGACATCCCCAAGATGCTG
TGGCAGCAGCAGAAGGGGTGTCCTTCCCCACTCATCTGAGCATCTCGGCCGATTGCCAG
GACCTGCTCAAGAGGCTCCTGGAACCCGATATGATCCTCCGGCCTTCAATTGAAGAAGTT
AGTTGGCATCCATGGCTAGCAAGCACTTGATAAAAGCAATGGCAAGTGCTCTCCAATAAA
GTAGGGGGAGAAAGCAAA

SEQ ID NO: 92_AA060026_M SGK022_M

CAGACGGAGAATGTTCTAGCCCTGGAGGCAGCTGTGAATGAAGTCCTTGGGGGGAAAGA
AGCAGGCCGAGGGCGATGGTGGAGTAGAGCTGCCTCGCAGAGGCAGCATGAGCTGAGAGG
GTGACAAGAAGGAGGCGCTACACAGCATGGAGGACTTTCTACTCTCCAATGGGTATCAGC
TGGGCAAGACCATTGGGGAAGGGACCTACTCAAAGTCAAAGAAGCATTTCACAAAAAC
ATCAAAGAAAAGTGGCAATTAAAATTATAGACAAGATGGGAGGGCCAGAAGAGTTTATCC
AGAGATTCTGCTCGTGAGCTCCAGATTGTCCGTACCCTGGACCACAAAAACATCATCC
AGGTGTATGAGATGCTGGAGTCAGCAGATGGAAAAATCTACCTGGTGTGGAAGTGGCTG
AGGGAGGGGATGTCTTTGACTGTGTGCTGAACGGAGGGCCACTTCCCGAGAGCCGGGCCA
AGGCCCTCTTCCGCCAGATGGTTGAGGCTATTCGCTATTGCCATGGCTGTGGCGTGGCCC

FIGURE 2UUU

ACCGGGACCTTAAGTGTGAGAACGCCTTGTTGCAGGGCTTCAACCTGAAGCTGACCGACT
TTGGCTTTGCCAAGGTGCTACCCAAGTCACGCAGGGAGCTGAGCCAGACCTTCTGTGGCA
GCACAGCCTATGCCGCCCCCTGAGGTGCTACAGGGCATACCCCATGATAGCAAGAAAGGTG
ATGTCTGGAGCATGGGTGTGGTCTGTATGTAATGCTCTGTGCAAGTCTACCTTTTGATG
ACACAGATATCCCCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATT
TGGGCATCTCAACCGAATGCCAGGACCTGCTCAAGCGGCTCCTGGAACCAGACATGATAC
TCCGGCCTTCAATCGAAGAAAGTTAGTTGGCACCCATGGCTAGCAAGCACTTGATAAAAGC
AATGGCAAGTCTTCCCCAATAAAGTAGGGGGAGAAAGCAAACCTG

SEQ ID NO: 93_AA399669_H

CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGCACTTCATTCTCAA
GTTTTGTGGCCAACGATGGATAGGAGGTGGATTGTGATGTATTGGAACATGGGACCTTG
AGGAGTTCGGTAACCAAAAGGAGAAAAGTAACAACAGCCAGTGGAGACAAAAAGAACTGCT
TCTCTTTCTTTCCCCCTCCAAGTTCCTAGTGGAGGGCTGAGTCCAGCATCCCAGACTCGT
GTGACTATATAGGCAAGCATTGTTGGGACCTACTTCACTTTGATACCCTAGCCTTCAGCAG
CTCAAGGTGTTGGCCTTTGGATAGGAGGCTTCCAAGTAGTAAAGCTCCCTGCTCTCAGCA
AGCCCAACACCATGGGGAAGGGAGATGTCTTAGAGGCAGCACCAACCACCACAGCCTACC
ATTCCTCATGGATGAATATGGTTATGAGGTGGGCAAGGCCATTGGCCATGGCTCCTATG
GGTCGGTATATGAGGCTTTCTACACAAAGCAGAAGGTTATGGTGGCAGTCAAGATCATCT
CAAAGAAGAAGGCCTCTGATGACTATCTTAACAAGTTCCTGCCCCGTGAAATACAGGTAA
TGAAAGTCTTGCGGCACAAGTACCTCATCAACTTCTATCGGGCCATTGAGAGCACATCTC
GAGTATACATCATTTCTGGAACCTGGCTCAGGGTGGTGTATGTCCTTGAATGGATCCAGCGCT
ACGGGGCCTGCTCTGAGCCCCCTTGCTGGCAAGTGGTTCTCCAGCTGACCCTGGGCATTG
CCTACCTGCACAGCAAGAGCATCGTGACCCGGGACTTAAAGTTGGAGAACCTGTTGCTGG
ACAAGTGGGAGAATGTGAAGATATCAGACTTTGGCTTTGCCAAGATGGTGCCTTCTAACC
AGCCTGTGGGTTGTAGCCCTKCTTACCGCCAAGTGAAGTGCCTTTTCCACCTCAGCCAGA
CTTACTGTGGCAGCTTTGCTTACGCTTGCCAGAGATCTTACGAGGCTTGCCCTACAACC
CTTTCTGTCTGACACCTGGAGCATGGGCGTCATCCTTTACACTCTAGTGGTCGCCCCATC
TGCCCTTTGATGACACCAATCTCAAAAAGCTGCTAAGAGAGACTCAGAAGGAGGTCACTT
TCCCAGCTAACCATAACCATCTCCAGGAGTGCAAGGTCCAAGTGCCTATTGCCTGTGTGG
CACAATGGAGAAAAACTCAGGCAAGACCTCTCTCTCCCTGCTCTAGAACCTGATCCTCC
AGATGCTACGCCAAGCCACTAAGCGTGCCACCATTCTGGACATCATCAAGGATTCCTGGG
TGCTCAAGTTCAGCCTGAGCAACCCACCCATGAGATCAGGCTGCTTGAGGCCATGTGCC
AGCTCCACAACACCACTAAACAGCACCAATCCTTGCAAATTACGACCTGAAAATGGCTGA
GGGAGGGGGCTAAGAGAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTTACCAA
AAATAAATCTAAGTCTGATTTAGTTTCATCAAAAAA

SEQ ID NO: 94_AA758539_H

GACCATTCAGACGCCTCCGGTAGTGTAATGAGGACAATGCCTGCTGGCCACATGACGG
GGGGATGTAGACGGCAGCGGCCAGTCGCTCCTGGCACCATGGACGATGCCACAGTCCT
AAGGAAGAAGGGTTACATCGTAGGCATCAATCTTGGCAAGGGTTCCTACGCAAAAGTCAA
ATCTGCCTACTCTGAGCGCCTCAAGTTCAATGTGGCTGTCAAGATCATCGACCGCAGGAA
AACACCTACTGACTTTGTGGAGAGATTCTTCTCGGGAGATGGACATCCTGGCAACTGT
CAACCACGGCTCCATCATCAAGACTTACGAGATCTTTGAGACCTCTGACGGACGGATCTA
CATCATCATGGAGCTTGGCGTCCAGGGCGACCTCCTCGAGTTCATCAAGTGCCAGGGAGC
CCTGCATGAGGACGTGGCACGCAAGATGTTCCGACAGCTCTCCTCCGCCGTCAAGTACTG
CCACGACCTGGACATCGTCCACCGGGACCTCAAGTGCGGAGAACCTTCTCCTCGACAAGGA
CTTCAACATCAAGCTGTCTGACTTTGGCTTCTCCAAGCGCTGCCTGCGGGACAGCAATGG
GCGCATCATCCTCAGCAAGACCTTCTGCGGGTTCGGCAGCATATGCAGCCCCCGAGGTGCT
GCAGAGCATCCCCACCAGCCCAAGGTGTATGACATCTGGAGCCTGGGCGTGATCCTGTA

FIGURE 2VVV

CATCATGGTCTGCGGCTCCATGCCCTATGACGACTCCGACATCAGGAAGATGCTGCGTAT
CCAGAAGGAGCACCGTGTGGACTTCCCCGCGCTCCAAGAACCTGACCTGCGAGTGCAAGGA
CCTCATCTACCGCATGCTGCAGCCCCGACGTCAGCCAGCGGCTCCACATCGATGAGATCCT
CAGCCACTCGTGGCTGCAGCCCCCAAGCCCAAGCCACGTCTTCTGCCTCCTTCAAGAG
GGAGGGGGAGGGCAAGTACCGCGCTGAGTGCAAAC'TGGACACCAAGACAGGCTTGAGGCC
CGACCACCGGCCCCGACCACAAGCTTGGAGCCAAAACCCAGCACCGGCTGCTGGTGGTGCC
CGAGAACGAGAACAGGATGGAGGACAGGCTGGCCGAGACCTCCAGGGCCAAAGACCATCA
CATCTCCGGAGCTGAGGTGGGGAAAGCAAGCACCTAGCATGACAATGGCCCCGTTGTGTG
TGGTGGGGGTGCGGGTTGGGGGGCATGGTGCAGTCGGCCTTCACGTAAACTAAGTAGGCA
GGTAGGATCTGAAGAAGGCACAGGTGCAAGTAAAATTCGTCAATTAAACCACTATTTTGA
TT

SEQ ID NO: 95_AA883975_H

ATGTCCGGAGACAACTTCTGAGCGAACTCGGTTATAAGCTGGGCCGCACAATTGGAGAG
GGCAGCTACTCCAAGGTGAAGGTGGCCACATCCAAGAAGTACAAGGGTACCGTGGCCATC
AAGGTGGTGGACCGGCGGAGCGCCCCCGGACTTCGTCAACAAGTTCCTGCCGCGAGAG
CTGTCCATCCTGCGGGGCGTGCGACACCCGCACATCGTGCACGTCTTCGAGTTCATCGAG
GTGTGCAACGGGAACTGTACATCGTGATGGAAGCGGCCGCCACCGACCTGCTGCAAGCC
GTGCAGCGCAACGGGCGCATCCCCGAGTTTCAGGCGCGCGACCTCTTTCGCGCAGATCGCC
GGCGCCGTGCGCTACCTGCACGATCATCACCTGGTGCACCGCGACCTCAAGTGCGAAAAC
GTGCTGCTGAGCCCGGACGAGCGCCGCGTCAAGCTCACCGACTTCGGCTTCGGCCGCCAG
GCCCATGGCTACCCAGACCTGAGCACCACCTACTGCGGCTCAGCCGCTACGCGTCAACC
GAGGTGCTCCTGGGCATCCCCTACGACCCCAAGAAGTACGATGTGTGGAGCATGGGCGTC
GTGCTCTACGTATGGTACCCGGGTGCATGCCCTTCGACGACTCGGACATCGCCGGCCTG
CCCCGGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC
AAGGCCCTGATCGCCGAGCTGCTGCAGTTTCAGCCCCGTCCGCCAGGCCCTCCGCGGGCCAG
GTAGCGCGCAACTGCTGGCTGCGCGCCGGGACTCCGGCTAG

SEQ ID NO: 96_AA905446_H

CTGGTAGAGAACAGGGGCTGGTGCCAAGGCCCATGGAGATGAGAAAACGGAAGACAGGGA
TCATGGAAAGAATTGTGGGGTCAGGGGACAGTGGCGGGAGGAGCTGGCTCACCACCCTGT
GGACAAATCAGGCCTTATAATTTGTGATTCTGTGGCTTTGTCTAAAAGTCCATAAAGCAC
CTTGATATCCAGTCTCACAGACTGCTCACAACAGTCCACAAGGCTGGTGGGGAGTGCTTC
TTTTGAATGATATACTAACGACAAAAATAATAGAAGTGAACATTCTTTGCAATGTCCAAG
CAGCTAGACACACTTAAGACCATTAAGAAAGCCAAGAAATAAGACCCAGACAAGGTGGGC
AGAAGTTGGAAGGCAGGAGACAGGTGTGAGGAGGTGGGCCTTTCTGATCTGCCAGCCCAT
CTCTCCTCCCCTTACTTCCTCAGAGTTTATCCAGAGATTCCCTCCCTCGGGAGCTCCAAAT
CGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCTGCCGA
CGGGAAAATCTGCCTGGTGTGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGCGTGCT
GAATGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTGAGATGGTTGAGGC
CATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAACGCCTT
GTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCCAAGTC
ACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAGGTGCT
GCAGGGCATTCCCNCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCA
TCTGAGCATCTCGGCCGATTGCCAGGACCTGCTCAAGAGGCTCCTGGAACCCGATATGAT
CCTCCGGCCTTCAATTGAAGAAGTTAGTTGGCATCCATGGCTAGCAAGCACTTGATAAAA
GCAATGGCAAGTGCTCTCCAATAAAGTAGGGGGAGAAAGCAAACCC

FIGURE 2WWW

SEQ ID NO: 97_H29974_H

TTACAGCCTGTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCAGTGGC
CGGGCGCAGCGGGGCCCCGGTGGCGGTCAAGAAGATCCGCTGCGACGCCCCGAGAACGT
GGAGCTGGCGCTGGCTGAATTCTGGGCCCTCACCAGCCTCAAGCGGCGCCACCAGAACGT
CGTGACGTTTGAGGAGTGCGTCCTGCAGCGCAATGGGTTAGCCCAGCGCATGAGTCACGG
CAACAAGAGCTCGCAGCTTTACCTGCGCCTGGTGGAGACCTCGCTGAAAGGAGAAAGGAT
CCTGGGTTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTTCATGGAGTTCTGTGAAGGTGG
AGACCTGAATCAGTATGTCTGTCCCGGAGGCCAGACCCAGCCACCAACAAAAGTTTCAT
GCTACAGCTGACGAGCGCCATTGCCTTCCTGCACAAAAACCATATTGTGCACAGGGACCT
GAAGCCAGACAACATCCTCATCACAGAGCGGTCTGGCACCCCCATCCTCAAAGTGGCCGA
CTTTGGACTAAGCAAGGTCTGTGCTGGGCTGGCACCCCCGAGGCAAAGAGGGCAATCAAGA
CAACAAAAATGTGAATGTGAATAAGTACTGGCTGTCTCAGCCTGCGGTTTCGGACTTCTA
CATGGCTCCTGAAGTCTGGGAGGGACACTACACAGCCAAGGCGGACATCTTTGCCCTGGG
CATTATCATCTGGGCAATGATAGAAAGAATCACTTTTATTGACTCTGAGACCAAGAAGGA
GCTCCTGGGGACCTACATTAAACAGGGGACTGAGATCGTCCCTGTTGGTGGGCGCTGCT
AGAAAACCCAAAGATGGAGTTGCACATCCCCAAAAACGCAGGACTTCCATGTCTGAGGG
GATCAAGCAGCTCTTGAAAGATATGTTAGCTGCTAACCACAGGACCGGCTGATGCCTT
TGAAGTTGAAACCAGAATGGACCAGGTACATGTGCTGCTTAAATTCAGGGCTAAGCAT
TTTGGGTGATTTTAAACTAGGTGCGATTCCCTCGGGACCCACAGTCTCACCACGTCTCCTCC
AGAGGACGGCAGAGGGTACAGGTGGTGGCCTGGCCGGTGGCGATCTCCCGACAGCTGGA
TCCGGCAATGTGAAGCTTTTGTGGTGGTTCCTTTTGGCTTTTGGCTTTTGGCTTTTATTTN
TNNCTTTTCTTTTCTTTTTTTTNTTNNCCACNTNCCTTTTTTAAATTTAAACCATTGAG
ACTTCAGAAGAGCAGGACACAATGCTGTGGACAGGCACCAATTTCTTTAAAGAAATTCAA
TGTGGGCAAGGCATATGTGTAAATTTCACTTTTACTTTTATAAGGGGTAGGGAGCTAT
TTTTGGTTTTGTCTTCACTTTCCCTCTGTCTTCTTCTTATACTTTTCTCAGTTCTAC
TTATGACACCTCACTTCCCTAGAGAAGGCCCTGCCTCCCCATAGGGAATCTGGGGGTANCT
TCTGGAACGGGGCGTGAGGANACAAGGAGCCTCTGGGCCACNCCTCCCTACCAGATGCAG
GAACCTCTGGAATCCTTGGTGGGCTGGCCCTGGCTAGCCCTTGGGCCTCGGAGATGATCA
GAGGTGAAGAACCGCC

SEQ ID NO: 98_AA498104_M H29974_M

CCGTTGCTGCTCCCCCGCCCCCGCAGCCATGGAAACGGGGAAAGAGAACGGAGCCCCG
AGAGGGACAAAAAGCCCCGAGCGGAAAAGGCGAAGCCAGTCCAGCGGGTACTGTGCGAG
AAGCTGAGGCCGGCGGCCAGGCCATGGATCCGGCTGGGGCCGAGGTCCCGGGCGAGGCC
TTCTGGCCCCGGCGGCCGGATGGCGCGCGCGGGATGTTCTGCACGGCCGCGCTAC
AGCCTCTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCTGTGGCTGGG
CGCAGTGGGGCCAGGGTGGCAGTCAAGAAGATCCGCTGCGACGCTCCCGAGAACGTGGAG
TTGGCACTAGCAGAATTCTGGGCCCTCACCAGTCTCAAGCGGCGGCACCAGAATATCGTG
CAGTTTGAGGAGTGCGTCCTACAGCGCAACGGGTAGCCCAGCGCATGAGTCACGGCAAC
AAGAACTCACAGCTTTACCTGCGCCTGGTGGAGACCTCGCTCAAAGGAGAAAGGATCCTG
GGCTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTTCATGGAGTACTGTGAAGGTGGAGAC
CTCAATCAGTATGTCTGTCCCGGAGACCTGACCCAGCCACCAACAAAAGTTTCATGCTA
CAGCTTACAAGCGCCATTGCCTTCCTGCATAAAAAACCATCGTGACAGGGACCTAAAG
CCAGACAACATCCTGATCACAGAGCGGTCTGGCACCCCCATCCTCAAGGTGGCAGACTTT
GGACTGAGCAAGGTCTGTGCAGGGCTGGCACCCCCGAGGCAAAGAGGGCAATCAAGATAAC
AAAAATGTGAATGTGAATAAATACTGGCTGTCTCAGCTTGTGGCTCAGACTTCTACATG
GCTCCCGAAGTCTGGGAGGGACACTATACAGCCAAGGCGGACATCTTTGCTCTGGGCATT
ATCATCTGGGCAATGATAGAAAGAATTACCTTTATTGACTCTGAAACCAAGAAGGAGCTC
CTGGGGACCTACATTAAAGCAAGGGACTGAGATCGTCCCTGTTGGTGGAGCGCTGCTAGAA
AACCCAAAGATGGAGTTGCATATCCCCCAGAAACGTAGGACTTCCATGTCTGAGGGGCTC

FIGURE 2XXX

AAGCAGCTCTTGAAAGACATGTTAGCTGCTAACCCACAGGACCGACCTGATGCTTTTGAA
CTTGAAACCCGAATGGACCAGGTACATGTGCTGCTTAAACTCCAGGGCTGAACGTCTTG
GGTGTTTTTTAAACTAGGTTCGATCCTTCGGGACCCACAGTCTCATCGTGTCTCGGACAGGA
TGGCAGAGGGTACAGGTGGTGGTGTATCTCCTGACAGCTGGACCTCCCACAATGTGAAGCT
CACGCTTGGGCTGCCCCTCTACCCTTCTCTTCTCCTTCAGTAGAATAATAATTGTTTT
TCTAAACATTAAACCATCAAGACTTCTGAAGAGCAGAAGGCTACACTCTG

SEQ ID NO: 99_AA215311_H

CGRCCGCGCTACGGAAAGCCGGAGGGGGGCGGGGCCGTCGGCGTAAGGGGGTGTGTCCGC
GCGCACCACGGGGGCGCGCCGGCTGCTGACTGGAGGCGGCGGCAGCGGAGGCGCGAGC
TGCCCGATAATGGCGGCCTGCAGAGCCCATGAGAGGGAGAAGCGGCAGCGTCTACCCTGA
GAAACCTCGACCTTGAAGATGGTGAAGTAGCCAGCCAAAGTACGATCTAATACGGGAGGTA
GGCCGAGGTAGTTACGGTGTGTGTATGAAGCAGTCATCAGAAAGACCTCTGCACGGGTG
GCAGTGAAGAAAATTCGATGTCACGCACCTGAAAATGTTGAACTAGCCCTTCGTGAGTTC
TGGGCACTAAGCAGTATCAAGAGCCAACATCCAAATGTGATTCACTTGGAGGAATGCATC
CTACAAAAGGATGGGATGGTGCAAAAGATGTCCCACGGCTCTAATTCTTCCCTTTATTTA
CAGCTTGTAGAACTTCATTAAGGAGAAATTGCCTTTGATCCCAGAAGCGCCTATTAT
TTGTGGTTTGTGATGGATTTTTGTGACGGAGGAGATATGAATGAGTATCTGTTGTCCAGG
AAGCCCAATCGTAAACTAACACCAGCTTCATGCTTCAGCTGAGCAGTGCCCTGGCTTTC
TTGCATAAAAACCAGATCATCCACCGAGATCTTAAGCCTGATAACATCCTGATTTCTCAA
ACCAGGTTGGATACCAGTGACTTGGAACTACCCTCAAAGTGGCTGATTTTGGTCTAAGT
AAAGTTTGTTCAGCCTCTGGGCAGAACCCAGAAGAACCTGTCAGTGTAAACAAGTGTTC
CTTTCCACAGCATGTGGAACAGATTTTTACATGGCTCCTGAAGTTTGGGAAGGACATTAC
ACAGCAAAAGCTGACATCTTTGCTCTGGGGATTATCATCTGGGCAATGCTGGAAAGGATC
ACATTATAGACACAGAGACAAAGAAGGAACCTTGGGGAGTTATGTAAACAAGGAACCT
GAGATTGTGCTGTGGGGAGGCACTTCTGGAAAATCCCAAATGGAACTTCTCATTCTC
GTGAAGAAAAATCTATGAATGGGCGAATGAAACAACTGATTAAGGAAATGCTGGCTGCA
AACCTCAGGATCGTCCAGATGCTTTTGAAGTAGAACTCAGATTAGTACAAATTGCATTT
AAAGATAGCAGCTGGGAAACGTGACACATATTATTTGCAAATACCATGGATGATATGCTG
CTTCTGTTTAAACAGTGATGCAACATTATGTGGCTGAAAAAGAATATAAAAAGCTAGACTC
TACCCTCTAAGGGTTTAGATTTTTTGTGGGATTTTTTTTTTCTCATTCTTAAATCC
AAGTTGGCCGTTTTATTAGTATGTTTCAAATGTGTATTACCAATGTGGGTGTAAATTTTT
AAAAATGATTATTGATAGAAGTTTGGCAGGAAAATTCTTTAAGAGCTAACAAGAGAAGA
GAGTCCAGTTTTCTGGAAATATGTCTTTAAGTATTTTAGACATTCCTCGTCAGTATTAGG
AATTTCCATGGGAAAAGAGTTTGCATGCTGGTAATGCAACCTTTGAACTTTGTAAAGG
AAACATATATGTATATATTTATGTATATGTAAGTATGTGAATGTGCGCATTTTGCATTCC
ATATGAAAAAATGCCACGTCTGTTTAAATTATTTGATGTAGGTTTGGGTTTTTGTAGATT
TGCTGGTGAAGTCAGTGACGAAAAATAAACCTTCCCTTATCTTCCCTACTCTGCCCTCCC
CCTAATGAAATCATATTAAGTNGTTTTTCCCTNNTTTTTTTTGTAATATACAGCTTTTTTTT
TAAGGCATCATTTTCGAGGGTCTAAAATTATCTGGTAAACAAATGAAATTAAGTGATCC
AAAGCTGCTGAAGTATGTTTGAAGTCTCCAGTGCCCTATAGCTGCAAGAGTTGAATTAGT
CATGCAGTCATATGGCAGCAGGTTGGTGATT

SEQ ID NO: 100_AA018361_H

GCGGGGCTCCGTATCCCCACGTGGGCCCTGCAGGAACTGGCGGGGCGCGTGACCCGGCG
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TGCATTTCCGGCGGGGCGCGCTGGGGGCGAGCTGGAGCCACCCAGTGCTCGGCCCGCCCC
GCAACCCGCCGGAACCGCCCGCAGCGAGGAAGCGCCCGCGCGGGCGCAGGCGGCCGG
AATGGCGGGGCGGGCTGGGGTCCCCCGCGCCTGGACGGCTTCATCCTCACCAGCGCCT
GGGCAGCGGCACGTACGCCACGGTGTACAAGGCCTACGCCAAGAAGGACACTCGTGAAGT

FIGURE 2YYY

GGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAGGCATCGGTGGAGAACCTCCT
CACGGAGATTGAGATCCTCAAGGGCATTCGACATCCCCACATTGTGCAGCTGAAAGACTT
TCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTGCGCAGGGGGCGACCTGTC
TCGCTTCATCCATACCCGAGGATTCTGCCTGAGAAGGTGGCGCGTGTCTTCATGCAGCA
ATTAGCTAGCGCCCTGCAATTCCTGCATGAACGGAATATCTCTCACCTGGATCTGAAGCC
ACAGAACATTCTACTGAGCTCCTTGGAGAAGCCCCACCTAAAACTGGCAGACTTTGGTTT
CGCACAAACATGTCCCCGTGGGATGAGAAGCACGTGCTCCGTGGCTCCCCCTCTACAT
GGCCCCCGAGATGGTGTGCCAGCGGCAGTATGACGCCCGGTGGACCTCTGGTCCATGGG
GGTCATCCTGTATGAAGCCCTCTTCGGGCAGCCCCCTTTGCCTCCAGGTCGTTCTCGGA
GCTGGAAGAGAAGATCCGTAGCAACCGGGTCATCGAGCTCCCCTTGGCGCCCCCTGCTCTC
CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCAGCCGTCGCATCTC
CTTCCAGGACTCTTTTGCACCCCTGGGTGGACCTGGAGCACATGCCAGTGGGGAGAG
TCTGGGGCGAGCAACCGCCCTGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATT
AGCAGCCGCCTTATCACTCTACTGCAAGGCTCTGGACTTCTTTGTACCTGCCCTGCACTA
TGAAGTGGATGCCCAGCGGAAGGAGGCAATTAAGGCAAAGGTGGGGCAGTACGTGTCCCG
GGCTGAGGAGCTCAAGGCCATCGTCTCCTCTTCCAATCAGGCCCTGCTGAGGCAGGGGAC
CTCTGCCCCGAGACCTGCTCAGAGAGATGGCCCGGACAAGCCACGCCTCCTAGCTGCCCT
GGAAGTGGCTTCAGCTGCCATGGCCAAGGAGGAGCGCCGGCGGGAGCAGGATGCCCT
GGACCTGTACCAGCACAGCCTGGGGGAGCTACTGCTGTTGCTGCGGAGCCCCGGGCGG
AGGCGGGAGCTGCTTCACACTGAGGTTTCAAGACCTCATGGCCCGAGCTGAATACTTGAAG
GAGCAGATGAGGGAATCTCGCTGGGAAGCTGACACCCTGGACAAAGAGGGACTGTGCGAA
TCTGTTTCGTAGCTCTTGCACCCTTCAGTGACCCTAGAAGAATGATTGGACAGATGTGAGC
CATCTGGAGCAGAGGGGCACTAACCAGGCTGACGCCAAGAATGAAGTGGCCCACTGCAG
CCCTGGCGAGCAGGCTTCTTGGATGGACAGTGCTGAGACCCCATATCCCAGAGTCCCCA
GCCTCCCTCAGGTTACTCTGCACCCACAGATGGTTTGTATGGCTGTGCTGTATACTGGAG
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TACTGGGTCTGTGCCTGTCCGTTTTGGGGCATGCAGCCCTCTATCATTTTTTGGCTCCGA
GAAGAGGGCAAGGGGCCCCCGCAGGGTACTTCTGTGCTTGGCCCTCGCCCTGCCAGCAGGC
AGCTGTGCCCTGGCCTGCCCTTCCCGGGACCCCTTATTCCAACCTCAGCTCCTCTTTGCA
CTGGAATGGGGCACTCCAACACCCCTCAGGGACCACCCCTCCCCACAGTATGCACTCAGCC
CCACAGAACCACCAAGTCTTTCTGGGAACCTCACACCTGCCCCGCCATCTTGGTACTTTAGG
TTAATCCCTCAAGCATGAAAGCTGGATCTTTTGGGGTTTAAGAAGCCCAAGCCTTGTTCC
TGCCCTGGCCTAGGGAGCACTCAGGAGGGTTCCCTTGGTCCCTCATCTCTCCACCTCCGTT
CCCTCTGGGCCCCACACTAGCCACAGCGCGGGCCTTGTGCTGGAGTTTGAGCCTGGGACA
GGGAGAGGGAGGCTTGGAGACAGTCTGACCCAGTGCCCTCTAGGCCACCCACTTCTAGGC
CTGCCCTGCCGCCGTGGAGCCCTGGGCAAGCTCTTTCCCTTTCTGGGCCTGGGTCTCCC
CATCTCTTCAATGGGGCTGATACCTTACAGCCCACAGCATGGGCACCTTATGAGGACAAA
GTGAATTTAACCCTGGAAAAGAATGTATTTGAGAGTTTCTTTTAAATAATCAGCGGGTGT
GGTGATTTGTAGCCCTTCTGCCCTTAAATGCTTCCTTGGGCAAGAGCTGTCTGTCTCTCC
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SEQ ID NO: 101_AA311714_H

TGGACCTGTCCTGAGGCAGAGGCCGAGATGCGCGCAACCGCGGGAGCAGCCAAGTGGACT
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GAAGTCGGCCAGAGATGGAACCTTTATTCTGTATGAGGAGATCGGAAGAGGAAGCAAG
ACTGTTGTCTATAAAGGGCGACGGAAGGGAACAATCAATTTGTAGCCATTCTTTGTACT
GATAAGTGCAGAAGGCCTGAAATAACCAACTGGGTCCGTCTCACCCGTGAAATAAAACAC
AAGAATATTGTAACCTTTTCATGAATGGTATGAAACAAGCAACCACCTCTGGCTAGTGXAT
GAAAACCTCCCAGAAGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGGATTACAT
CATCTTCATAAACTTGGCATTCTCTTTTGTGACATTTCTCCTAGGAAGATACTCTTGAA

FIGURE 2ZZZ

GGGCCTGGCACACTGAAGTTTAGCAACTTTTGCTTGGCAAAAGTGGAAGGTGAAAATTTG
GAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGTGATAATGGGGAAAATGTC
CTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCAGAAGTT
GTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTAT
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ATCTTATGTGAAGATCCTTTGCCACCTATTCCGAAAGATTCTTCTCGTCCTAAAGCTTCT
TCAGATTTTATTAATTTGCTTGATGGGTACTTCAAAGAGATCCTCAGAAAAGATTGACT
TGGACAAGGCTACTGCAGCATTCATTTTGGAAGAAAGCTTTTGCTGGAGCAGATCAGGAA
TCAAGCGTCGAAGATCTCAGTCTCAGCAGAAACACTATGGAGTGTTCTGGGCCACAAGAT
TCCAAGGAGCTTTTGCAAGACTCTCAGAGTAGACAAGCAAAAGGGCACAAGAGTGGTCAA
CCACTAGGTCACTCTTTCAGACTAGAAAATCCAAGTGAAGTTTCGGCCTAAGAGTACTCTT
GAGGGTCAATTGAATGAATCCATGTTTCTTCTCAGTTCCTCGTCTACTCCCAGAACTAGC
ACTGCAGTGGAAGTAAGTCTTGGTGAGGATATGACTCACTGTTCAACACAGAAGACTTCT
CCTCTGACCAAGATTACAAGTGGACACCTGAGTCAGCAGGACCTGGAATCCCAGATGAGA
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ATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCTACCAACATATTCAGTG
GATAAGTTATTATTTCTGAAAGATCAAGATTGGAATGACTTTTTTGCAACAAGTGTGCTCG
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TTCCAATTGCTAATCCAGCATTTGCGGATAGCTCCAACTGGGATATACGGGGCCAAGGTT
GCTCACGTGATTGGTTTACTGGCTTCGCACACAACTGAGCTCCAGGAAAATACACCTGTT
GTTGAGACTACAAGCTCCATTGGAATCGGGATTTTGAAGTGTCTTGTTCAACACTCCACT
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AAACTGTATCAGCATT

SEQ ID NO: 102_SGK384_H

TCTTTGGCCACGTGCTGAGGGCGCGGCAGATCCTGACGGAGCCAGAAGTGCGCGACTAC
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SEQ ID NO: 103_AA210451_M SGK384_M

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GGTTGTGAGCTGCCATGTTGAACCAAGCAGGTCACTGAGGGACACAGGCATGTGGATGGA
AACCCTGCTGGGAGAAAAAAGAACTGCTGAAGGGACTGACATGGGACAGCAACATGGAA
CCAGGAATGGTCTCACGCATAGAGAGCTCCCCCGGGGCGTGGGGCTGCTGCTCGCCATGG
CCCTTATGAACGTGGCGCTCTACCTCTGCCTTGATCAGCTTTTCATCTCCCCCTGGACGAT
CCACCGCGGACTCTAGGCGCTGTCTCCGGGCTACTTCAGAATGGGGCGGATGAGAACT
GCTCACGCTGGCTGTCTGTGAAGAGCTGAGGACAGAAGTCAGGCAGCTGAAGCGCGTTG
GGGAGGGAGCCGTGAAGAGAGTCTTTCTGTCTGAATGGAAGGAACACAAAGTCGCTCTCT
CCCGGCTCACAGGCTGGAGATGAAGGAGGACTTCCTGCATGGGCTGCAGATGCTGAAGT
CTCTACAGAGTGAGCACGTGGTCACGCTGGTGGGCTACTGTGAGGAAGATGGCACTATTC
TCACCGAATATCAACCTTAGGTTCTTTGAGCAACCTGGAAGAAACACTAAACCTTTCAA
AGTACCAAGACGTGAACACTTGGCAGCACAGGCTGCAGCTGGCCATGGAGTACGTACGCA
TCATTAACATCTGCATCACAGCCCCCTGGGCACGAGGGTCATGTGTGACTCTAACGACC
TGCCCAAAACATTGTCCAGTACCTGCTAACAAGTAACTTCAGCATTTGTGGCAAACGACC
TGGACGCTCTGCCCCTGGTAGACCATGACTCTGGGGTACTTATAAAGTGTGGCCACAGAG
AGCTCCATGGGGATTTTGTGGCTCCAGAGCAGCTGTGGCCCTACGGAGAAGACACGCCCT
TCCAAGACGATCTCATGCCTTCTTACAATGAGAAGGTTGACATCTGGAAGATTCCAGATG
TCTCCAGTTTCTCTTGGGGCACGTGGAAGGGAGTGATATGGTTAGATTCCATTTGTTG
ATATCCATAAGGCGTGCAAGAGCCAGATCCCGGCAGAAAGACCCACTGCTCAGAACGTGC

FIGURE 2AAAA

TAGACGCTTACCAGAGGGTTTTCCATTCACTCCGAGACACTGTGATGTGCGAGACGAAAG
AAATGCTGTAAAAATGAGCCATCGAGTGACGTGCTTGATGGCTGAATGGCATCCCAGCTG
TTCCGCTCTTGATGATGGAAGAGCTTTGCATGGATGGATGTTGACCCTGGCTGTTACGCC
ACGTAGGCCTCCTCTACGTCTGCCTGCATGTTTGAGTGTTCTGCTCTCCTGGCAGCCCCGG
ATGGAAGCTGCCAAGCGAGAAAGCCTGGCTTCAGGATGCTCCCTGGTGAAGATGCAGAGG
ATTCTGGATCTGCATAGTTTCAAGGGAGTGATCAAACGGTGACCTTGAAGACATGCTGCC
TGCCTTGGTAACTTTTTATAGACTAGTAGGAAACAGAAATCTTTTGGGGGAGGGGGGGAC
AACCCACTAGTTCCTCAGAGACAATTTCTTCTCATTCAAGAAAGCCCTGTTGGAAGCTGGG
GATGTTTTAACTCCGTGGCAGGGCACTTGCCTAGTTGTGTGCAAAGCCTTGATCTGACC
CATGGCATGTGCACACACAAATGCTCAAAGAAAATCCCAGACGCCAGAAGTGTGCCCC
TTTCTTGTCAATAAGGTCAATGTTCAGTACCGGAGATGATTTTTTTTTATGAAGCGTTTATG
CTGACTCGTGTCACTGAGCCAAGTGTGCATGGTCGTTAGCTACTTTGTGGGTTCTTCTTT
CTTTCTACCCTACTTCTTCCCTTCCACCCCTAACACTAGATAGGAGAGAGGAGAGAGA
AAGGAAAGTGGGCACTGTTATATTGTTGGACGACTTCTTGCTGATTAAGGGGTGTCGAGT
TCCTTGGAGCAATGATCTTTGCTGCCAAGATATCTCATTCTTCTTGTCTTCTTCTCGCC
CACGACCACTTCACAAACACCGACCAACAGCAAACAACCAACCCACCCCGCTTCTCGGGGG
CCCTAGCACTTATGTACTTCTGAAAAGTCCCCAGAAATCCAATCATCACACACTCAGAG
AACTGTCTGCTGCTGGCAAACTACACCCCTGCTAGAGCATGAGGCAAATCATAGTCAG
CTGCTGTGGACAGTCTGAAGCAGCCTGGCATCCACACCTGAGATTAAAACAAAAACATT
CTTACCTGTGTTTTGTTTTGTTTTAAGAAACCAAAGTGCACCAAGATAGCATGCTCTTG
AGATTGTGGCTGTCTAGAGATTTTTGGAACAGCAAGTTGAAGGAACTTTCTTACCTGCCT
TGAATGGTGCTTTGAACTTCTGCTGACCTGGAGTTTCTGTGTGAATATTTCTATCCAGT
GTCCCCCTGTACCGGAAAGTACAAAGTCTGCTCTGGGCTTGCATGCCTGAACACTTTAAA
ACACTGTGGAGCCAGGAATAATGGTACCCACCTGTAATCCCAGCACCTGGGAGACAGGAG
GAACCAGGAGTTCAGGGTTATCCTGGGCTATATACCGTGACCCTGTCTACCCCCACACCC
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SEQ ID NO: 104 SGK071_2_H

GAGGTGGTGGCTGTGCAGATGATGGTGGAAATGCATGGATGACCATTACGCCAGTCAGGCC
CTGGAGGAGCTGATGCCACTGCTGAAGCTGCGGCACGCCCACATCTCTGTGTACCAGGAG
CTGTTTCATCAGTGGAATGGGGAGATCTCTTCTCTGTACCTCTGCCTGGTGTGAGGTTT
AATGAGCTCAGCTTCCAGGAGGTCAATGAGGATAAGAGGAAGGCAAAGAAAATCATTGAC
TCTGAGTGGATGCAGAAATGTGCTGGGCCAGGTGCTGGACGCGCTGGAATACCTGCACCAT
TTGGACATCATCCACAGGAATCTCAAACCCCTCCAACATCATCCTCATCAGCAGTGACCAC
TGCAAACCTGCAGGACCTGAGTTCCAATGTGCTAATGACAGACAAAGCCAAATGGAATATT
CGTGCGGAGGAAGACCCCTTTTCGTAAGTCCCTGGATGGCCCCCTGAAGCCCTCACTTCTCC
TTCAGCCAGAAATCAGACATCTGGTCCCTGGGCTGCATCATTCTGGACATGACCAGCTGC
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AGCCTGAAGGCCGTCTGAAGACAATGGAGGAGAAGCAGATCCCGGATGTGGAAACCTTC
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GTGGTGCACATCACCTTCTTGAGAGGCTCCTTCAAGTCTCGTGCGTCTCTCTGACCCCTG
CACCGGCAGATGGTGCCTGCCATCACCGACATGCTGTTAGAAGGCAACGTGGCCAGC
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TTGGCATCCTATTGTTTAGTTCCAGAGGGTTCAATATTTATGCCCCCTGGCCTTGCTCCAC
ATGCACGACCAGTGGCTCAGCTGTGACCAGGACAGAGTCCCTGGGAAGAGAGACTTTGCC
TCCCTGGGGAACTAGGGAAGCTGTTGGGCCCCATCCCAAAGGGTCTGCCGTGGCCCCCG
GAGCTGGTGGAGGTGGTGGTCACGACCATGGAGCTACATGACAGGGTCTCGATGTCCAG
CTGTGTGCCTGCTCCCTGCTGCTGCACCTCCTGGGCCAAGCGCTGGTGCACCACCCGGAA
GCCAAGGCTCCCTGCAACCAAGCCATCACCTCCACCCTGCTGAGTGCTCTTACAGAGCCAC
CCCGAGGAGGAGCCACTTCTTGTCAATGGTCTACAGCCTGCTAGCCATCACCACAACCCAG

FIGURE 2BBBB

GAGTCAGAGTCACTGTCAGAGGAGCTGCAGAACGCTGGGCTGCTGGAGCACATCCTGGAG
CACCTCAACAGCTCCCTCGAAAGCAGGGACGTCTGCGCCAGCGGCCTGGGCCTGCTCTGG
GCCCTCCTGCTGGACGACCCCATCTTGGCACTCCAGCGCCCCAGGAAAAAGAGAGCTCCA
AACCACGGAAGCCCGGAAACCAAGAACCTGCCAGCACCCAAAGTATCATTGTGAAC
AAGGCCCCCTTGGAGAAGGTCCCGGACCTCATCAGCCAGGTGTTGGCCACCTACCCTGCG
GATGGGGAAATGGCAGAAGCCAGCTGCGGAGTCTTCTGGCTGCTGTCCCTGCTGGGCTGC
ATCAAGGAGCAGCAGTTTGAACAAGTGGTGGCGCTGCTCCTGCAAAGCATCCGGCTGTGC
CAGGACAGAGCCCTGCTGGTGAACAATGCCTACCGGGGACTGGCCAGCCTGGTGAAGGTG
TCAGAGCTGGCGGCCCTTCAAGGTGGTGGTGCAGGAGGAGGGCGGCAGTGGCCTCAGCCTC
ATCAAGGAGACCTACCAGCTCCACAGGGACGACCCGGAGGTGGTGGAGAACGTGGGCATG
CTGCTGGTCCACCTGGCTTCCTATGAGGAGATCCTGCCGGAGCTGGTGTCCAGTAGTATG
AAGGCCCTGCTCCAGGAGATCAAGGAGCGCTTCACCTCCAGCCTGGTGAAGTACAGCAGC
GCCTTCAGCAAACCAGGCCTCCCTCCAGGTGGAAGCCCCAGCTGGGGTGCACCACGTCT
GGGGGACTGGAATAG

SEQ ID NO: 105_AA118352_M SGK071_M

CAGAAGAAGACCCCTGCCAGAAGTCTGGATGGCTCCTGAAGCTCTCAAATTCTCCTTCT
CCACCAAATCCGACATCTGGTCTCTGGGCTGCATCATTCTAGACATGGCCACTTGCTCCT
TCCTGAACGACACAGAAGCCATGCAACTGCCGAAGGCCATCCGCCATCATCCAGGCAGCC
TGAAGCCCATCCTGAAAACCATGGAGGAGAAGCAAATCCCTGGTACAGATGTCTACTATT
TGCTTCTGCCCTTCATGTTGCATATCAACCCCTCCGATCGACTGGCAATCAAGGATGTGA
TGCAAGTCACCTTCATGAGCAACTCCTTCAAAGCTCCTCTGTTGCGCTGAATATGCAGC
GGCAGAAGGTCCCATCTTCATCACTGACGTGCTGCTTGAAGGCAACATGGCCAACATCT
TAGGCAGCTGGCTGTGTGCTTCTTTGTGAACGACAGCAGGCACTGTGACTCAGGGATTG
GCTCGCAGAGACTTGGGTTTGATTTTCAGTCAGTCTCTTGGACAGAGCACCCCTCTGAAAG
ATGTCATGCAGAATTTCTCCAGTCGACCAGAGGTCCAGCTCAGAGCCATTAACAAGTTGT
TGACAATGCCAGAGGACCAGCTAGGGCTGCCATGGCCACAGAGCTGCTGGAAGAGGTGA
TCAGCATCATAAAGCAGCATGGGCGGATCCTGGATATTCTGCTCAGCACCTGCTCCCTTC
TGCTGCGTGTCTTGGCCAAGCACTGGCAAAGGACCCAGAAGCTGAGATCCCAAGGAGCA
GTTTGATCATCTCCTTCTGATGGATACCTTGCGGAGCCATCCTAACTCTGAAAGGCTTG
TTAATGTGGTCTACAACGTGCTTGCCATTATTTCCAGCCAAGGACAGATCTCAGAAGAGC
TGGAAGAGGAGGGGTTGTTTCAGCTTGCCCAAGAGAACCCTGGAGCACTTCCAAGAGGACA
GGGACATCTGCCTCTCTATCCTGAGCCTGCTCTGGTCCCTCCTGGTAGATGTTGTCACTG
TGGACAAAGAGCCCTTGGAGCAGCTCTCTGGCATGGTCACTGGGTGCTGGCTACTCATC
CGGAGGACGTGGAAATAGCAGAGGCTGGCTGTGCGGTGCTCTGGCTGCTGTCTTGTGG
GCTGCATAAAGGAGAGTCAGTTTGAGCAGGTGGTAGTGCTGCTCCTGAGAAGCATCCAGC
TGTGCCCTGGCAGAGTACTGCTGGTGAACAATGCATTCCGTGGCTTGGCCAGCCTCGCAA
AGGTGTCCGAACCTGGTGGCCTTCCGAATAGTAGTACTGGAAGAGGGCAGCAGCGGCCTCC
ACCTCATCCAAGATATCTACAAGCTCTACAAGGATGACCCTGAGGTGGTGGAGAACCCTCT
GCATGCTGTTGGCCCATCTGACCTCCTACAAGGAGATCCTGCCAGAGATGGAGTCTGGAG
GCATCAAAGACCTAGTCCAGGTGATCCGGGGGCGCTTTACCTCCAGCCTGGAGCTGATTT
CTTACGCTGATGAGATACTCCAGGTACTGGAAGCAAATGCACAACCTGGCCTCCAGGAGG
ATCAGCTTGAGCCTCCTGCAGGGCAGGAAGCCCCACTGCAGGGAGAGCCCTCTTTCAGGC
CCTGACATGCTGCCCTTCTGGTCTGTGGTAAGAGAAAGTATCACTAGGTCCAGTATTAA
TTTCGTACCCCATGGTGAATAATAAAGAAGCCCTAGGCTGTTTCTGGC

SEQ ID NO: 106_018653.9_H

GGCCGGGGTTCGGGGCGCGGGGCATGCGCGCGGGCTGGGCAGGGGGCCGGCGGGGCGCAGA
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GCCGGCCGGGGGAGGGGAGCGATGCGGCGCGGGCGGGCGGCAGTGGCCGCGGGTTTCTG

FIGURE 2CCCC

CGCCTCCTTCCTGCTGGGCTCCGTCCTCAACGTGCTCTTCGCTCCGGGTCCGAGCCTCCG
AGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCGGGTGCGGGCCGTGCGGGGGCCGC
GGGGAGCTGGCCCGGCAGATCCGGGCGCGCTACGAGGAGGTGCAGCGCTATTCCCGCGGG
GGCCCCGGGCCCGGGGCGGGCCGGCCGGAGCGGCGGCGCCTGATGGACCTGGCTCCGGGC
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GGCTGGCCCCCGGCTCCCGGCCAGGCTCCCCCGGCCCGGGCCCCGCGCTGGGCTGCGCC
GCGCTTCGCAACGTGTCCGGCGCGCAGTACATGGGCTCAGGCTACACCAAGGCCGTGTAC
CGGGTCCGCCTGCCCGGCGGTGCCGCGGTGGCGCTCAAGGCGGTGGACTTTAGCGGCCAC
GATCTGGGCAGCTGCGTGCGGAGTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGTGCGGCACCCCAACGTGCTGCAG
CTCTATGGCTACTGCTACCAGGACAGCGAGGACATCCAGACACCCTGACCACCATCACG
GAGCTGGGCGCCCCCTGTAGAAATGATCCAGCTGCTGCAAACCTTCTGGGAGGATCGATT
CGAATCTGCCTGAGCCTGGGCGCGCTCCTCCACCACCTGGCCCCACTCCCCACTGGGCTCC
GTCACCTCTGCTGGACTTCCGCCCCCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATA
CTCGAGTTTCCGGCCAGGAACCTTACCCTGCCCTGCTCAGCCCAGGGCTGGTGCAGGGGC
ATGAACGAGAAGCGGAACCTCTATAATGCCTACAGTTTTTCTTACATACCTCCTGCCT
CACAGTGCCCCGCTTCACTGCGTCTCTGCTGGACAGCATCGTCAACGCCACAGGAGAG
CTCGCCTGGGGGGTGGACGAGACCCTGGCCCAGCTGGAGAAGGTGCTGCACCTGTACCGG
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCA
GACAGCACCATCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGC
CTCCTTTCACTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCCAGTGT
CGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCCGCAGCTGGTCTTTTCAAG
ACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCCTTGGC
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GAGGGAGTGACTTGCACTGGCAGCACTGCATGTACCTGGGAACCCCTGCAGACAAAGCT
AACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAT
GTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTAT
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TGGGGACAATCCATCGTGGAGTGTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGG
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GGGACACTCCAGGCCAGCCAGGGGTGAGGGGAGAGGTGCACACCTCAGCATGAGCCA
AGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGG
GGCCTTTCTGCCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCC
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T

SEQ ID NO: 107_AA396601_M

CCACGCGTCCGGGCTGCGCCGCGCTCCGCAACGTGTCTGGCGCGCAGTACGTGGGCTCAG
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GCTGCTATCGCCTGGCGGCCACAAAGCTGCTCAAAGAGATGGTGCTGCTGGAGCGGCTGC
GGCACCCCAACGTGCTGCAGCTCTATGGCTATTGCTACCAGGACAGTGAGGGCATCCCAG
ACACGCTGACCACCATCACAGAGCTGGGTGCCCCCTGTGGAGATGATCCAGCTGTTGCAGA
CTTCCTGGGAGGATCGATTCCGAATCTGCCTCAGCCTTGGCCGCCTCCTCCACCACCTGG
CCCACTCCCCGCTGGGCTCGGTACCCCTGCTTGACTTCCGCCCCCGGCAGTTTGTGCTAG
TGAACGGGGAGCTGAAAGTGACAGACCTGGATGATGCCCGCGTGGAAGAGACACCGTGCA

FIGURE 2DDDD

CCAGCAGTGCCGACTGCACGCTAGAGTTTCCAGCCAGGAACTTCAGCCTGCCCTGCTCGG
CCCAGGGCTGGTGCGAGGGCATGAATGAGAAACGGAACCTCTACAATGCCTACAGGTTCT
TCTTCACATACCTCCTGCCACACAGTGCCCCGCTTCCCTCCGACCTCTCCTGGATAGCA
TCGTCAATGCCACGGGAGAGCTCGCCTGGGGGGTGGATGAGACCCTGGCCCAGCTGGAGA
CAGCGCTACACTTGTTCCGAAGTGGGCAGTACCTGCAGAACTCTACAAGCAGCAGGGCTG
AGTACCAGCGCATCCCAGGACAGTGCCATCACACAGGAGGACTATCGCTGCTGGCCATCCT
ATCACCACGGCGGCTGCCTCCTGTCCGTGTTCAACCTGGCTGAGGCTATAGATGTCTGTG
AGAGCCATGCTCAGTGTCTGTCCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTGCGA
AGCTGGTCTTTTAAAGACTGGATGGAACCAAGTGGTCCCTGATGCCGCAAGACCACAT
ATGTGAAGGCCCTGGTTGACTGGTTGTGGGCTCAGCTGACCAGCTGGGCTTGCCTGCTG
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CTGATGTGACCAGGACAAAACGTGCAATATGCAAAAATGTTAAAATGTGAGTTTGCCAGC
TTCAGTCCCAGACTGGTTGGAACCCGATTGCCTCTCTGGAGCTGTAGGCTGTGAGCAGGG
CTCAGGCTGGTCTTAAGTGGGACAGTCCCGTGGGCAGCCATTACTGCATTTCATGCTTTG
AGAATGTAGCCAGAACACTGCTGCTGCATAAGCCACCGTGGGCAGGAGCTGCCTGGGGAC
AACCAGTCTCAGAGTGTCTCTCAGCTCAGCTCCGCTCCAAATGGAGAGCGCGGGATGCG
GAGATGTGAGTGAACCAGCACTGGGAAGAAGGCTCTCGGGCCTCTCCCTAGAGGTTGCTC
CTAGGCCAGCCCCGAGGCCGTGGGCAGCAGTGCTCGCATCCATATGAGCCAAGACTAGAG
TGGAGGAGCAGATTGCATTTGAGCCAGGACTGGGGTGGGGGTAGGGTCGGGGCCTCTCTG
CCTCATTTGCTTTAGTGAAGCCAGGGAGCAGCCGAGCCAGGCTCCTCCCCTCCTGG
AGGCCAGGCTCCTCCCCCTCCTGGAGGCCAGGCTCCTCCCCCTCCTGGAGTTTGCGTACC
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CAATTAATAAAATGATGTTTTGTGAC

SEQ ID NO: 108_VRK3_H

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CATGTGTCATCCTTCCAAGGCTCAAAGAGAGGGCTGAACTCCAGTTTTGAAACCTCTCCT
AAGAAAGTGAAATGGTCCAGCACCGTCACCTCTCCCCGATTATCCCTCTTCTCAGATGGT
GACAGTTCTGAGTCTGAAGATACTCTGAGTTCTCTGAGAGATCCAAGGCTCCGGGAGC
AGACCCCCAACCCCCAAAAGCAGCCCTCAGAAGACCAGGAAGAGCCCTCAGGTGACCAGG
GGTAGCCCTCAGAAGACCAGCTGTAGCCCTCAGAAGACCAGGCAGAGCCCTCAGACGCTG
AAGCGGAGCCGAGTGACCACCTCACTTGAAGCTTTGCCCACAGGGACAGTGCTGACAGAC
AAGAGTGGGCGACAGTGGAAGCTGAAGTCCTTCCAGACCAGGGACAACCAGGGCATTCTC
TATGAAGCTGCACCCACCTCCACCTCACCTGTGACTCAGGACCACAGAAGCAAAAGTTC
TCACTCAAACCTGGATGCCAAGGATGGGCGCTTGTTCAATGAGCAGAACTTCTTCCAGCGG
GCCGCCAAGCCTCTGCAAGTCAACAAGTGAAGAAGCTGTACTCGACCCCACTGCTGGCC
ATCCCTACCTGCATGGGTTTTCGGTGTTCACCAGGACAAATACAGGTTCTTGGTGTTACCC
AGCCTGGGGAGGAGCCTTCAGTCGGCCCTGGATGTCAGCCCAAAGCATGTGCTGTCAGAG
AGGTCTGTGCTGCAGGTGGCCTGCCGGCTGCTGGATGCCCTGGAGTTCCTCCATGAGAAT
GAGTATGTTTCATGGAAATGTGACAGCTGAAAATATCTTTGTGGATCCAGAGGACCAGAGT
CAGGTGACTTTGGCAGGCTATGGCTTCGCCTTCCGCTATTGCCCAAGTGGCAAACACGTG
GCCTACGTGGAAGGCAGCAGGAGCCCTCACGAGGGGGACCTTGAGTTCATTAGCATGGAC
CTGCACAAGGGATGCGGGCCCTCCCGCCGAGCGACCTCCAGAGCCTGGGCTACTGCATG
CTGAAGTGGCTCTACGGGTTTCTGCCATGGACAAATTGCCCTCCCAACACTGAGGACATC
ATGAAGCAAAAACAGAAGTTTGTGATAAGCCGGGGCCCTTCGTGGGACCCTGCGGTAC
TGGATCAGGCCCTCAGAGACCCTGCAGAAGTACCTGAAGGTGGTGATGGCCCTCACGTAT
GAGGAGAAGCCGCCCTACGCCATGCTGAGGAACAACCTAGAAGCTTTGCTGCAGGATCTG
CGTGTGTCTCCATATGACCCCATTTGGCCTCCCGATGGTGCCCTAG

FIGURE 2EEEE

SEQ ID NO: 109_S71575_M VRK3_M

CCATCCCCACCTGTATCGGCTTTGGCATTACACAGGACAAGTACAGGTTCCCTAGTATTCC
CCAGCCTGGGGAGGAGCCTTCAGTCAGCCCTGGATGACAACCCAAAGCATGTGGTATCAG
AGAGATGTGTGCTTCAGGTGGCCTGCAGGCTGCTGGATGCTCTGGAGTATCTCCATGAAA
ATGAGTATGTTACGGGAACCTGACAGCTGAGAATGTCTTTGTGAATCCAGAGGATCTGA
GCCAGGTGACCCTGGTGGGCTATGGCTTACCTACCGATACTGCCAGGTGGCAAACACG
TGGCCTACAAAGAAGGCAGCAGGAGTCCACACGATGGGGACTTGGAGTTCATTAGCATGG
ACCTGCACAAGGGATGCGGACCCTCCCGCCGACGCGATCTCCAGACCTTGGGCTACTGTA
TGCTCAAGTGGCTTTATGGGTCCCTGCCATGGACAAATTGCCTTCCCAACACCGAAAAGA
TAAGTAGGCAGAAGCAGAAGTATCTGGACAGCCCCGAGCGCCTCGTGGGACTGTGTGGCC
GCTGGAACAAGGCCTCAGAGACCCTGCGGGAGTACCTGAAGGTGGTGTATGGCCCTCAATT
ATGAGGAGAAGCCACCCTATGCCACGCTGAGGAACAGCCTAGAAGCTCTGCTGCAGGATA
TGCGGGTGTACCCCTATGACCCTCTGGACCTCCAGATGGTGCCTTAGATGGAATCCAGAG
CTTCCGACTTGCAGCTTGAAGTAGAACATGAAGTAGTGTGACTGGAGGCCTGTTTGAAC
CATAGCTCCTAAAAGAATCCCTTGAATGTGCATTCTCACCGCTCCCTTAGGACATATGAA
TCAGCACTTGTGTTGGGGAACCTGAGTCATGTATGTAATGTGAACTCCTCCCTGTCTC
AGCTCTGGCAGCTGTGGATGGAGGTAAGTGGATGCTGGCGGCGGCGGCGGAGCAGCCAC
TCCACTCCCTATGGCATTTCTGTGATGGCATAATAAACTGTTTTTAATC

SEQ ID NO: 110_AA45427_H

ATGGGCCACGCGCTGTGTGTCTGCTCTCGGGGAAGTGTATCATTGACAATAAGCGCTAC
CTCTTCATCCAGAACTGGGGGAGGGTGGGTTTCACTATGTGGACCTAGTGGAAAGGGTTA
CATGATGGACACTTCTACGCCCTGAAGCGAATCCTGTGTCACGAGCAGCAGGACCGGGAG
GAGGCCCAGCGAGAAGCCGACATGCATCGCCTCTTCAATCACCCCAACATCCTTCGCCTC
GTGGCTTACTGTCTGAGGGAACGGGGTGCTAAGCATGAGGCCTGGCTGCTGCTACCATTC
TTCAAGAGAGGTACGCTGTGGAATGAGATAGAAAGGCTGAAGGACAAAGGCAACTTCCTG
ACCGAGGATCAAATCCTTTGGCTGCTGCTGGGGATCTGCAGAGGCCTTGAGGCCATTCTAT
GCCAAGGGTTATGCCCACAGAGACTTGAAGCCCACCAATATATTGCTTGGAGATGAGGGG
CAGCCAGTTTTTAATGGACTTGGGTTCCATGAATCAAGCATGCATCCATGTGGAGGGCTCC
CGCCAGGCTCTGACCCTGCAGGACTGGGCAGCCGAGCGGTGCACCATCTCCTACCGAGCC
CCAGAGCTCTTCTGTGTCAGAGTCACTGTGTCATCGATGAGCGGACTGATGTCTGGTCC
CTAGGCTGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTGTTCCTAA
AAGGGTGACAGTGTGGCCCTTGCTGTGTCAGAACCAACTCAGCATCCCAAGAGCCCGAGG
CATTCTTCAGCATTGCGGCAGCTCCTGAACTCGATGATGACCGTGGACCCGCATCAGCGT
CCTCACATTCCTCTCCTCCTCAGTCAGCTGGAGGCGCTGCAGCCCCCAGCTCCTGGCCAA
CATACTACCCAAATCTGA

SEQ ID NO: 111_H05721_H

CCCTGAGGCACCGCCCCAAGTTTGGTGTGACCGGCGGGGGACGCCGGTGGTGGCGGCAGC
GACGGCTGCGGGGGACCGGGCCGCGGCGCCACCATGGCGGTGCGACAGGCGCTGGGCCG
CGGCCTGCAGCTGGGTGAGCGCTGCTGCTGCGCTTACGGGCAAGCCCGGCCGGGCCTA
CGGCTTGGGGCGGCGGGCCCGGCGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGC
CGCAGGACCGGGCGCGGAGCCTCGCAGGGTGGGGCTCGGGCTCCCTAACCGTCTCCGCTT
CTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTTGCAGCGGCAGTTCGTGGTGGCGGC
CTGGGGCTGCGCGGGCCCTTGCGGCGGGCAGTCTTCTGGCCTTCGGGCTAGGGCTGGG
CCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTCAGGAGATCCA
GGCAATTTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGGACACGAGACGCTTGCA
GGGCTTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGTCTGC
TGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCCTGGAGGTGACAAAGAGCACCGG
GTTGCTTCCAGGGAGAGGCCAGGTACCAAGTGCACAGGAGAAGGGCAGGAGCGAGCTCC

FIGURE 2FFFF

GGGGGCCCCCTGCCTTCCCCTTGGCCATCAAGATGATGTGGAACATCTCGGCAGGTTCCCTC
CAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCTT
GGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAGGTCCCAAGCAACTAGC
CCCTCACCCCAACATCATCCGGGTTCTCCGCGCCTTCACCTCTTCCGTGCCGCTGCTGCC
AGGGGCCCCCTGGTCGACTACCCTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGG
CCATGGCCGGACGCTGTTCTCGTTATGAAGAACTATCCCTGTACCCTGCGCCAGTACCT
TTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGCTGCAGCTGCTGGAAGG
CGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGAAATCCGACAACATCCT
TGTGGAGCTGGACCCAGACGGCTGCCCTGGCTGGTGATCGCAGATTTTGGCTGCTGCCCT
GGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGTACGTGGATCGGGGCGG
AAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCCTGGCCCCAGGGCAGTGAT
TGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCGGGCT
TGTCAATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCCGAGCTACCAAGAGGC
TCAGCTACCTGCACTGCCCGAGTCAGTGCCTCCAGACGTGAGACAGTTGGTGAGGGCACT
GCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCGCAAATGTGCTTCATCT
AAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGG
CTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGCTCACAGAGAAGTGTTG
TGTGGAACAACAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGTGTAACCGCTCTGCCA
GGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGT
GAATTACTAAAAGAACATGGCATCCTCTGTGTCGTGATGGTCTGTGAATGGTGAGGGTGG
GAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGAAAAGGCCTCGGGCTTGG
CAAATGGAAGAACTTGAGTGAGAGTTAGTCTGCAGTCTCTGCTCACAGACATCTGAAA
AGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATC
CACAGAGAGGATCCAGGCCAAGGCACTGGCTGTGAGTGGCAGAGTTTGGCTGTGACCTTT
GCCCCTAACACGAGGAACCTCGTTTGAAGGGGGCAGCGTAGCATGTCTGATTTGCCACCTG
GATGAAGGCAGACATCAACATGGGTGAGCACGTTTCAAGTACGGGAGTGGGAAATTACATG
AGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATC
TCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTGGGGATTTAAACTTGAG
GGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATATTAAATGCAAATTTACA
ACTGCAGATGACGTATGTGCCCTGAACTGAATATTTGGCTTTAAGAATGATTCTTCTTAT
ACTCTGAAGGTGAGAATATTTTGTGGGCAGGTATCAACATTGGGGAAGAGATTTATGTC
TAACTAATACTTTTATACATGATTTTTAGGAAGCTATTGCCTAAATCAGCGTCAACATG
CAGTAAAGGTTGTCTTCAACTGACAAA

SEQ ID NO: 112_AI086865_H

AATGAGATGGAGAAGTACGAGCGGATCCGAGTGGTGGGGAGAGGTGCCTTCGGGATTGTG
CACCTGTGCCTGCGAAAGGCTGACCAGAAGCTGGTGATCATCAAGCAGATTCCAGTGGA
CAGATGACCAAGGAAGAGCGGCAGGCAGCCAGAATGAGTGCCAGGTCTCAAGCTGCTC
AACCACCCCAATGTCATTGAGTACTACGAGAACTTCCTGGAAGACAAAGCCCTTATGATC
GCCATGGAATATGCACCAGGCGGCACTCTGGCTGAGTTCATCCAAAAGCGCTGTAATTCC
CTGCTGGAGGAGGAGACCATCCTGCACTTCTTCGTGCAGATCCTGCTTGCATGCATCAT
GTGCACACCCACCTCATCCTGCACCGAGACCTCAAGACCCAGAACATCCTGCTTGACAAA
CACCGCATGGTTCGTCAAGATCGGTGATTTCCGCATCTCCAAGATCCTTAGCAGCAAGAGC
ACCCCATGCTATATCTCCCCTGAGCTGTGTGAGGGCAAGCCCTACAACCAGAAGAGTGAC
ATCTGGGCCCTGGGCTGTGTCTCTACGAGCTGGCCAGCCTCAAGAGGGCTTTTCAGGGCT
GCGAACTTGCCAGCACTGGTGCTGAAGATCATGAGTGGCACCTTTGCACCTATCTCTGAC
CGGTACAGCCCTGAGCTTCGCCAGCTGGTCTGAGTCTACTCAGCCTGGAGCCTGCCAG
CGGCCACCACTCAGCCACATCATGGCACAGCCCTCTGCATCCGTGCCCTCCTCAACCTC
CACACCGACGGCAGAGAAGTCCGTGGCCCCCAGCAACACAGGGAGCAGGACCACCAAGTGT
CCGTGCAGAGAGGCATCATCATGACATTCGGCAGCGGCAGCAATGGGTGCCTAGGCCAT

FIGURE 2GGGG

GGCAGCCTCACTGACATCAGCCAGCCCAcCATTTGTGGAGGCTTTGTTGGGCTATGAAATG
GTGCAGCAAGTGGAGGAGGCCCTGAGCTTCACACTACTAGGCTCTGCACCCCTGGACCAG
GAGCCTCTGCTGAGTATAGACCTGGGCACTGCTCACTCAGCTGCTGTGACTGGTGAGGAG
GACTTGGGCTCTGGAGATGTAAACAGGTTACCCAGCTGGGAGAGAGGACATCTGCTGGCT
GGTGTGGCGTCCAGCACTGATGTGTCTACCTTCTCTGAAGGTGACTGCAAGGAGCCTGAC
AAGTGTCTGTGGAGACACAAGCAGTGCCTGGGCACATCATCTACCCTTTTCGCTCTGAC
TGTGTCCGCCACAGCCTGCACCTACACTCTGTCAACCCTGCAACTGTAATTCTAGGCTG
AAGGACTCTTCAGAGGATAGCAGCAGCTCCCGGGGCGCGGGCCCAACCTGCTCCCATGTC
ATCGAGTCCCTTTGCTTTGAGCTCACACCGGAGGAGGAGCATGTGGAGCGATTCCGGTAT
GGCTGGTGCAAAAGCTACAGACCTGTCTCTGTGGCAGTGATCCACCATCCACTCTACCAT
GAGTGTGGGGCAGATGATCTAAATGXAAAGAAGAGGAAGAGGAGGAGGAGGAAAAGCAAG
CCCCCATCCCGACACAGGTGGGGCCCGCCACCGCCTCCCCTGACCTAGGCACCAGCATG
GCCACTGGTACCCCTGACTCCACAGCGCCCATCACCATCTGGCGCTCTGAGAGCCCCACA
GGGAAGGGTCAGGGCAGCAAGGTGATCAAGAAGGTAAAGAAGAAAAAGGAAAAAGAGAAA
GACAAGGAGGAGATGGATGAGAAGGCAAAGCTGAAGAAAAAAGCCAAGAAAGGCCAGTTG
ACTAAGAAGAAAAAGCCCGTTAAATTGGAGCCTTCCCGCCAGACGTGAGCCGATCATTA
AGCGCAAGACAGCTGGCCAGGATGTCCGAGTCCAGCCAGAAAGCCGGGAAGAGCTGGAG
AGCGAGGACAGTTACAATGGCCGGGGGCGAGGAGAACTGTCCAGCGAGGATATTGTGGAA
TCATCATCGCCAGGAAGAGAGAGAAACACAGTCCAGGCCAAAAAGACAGGGGCCAAAGCCC
TCACAAGCCAGGAAGGTAAACAAGAGAAAAATCTCCCCAGGATCAAACCCCAACCTCAGT
TGAGGCCAGGGTGGTCAGGGTGCAGAATAAATGCCATCGAGCCTGTGGCTGGCCCTCTGC
TGCTGTTCTCTCCCTCCAACCTGGCTGTTTCTTGCGGGGCAAGGGGTGGGCTCAGGGCTG
CAGGGGTTTCTCAAAGGCAATCCAGCTTTCACAAAGGAAGCCCATGGGAAGGCAGGTGGG
AGGGAAAGGAAGGGGCACAGCCCTATTTCTTCCTACCTGCTAGGACAAGGTGGAAGAGTG
TATCTGGGGTGGGAAGGAGGGCTTCCCTCTCTGCTGCGAGAGACTGGTCTGTGTGAAAT
CCACTTCTGGGACAGGCAGTACTGTCTGCAGCGATACCCCCAATAAACGGAACTTTTTTAA
CCC

SEQ ID NO: 113_AA836348_H

ATGTCCGGTGTGGGCGAGTACGAGCGACACTGCGATTCCATCAACTCGGACTTTGGGAGC
GAGTCCGGGGGTTGCGGGGACTCGAGTCCGGGGCCTAGCGCCAGTCAGGGGCCGCGAGCC
GGCGGCGGCGCGGCGGAGCAGGAGGAAGTGCCTACATCCCCATCCGCGTCTCTGGGCCGC
GGCGCCTTCGGGGAAGCCACGCTGTACCGCCGCACCGAGGATGACTCACTGGTTGTGTGG
AAGGAAGTCTGATTTGACCCGGCTGTCTGAGAAGGAACGTCGTGATGCCTTGAATGAGATA
GTTATTCTGGCACTGCTGCAGCACGACAACATTATTGCCTACTACAATCACTTCATGGAC
AATACCACGCTGCTGATTGAGCTGGAATATTGTAATGGAGGGAACCTGTATGACAAAATC
CTTCGTGAGAAGGACAAGTTGTTGAGGAAGAGATGGTGGTGTGGTACCTATTTAGATT
GTTTCAGCAGTGAGCTGCATCCATAAAGCTGGAATCCTTCATAGAGATATAAAGACATTA
AATATTTTTCTGACCAAGGCAAACCTGATAAACTTGGAGATTATGGCCTAGCAAAGAAA
CTTAATTCTGAGTATTCCATGGCTGAGACGCTTGTGGGAACCCCATATTACATGTCTCCA
GAGCTCTGTCAAGGAGTAAAGTACAATTTCAAGTCTGATATCTGGGCAGTTGGCTGCGTC
ATTTTTGAACTGCTTACCTTAAAGAGGACGTTTGATGCTACAAACCCACTTAACCTGTGT
GTGAAGATCGTGCAAGGAATTGCGGCCATGGAAGTTGACTCTAGCCAGTACTCTTTGGAA
TTGATCCAAATGGTTCATTCTGTCCTTGACCAGGATCCTGAGCAGAGACCTACTGCAGAT
GAACTTCTAGATCGCCCTCTTCTCAGGAAACGCAGGAGGTCAAGCACTGTGACTGAAGCA
CCCATGCTGTAGTAACATCACGAACAGTGAAGTCTATGTTTGGGGTGGTGGAAAATCC
ACCCCCAGAACTGGATGTTATCAAGAGTGGCTGTAGTGCCCGGCAGGTCTGTGCAGGG
AATACCCACTTTGCTGTGGTCACAGTGGAGAAGGAAGTGTACACTTGGGTGAACATGCAA
GGAGGCACTAACTCCATGGTCAGCTGGGCCATGGAGACAAAGCCTCCTATCGACAGCCA
AAGCATGTGGAAGGTTGCAAGGCAAAGCTATCCGTCAGGTGTCATGTGGTGATGATTTT

FIGURE 2HHHH

ACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTCGGATCAGATTATTATGGCTGC
ATGGGGGTGGACAAAGTTGCTGGCCCTGAAGTGCTAGAACCCATGCAGCTGAACCTCTTC
CTCAGCAATCCAGTGGAGCAGGTCTCCTGTGGAGATAATCATGTGGTGGTTCTGACACGA
AACAAGGAAGTCTATTCTTGGGGCTGTGGCGAATATGGACGACTGGGTTTGGATTTCAGAA
GAGGATTATTATACACCACAAAAGGTGGATGTTCCCAAGGCCTTGATTATTGTTGCAGTT
CAATGTGGCTGTGATGGGACATTTCTGTTGACCCAGTCAGGCAAAGTGCTGGCCTGTGGA
CTCAATGAATTCAATAAGCTGGGTCTGAATCAGTGCATGTCGGGAATTATCAACCATGAA
GCATACCATGAAGTTCCCTACACAACGTCCTTTACCTTGGCCAAACAGTTGTCCTTTTAT
AAGATCCGTACCATTGCCCCAGGCAAGACTCACACAGCTGCTATTGATGAGCGAGGCCGG
CTGCTGACCTTTGGCTGCAACAAGTGTGGGCAGCTGGGCGTTGGGAACAAGAAGCGT
CTGGGAATCAACCTGTTGGGGGGACCCCTTGGTGGGAAGCAAGTGATCAGGGTCTCCTGC
GGTGATGAGTTTACCATTGCTGCCACTGATGAGAAAGTATTGAATTCTAAGACCATCCGT
TCCAATAGCAGTGGCTTATCCATTGGAAGTGTGTTTCAGAGCTCTAGCCCGGGAGGAGGC
GGCGGGGGCGGCGGTGGTGAAGAAGAGGACAGTCAGCAGGAATCTGAAACTCCTGACCCA
AGTGGAGGCTTCCGAGGAACAATGGAAGCAGACCGAGGAATGGAAGGTTTAATCAGTCCC
ACAGAGGCCATGGGGAACAGTAATGGGGCCAGCAGCTCCTGTCCTGGCTGGCTTCGAAAG
GAGCTGGAAAATGCAGAAATTTATCCCCATGCCTGACAGCCCATCTCCTCTCAGTGCAGCG
TTTTCAGAATCTGAGAAAGATAACCTGCCCTATGAAGAGCTGCAAGGACTCAAAGTGGCC
TCTGAAGCTCCTTTGGAACACAAACCCCAAGTAGAAGCCTCGGTAAGTGAAGCTTTTTGCC
TTTGAATCACAAGTAGTCACCTCGGCTGAATCCTGCAGTAACCTGTGCTGGGAAGGGAAC
ACCACTGACTCCTCCTGCGTGTGCGTGCAGCTCTCTGCAGGTGGAGGTTGA

SEQ ID NO: 114_R86668_H, MKK6_H

ATGAACCTTGCTGCTCTCCTACCGCGATGTGCAGGACTACTCGGCCATCATTGAGCTGGTG
GAGACGCTGCAGGCCCTTGCCACCTGTGATGTGGCCGAGCAGCATAATGTCTGCTTCCAC
TACACTTTTGCCCTCAACCGGAGGAACAGGCCTGGGGACCGGGCGAAGGCCCTGTCTGTG
CTGCTGCCGCTGGTACAGCTTGAGGGCTCTGTGGCGCCCGATCTGTACTGCATGTGTGGC
CGTATCTACAAGGACATGTTCTTCAGCTCGGGTTTCCAGGATGCTGGGCACCGGGAGCAG
GCCTATCACTGGTATCGCAAGGCTTTTGACGTAGAGCCCAGCCTTCACTCAGGCATCAAT
GCAGCTGTGCTCCTCATTGCTGCCGGGCAGCACTTTGAGGATTCCAAAGAGCTCCGGCTA
ATAGGCATGAAGCTGGGCTGCCTGCTGGCCCGCAAAGGCTGCGTGGAGAAGATGCAGTAT
TACTGGGATGTGGGTTTCTACCTGGGAGCCAGATCCTCGCCAATGACCCACCCAGGTG
GTGCTGGCTGCAGAGCAGCTGTATAAGCTCAATGCCCCATATGGTACCTGGTGTCCTGTG
ATGGAGACCTTCTGCTCTACCAGCACTTCAGGCCCACGCCAGAGCCCCCTGGAGGGCCA
CCACGCCGTGCCACTTCTGGCTCCACTTCTTGCTACAGTCTGCCAACCATTCAGACA
GCCTGTGCCAGGGCGACCAGTGCTTGGTGCTGGTCTGAGATGAACAAGGTGCTGCTG
CCTGCAAAGCTCGAGGTTCCGGGTAAGTACCCAGTAAGCACAGTGACCCTGAGCCTGCTG
GAGCCTGAGACCCAGGACATTCCCTCCAGCTGGACCTTCCAGTCGCCTCCATATGCGGA
GTCAGCGCCTCAAAGCGCGACGAGCGCTGCTGCTTCTCTATGCACTCCCCCGGCTCAG
GACGTCCAGCTGTGCTTCCCCAGCGTAGGGCACTGCCAGTGGTTCTGCGGCCTGATCCAG
GCCTGGGTGACGAACCCGATTCCACGGCGCCCGCGGAGGAGGCGAGGGCGCGGGGGAG
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AGACGCCTGCGCCACAAGAACATAGTGCGCTATCTGGGCTCAGCTAGCCAGGGCGGCTAC
CTTAAGATCTTCATGGAGGAAGTGCTGGAGGCAGCCTGTCTCCTTGTGCTGCGGTGCGTG
TGGGGACCCCTGAAGGACAACGAGAGCACCATCAGTTTCTACACCCGCCAGATCCTGCAG
GGACTTGGCTACTTGCACGACAACCACATCGTGCACAGGGACATAAAAGGGGACAATGTG
CTGATCAACACCTTCAGTGGGCTGCTCAAGATTTCTGACTTCGGCACCTCCAAGCGGCTG
GCAGGCATCACACCTTGCACTGAGACCTTCACAGGAACCTCTGCAGTATATGGCCCCAGAA

FIGURE 2III

ATCATTGACCAGGGCCACGCGGGTATGGGAAAGCAGCTGACATCTGGTCACTGGGCTGC
ACTGTCAATTGAGATGGCCACAGGTCGCCCCCCTTCCACGAGCTCGGGAGCCACAGGCT
GCCATGTTTCAGGTGGGTATGTACAAGGTCCATCCGCCAATGCCAGCTCTCTGTCGGCC
GAGGCCCAAGCCTTTCTCCTCCGAACCTTTGAGCCAGACCCCGCCTCCGAGCCAGCGCC
CAGACACTGCTGGGGGACCCCTTCTGTCAGCCTGGGAAAAGGAGCCGCAGCCCCAGCTCC
CCACGACATGCTCCACGGCCCTCAGATGCCCCCTTCTGCCAGTCCCACTCCTTCAGCCAAC
TCAACCACCCAGTCTCAGACATTCCCGTGCCCTCAGGCACCCCTCTCAGCACCCACCCAGC
CCCCGAAGCGCTGCCTCAGTTATGGGGGCACCAGCCAGCTCCGGGTGCCCGAGGAGCCT
GCGGCCGAGGAGCCTGCGTCTCCGGAGGAGAGTTGCGGGCTGAGCCTGCTGCACCAGGAG
AGCAAGCGTCGGGCCATGCTGGCCGCAGTATTGGAGCAGGAGCTGCCAGCGCTGGCGGAG
AATCTGCACCAGGAGCAGAAGCAAGAGCAGGGGGCCCGTCTGGGCAGAAACCATGTGGAA
GAGCTGCTGCGCTGCCTCGGGGCACACATCCACACTCCCAACCGCCGGCAGCTCGCCAG
GAGCTGCGGGCGCTGCAAGGACGGCTGAGGGCCAGGGCCTTGGGCCTGCGCTTCTGCAC
AGACCGCTGTTTGCCCTTCCCGGATGCGGTGAAGCAGATCCTCCGCAAGCGCCAGATCCGT
CCACACTGGATGTTTCTGTTCTGGACTCACTGCTCAGCCGTGCTGTGCGGGCAGCCCTGGGT
GTGCTAGGACCGGAGGTGGAGAAGGAGGCGGTCTCACCAGGTCAGAGGAGCTGAGTAAT
GAAGGGGACTCCCAGCAGAGCCCAGGCCAGCAGAGCCCGCTTCCGGTGGAGCCCGAGCAG
GGCCCCGCTCCTCTGATGGTGCAGCTGAGCCTCTTGAGGGCAGAGACTGATCGGCTGCGC
GAAATCCTGGCGGGGAAGGAACGGGAGTACCAGGCCCTGGTGCAGCGGGCTCTACAGCGG
CTGAATGAGGAAGCCCGGACCTATGTCTGGCCCCAGAGCCTCCAACCTGCTCTTTCAACG
GACCAGGGCCTGGTGCAGTGGCTACAGGAAGTGAATGTGGATTGAGGCACCATCCAAATG
CTGTTGAACCATAGCTTACCCCTCCACACTCTGCTCACCTATGCCACTCGAGATGACCTC
ATCTACACCCGCATCAGGGGAGGGATGGTATGCCGCATCTGGAGGGCCATCTTGGCACAG
CGAGCAGGATCCACACCAGTCACCTCTGGACCCTGA

SEQ ID NO: 115_PAK6_H

ATGTTTGGGAAGAAAAGAAAAGATTGAAATATCTGGCCCGTCCAACCTTTGAACACAGG
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AGCCTGTAGCAGATACGGCCAACAGGCCAAAGCCTATGGTGGACCCCTCATGCATCACA
CCCATCCAGCTGGCTCCTATGAAGACAATCGTTAGAGGAAACAAACCCTGCAAGGAAACC
TCCATCAACGGCCTGCTAGAGGATTTTGACAACATCTCGGTGACTCGCTCCAACCTCCCTA
AGGAAAGAAAGCCACCCACCCAGATCAGGGAGCCTCCAGCCACGGTCCAGGCCACGCG
GAAGAAAATGGCTTCATCACCTTCTCCAGTATTCCAGCGAATCCGATACTACTGCTGAC
TACACGACCGAAAAGTACAGGGAGAAGAGTCTCTATGGAGATGATCTGGATCCGTATTAT
AGAGGCAGCCACGCAGCCAAGCAAAATGGGCACGTAATGAAAATGAAGCACGGGGAGGCC
TACTATTCTGAGGTGAAGCCTTTGAAATCCGATTTTGCCAGATTTTCTGCCGATTATCAC
TCACATTTGGACTCACTGAGCAAACCAAGTGAATACAGTGACCTCAAGTGGGAGTATCAG
AGAGCCTCGAGTAGCTCCCCCTCTGGATTATTTCATTCCAATTACACCTTCTAGAAGTGA
GGGACCAGCGGGTGCTCCAAGGAGAGCCTGGCGTACAGTGAAAGTGAATGGGGACCCAGC
CTGGATGACTATGACAGGAGGCCAAAGTCTTCGTACCTGAATCAGACAAGCCCTCAGCCC
ACCATGCGGCAGAGGTCCAGGTGAGGCTCGGGACTCCAGGAACCGATGATGCCATTTGGA
GCAAGTGCATTTAAACCCATCCCCAAGGACACTCCTACAACCTCCTACACCTACCCTCGC
TTGTCCGAGCCCACAATGTGCATTCCAAGGTGGATTACGATCGAGCACAGATGGTCCCTC
AGCCCTCCACTGTGAGGTCTGACACCTACCCAGGGGCCCTGCCAAACTACCTCAAAGT
CAAAGCAAATCGGGCTATTCTCAAGCAGTACCAGTACCCGTCTGGGTACCACAAAGCC
ACCTTGTAACCATACCCCTCCCTGCAGAGCAGTTTCGAGTACATCTCCACGGCTTCCTAC
CTGAGCTCCCTCAGCCTCTCATCCAGCACCTACCCGCCGCCAGCTGGGGCTCCTCCTCC
GACCAGCAGCCCTCCAGGGTGTCCCATGAACAGTTTCGGGCGGCCCTGCAGCTGGTGGTC
AGCCCAGGAGACCCAGGGAATACTTGGCCAACCTTTATCAAAATCGGGGAAGGCTCAACC
GGCATCGTATGCATCGCCACCGAGAAACACAGGGAAACAAGTTGCAGTGAAGAAAATG

FIGURE 2JJJJ

GACCTCCGGAAGCAACAGAGACGAGAACTGCTTTTCAATGAGGTCGTGATCATGCGGGAT
TACCACCATGACAATGTGGTTGACATGTACAGCAGCTACCTTGTCGGCGATGAGCTCTGG
GTGGTCATGGAGTTTCTAGAAGGTGGTGCCTTGACAGACATTGTGACTCACACCAGAATG
AATGAAGAACAGATAGCTACTGTCTGCCTGTCAGTTCTGAGAGCTCTCTCCTACCTTCAT
AACCAAGGAGTGATTCACAGGGACATAAAAAGTGAATCCATCCTCCTGACAAGCGATGGC
CGGATAAAGTTGTCTGATTTTGGTTTCTGTGCTCAAGTTTCCAAAGAGGTGCCGAAGAGG
AAATCATTGGTTGGCACTCCCTACTGGATGGCCCCCTGAGGTGATTTCTAGGCTACCTTAT
GGGACAGAGGTGGACATCTGGTCCCTCGGGATCATGGTGATAGAAATGATTGATGGCGAG
CCCCCTACTTCAATGAGCCTCCCTCCAGGCGATGCGGAGGATCCGGGACAGTTTACCT
CCAAGAGTGAAGGACCTACACAAGGTTTCTTCAGTGCTCCGGGGATTCTAGACTTGATG
TTGGTGAGGGAGCCCTCTCAGAGAGCAACAGCCCAGGAACTCCTCGGACATCCATTCTTA
AAACTAGCAGGTCCACCGTCTTGCATCGTCCCCCTCATGAGACAATACAGGCATCACTGA

SEQ ID NO: 116_SURTK106_H

ATGAATGATAGGAATGAGATTCAAATGGAAGCCAAACTCCAAAGTCTTACCATTATAGCA
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AAACTAGGAAGGCAAGGAATGGCAAGGTGAGGAATTACTCACAGCTGTGCTGTGTGCATT
CTCTGTGGGCCTAGCAGGGAAGGGACAGCCCTGTGGCAATGGGCATGACACGGATGCTC
CTGGAATGCAGTCTCAGTGACAAGTTGTGTGTCATCCAGGAGAAGCAGTATGAAGTGATT
ATCGTCCCAACTTTGTTGGTTACTATCTTCTCATCCTTCTTGGGGTCATCCTGTGGCTT
TTTATCAGAGAACAAGAACTCAACAGCAGCGTTCTGGACCTCAAGGCATTGCCCTGTT
CCTCCACCTAGGGACCTAAGCTGGGAAGCAGGACATGGAGGAAATGTGGCTTTGCCACTT
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FIGURE 2KKKK

GAACATTCAACATGTATTGTTTCATTAAGCTAGCTTCCTAGTTCCGATTAGACTAAGGAGA
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SEQ ID NO: 117_AA098024_M

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SEQ ID NO: 118_SGK2ALPHA_H

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FIGURE 2LLLL

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SEQ ID NO: 120_CCRK_H

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SEQ ID NO: 121_TESK2_H

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FIGURE 2MMMM

CCCACCGCCTCCGCAGGCTAAGGAGCCGCTGCCACCAACGAGCTGTGAGGGTTACTATGC
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